

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: May 11, 2005, 21:05:14 ; Search time 117.489 Seconds  
(without alignments)  
72.421 Million cell updates/sec

Title: US-10-712-812-5

Perfect score: 112  
Sequence: 1 MADNGTIVEELKQLLEQWNLV 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneeqp19808:\*  
2: geneeqp19908:\*  
3: geneeqp20005:\*  
4: geneeqp20018:\*  
5: geneeqp20028:\*  
6: geneeqp20038:\*  
7: geneeqp20038:\*  
8: geneeqp20048:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	221	8	ADI95325
2	52	46.4	16368	6	ABM67171
3	51	45.5	54	4	AAU19303
4	51	45.5	54	4	ABM38585
5	51	45.5	54	4	AAU32049
6	51	45.5	54	4	ABM32710
7	51	45.5	54	4	AAU1757
8	51	45.5	54	4	AAU59222
9	51	45.5	54	4	ABG53442
10	51	45.5	54	4	ABG41571
11	51	45.5	206	6	ABU03494
12	51	45.5	206	6	ABU62881
13	51	45.5	206	6	ADG10624
14	51	45.5	206	7	ADJ70216
15	51	45.5	206	8	ADQ20631
16	51	45.5	206	8	ADQ34469
17	51	45.5	209	7	ADU14139
18	51	45.5	209	8	ADP24705
19	51	45.5	209	8	ADG34490
20	51	45.5	246	4	AAU31548
21	51	45.5	351	6	ABU23569
22	51	45.5	572	2	AAU68488
23	50	44.6	469	7	ABU48797
24	50	44.6	673	6	ABU48797
25	49	43.8	123	3	AAU32530

26	49	43.8	123	7	ADU10302	Adel0302 S. lavend
27	48.5	43.3	842	3	AAU69350	AAU69350 HIV-1 non
28	48	42.9	300	7	ADU7641	ADU7641 Bacterial
29	48	42.9	401	8	ADU21407	ADU21407 Bacterial
30	48	42.9	4437	6	ABU11384	ABU11384 Protein e
31	47	42.0	159	8	ADU18885	ADU18885 Glucosam
32	47	42.0	159	8	ADU64176	ADU64176 S. cerevi
33	47	42.0	508	8	ADU10681	ADU10681 Nicotiana
34	47	42.0	508	8	ADU10653	ADU10653 Nicotiana
35	47	42.0	509	8	ADU10655	ADU10655 Nicotiana
36	47	42.0	659	8	ADU19947	ADU19947 Bacterial
37	46.5	41.5	428	6	ABU49306	ABU49306 Protein e
38	46.5	41.5	849	3	AAU69645	AAU69645 HIV synth
39	46	41.1	100	3	AAU20204	AAU20204 Human sec
40	46	41.1	114	4	ABU70970	ABU70970 Drosophi
41	46	41.1	189	5	ABG59978	ABG59978 Human DIT
42	46	41.1	216	4	AAU82765	AAU82765 S. epider
43	46	41.1	216	6	ABU19037	ABU19037 Pathogen
44	46	41.1	253	8	ADQ37007	ADQ37007 Cell prol
45	46	41.1	253	8	ADQ15677	ADQ15677 Rice stre
46	46	41.1	274	5	ABP40434	ABP40434 Staphyloc
47	46	41.1	274	8	ADU05966	ADU05966 Staphyloc
48	46	41.1	300	6	ADU12194	ADU12194 Actinobac
49	46	41.1	300	7	AAU39415	AAU39415 Actinobac
50	46	41.1	385	3	AAU34981	AAU34981 Arabidops
51	46	41.1	398	3	AAU33096	AAU33096 Arabidops
52	46	41.1	420	3	AAU34980	AAU34980 Arabidops
53	46	41.1	433	3	AAU23085	AAU23085 Arabidops
54	46	41.1	469	4	ABG09202	ABG09202 Novel hum
55	46	41.1	469	4	ABG21331	ABG21331 Novel hum
56	46	41.1	512	6	AAU38226	AAU38226 Human enz
57	46	41.1	516	4	AAU35470	AAU35470 Human cyc
58	46	41.1	532	7	ABO63494	ABO63494 Klebsiell
59	46	41.1	534	8	ABM83406	ABM83406 Human dia
60	46	41.1	536	2	AAU95110	AAU95110 Human RPN
61	46	41.1	536	8	ADU58253	ADU58253 Human pro
62	46	41.1	536	8	ADU40394	ADU40394 Human pho
63	46	41.1	536	8	ADU75985	ADU75985 Human pho
64	46	41.1	537	7	ADU04444	ADU04444 Bacterial
65	46	41.1	545	6	ABU26622	ABU26622 Protein e
66	46	41.1	553	2	ABU68489	ABU68489 Human par
67	46	41.1	553	8	ABM83407	ABM83407 Human dia
68	46	41.1	572	5	ABG32231	ABG32231 Human U1
69	46	41.1	572	6	ABP97910	ABP97910 Amino aci
70	46	41.1	572	8	ADP65307	ADP65307 Human dth
71	46	41.1	572	8	ADU18668	ADU18668 Human sof
72	46	41.1	792	6	ABU55389	ABU55389 Human col
73	46	41.1	1052	3	AAU60335	AAU60335 Rat subtl
74	46	41.1	422	6	ABU05276	ABU05276 Protein e
75	45.5	40.2	119	8	ABO58567	ABO58567 Human gen
76	45	40.2	329	8	ABO58567	ABO58567 Human gen
77	45	40.2	377	3	AAU20649	AAU20649 Arabidops
78	45	40.2	377	3	AAU45918	AAU45918 Arabidops
79	45	40.2	399	3	AAU20648	AAU20648 Arabidops
80	45	40.2	399	3	AAU45917	AAU45917 Arabidops
81	45	40.2	404	3	AAU20647	AAU20647 Arabidops
82	45	40.2	404	3	AAU45916	AAU45916 Arabidops
83	45	40.2	467	6	ABU25173	ABU25173 Protein e
84	45	40.2	497	7	ADU64193	ADU64193 Human pro
85	45	40.2	508	8	ADU10589	ADU10589 Nicotiana
86	45	40.2	534	2	AAU28404	AAU28404 63 kd Cam
87	45	40.2	534	2	AAU69720	AAU69720 Cyclic-GM
88	45	40.2	534	2	AAU11251	AAU11251 63 kd cal
89	45	40.2	534	2	AAU18038	AAU18038 Bovine br
90	45	40.2	534	2	AAU71223	AAU71223 63 kDa Ca
91	45	40.2	534	2	AAU77039	AAU77039 Bovine br
92	45	40.2	534	2	AAU60751	AAU60751 63 kDa bo
93	45	40.2	534	3	AAU80977	AAU80977 Bovine br
94	45	40.2	534	6	ABU58716	ABU58716 Bovine br
95	45	40.2	534	8	ADU94947	ADU94947 Rat Prote
96	45	40.2	535	7	ADU58251	ADU58251 Rat Prote
97	45	40.2	548	4	ABU62383	ABU62383 Drosophi
98	45	40.2	626	5	ABU49107	ABU49107 Listeria

99	45	40.2	626	6	ABU32651	Abu32651 Protein e	172	44	39.3	952	7	ABO68769	AbO68769 Pseudomon
100	45	40.2	643	4	AAU35641	Aau35641 Haemophil	173	44	39.3	1577	2	AAR91047	Aar91047 Alpha-D-g
101	45	40.2	633	6	ABU30579	Abu30579 Protein e	174	43.5	38.8	189	8	ADG45845	AdG45845 Staphyloc
102	45	40.2	666	5	ABB90255	Abb90255 Human pol	175	43.5	38.8	384	3	AAI10103	Aai10103 Arabidops
103	45	40.2	808	7	ADB64170	Adb64170 Human pro	176	43.5	38.8	426	3	AAI10102	Aai10102 Arabidops
104	45	40.2	867	7	ADB71288	Adb71288 Novel hum	177	43.5	38.8	429	6	ABU47911	Abu47911 Protein e
105	45	40.2	1052	3	AAAB06336	AaB06336 Mouse sub	178	43.5	38.8	434	7	ADG94448	AdG94448 E. faeciu
106	45	40.2	1052	3	AAAB06334	AaB06334 Human sub	179	43.5	38.8	437	4	AAU38398	Aau38398 Salmonell
107	45	40.2	1052	3	AAAY54619	Aay54619 Human sub	180	43.5	38.8	523	3	AAI10101	Aai10101 Arabidops
108	45	40.2	1052	3	AAAY66982	Aay66982 Human sub	181	43.5	38.8	523	8	ADN73153	Adn73153 Thale cre
109	45	40.2	1052	3	AAAY84227	Aay84227 Amino aci	182	43.5	38.8	540	7	ADFO5702	Adfo5702 Bacterial
110	45	40.2	1052	3	AAAY84228	Aay84228 Amino aci	183	43.5	38.8	619	8	ADS30170	Ads30170 Bacterial
111	45	40.2	1052	3	AAU385520	Aau385520 Human sub	184	43	38.4	42	8	ABO58010	AbO58010 Human gen
112	45	40.2	1052	5	AAE14527	Aae14527 Human sit	185	43	38.4	126	4	ABB62908	Abb62908 Drosophil
113	45	40.2	1052	5	AAE14528	Aae14528 Hamster s	186	43	38.4	162	7	ADFO6342	Adfo6342 Bacterial
114	45	40.2	1052	5	ABG91096	Abg91096 Human sub	187	43	38.4	172	6	ABU40649	Abu40649 Protein e
115	45	40.2	1537	4	AAAB83971	Abg83971 Amino aci	188	43	38.4	172	8	ADS42775	Ads42775 Bacterial
116	45	40.2	1677	4	ABG10016	Abg10016 Novel hum	189	43	38.4	196	4	ABR03863	AbR03863 Human mus
117	45	40.2	1696	7	ADU69016	Adj69016 Human hea	190	43	38.4	196	6	ABU13177	AbU13177 Novel hum
118	45	40.2	1720	6	AAW78886	Aaw78886 Human pro	191	43	38.4	196	6	ADJ29203	Adj29203 Human mus
119	45	40.2	1720	6	ABO07115	AbO07115 Novel hum	192	43	38.4	256	3	AAAY82452	Aay82452 Spinnach c
120	45	40.2	1721	4	AAW79870	Aaw79870 Human pro	193	43	38.4	311	6	ABP96401	Abp96401 Prochloro
121	45	39.7	403	4	AAU54649	Aau54649 Propionib	194	43	38.4	394	5	ABG93276	Abg93276 C. albica
122	44.5	39.7	403	6	ABM51168	Abm51168 Propionib	195	43	38.4	407	7	ADM05407	Adm05407 Human pro
123	44.5	39.7	417	8	ADS42706	AdS42706 Bacterial	196	43	38.4	429	6	ABM15850	Abm15850 Mycobacte
124	44.5	39.7	424	6	ABM67843	Abm67843 Phototrab	197	43	38.4	467	7	ADG33780	Adg33780 Actinomyc
125	44.5	39.7	499	8	ADG26143	AdG26143 HIV gp120	198	43	38.4	469	8	ADN20290	Adn20290 Bacterial
126	44.5	39.7	549	5	AAU52842	Aau52842 Physcomit	199	43	38.4	481	8	ADN01952	Adn01952 Staphyloc
127	44.5	39.7	619	5	AAU75156	Aau75156 N-termina	200	43	38.4	481	8	ADN01939	Adn01939 Staphyloc
128	44.5	39.7	646	5	AAU75155	Aau75155 Modified	201	43	38.4	481	8	ADN01953	Adn01953 Staphyloc
129	44.5	39.7	842	5	ABB06211	Abb06211 HIV Env 1	202	43	38.4	481	8	ADN01955	Adn01955 Staphyloc
130	44.5	39.7	842	6	ABU66565	Abu66565 Human imm	203	43	38.4	481	8	ADN01946	Adn01946 Staphyloc
131	44.5	39.7	842	6	ABR55684	AbR55684 HIV IsoLa	204	43	38.4	486	6	ABW71573	Abw71573 Staphyloc
132	44.5	39.7	842	7	ADC13218	AdC13218 Protein o	205	43	38.4	490	2	AAW89764	Aaw89764 Staphyloc
133	44.5	39.7	842	8	ADM73868	Adm73868 HIV-1 pol	206	43	38.4	490	8	ADN01954	Adn01954 Staphyloc
134	44.5	39.7	847	3	AAW97073	Aay97073 Variant H	207	43	38.4	510	8	ADN17403	Adn17403 Bacterial
135	44.5	39.7	847	8	ADOO5103	Adoo5103 Human imm	208	43	38.4	521	7	ABD23592	Abd23592 Ricketsei
136	44	39.3	114	2	ADC96973	Adc96973 E. faeciu	209	43	38.4	555	6	ABU39997	AbU39997 Protein e
137	44	39.3	136	2	AAU12478	Aay12478 Human 5'	210	43	38.4	587	6	ABU29807	Abu29807 Protein e
138	44	39.3	138	4	AAU31547	Aau31547 Novel hum	211	43	38.4	594	8	ADN20584	Adn20584 Bacterial
139	44	39.3	143	2	AAV36077	Aav36077 Extended	212	43	38.4	597	7	ADC97426	Adc97426 E. faeciu
140	44	39.3	143	8	ADP19385	Adp19385 Human sec	213	43	38.4	759	6	ABM70917	Abm70917 Staphyloc
141	44	39.3	157	8	ADN17554	Adn17554 Bacterial	214	43	38.4	798	4	ABB61410	Abb61410 Drosophil
142	44	39.3	176	3	AAAG54430	Aag54430 Zea mays	215	43	38.4	1188	8	ADOB0423	AdoB0423 Zebrafish
143	44	39.3	206	5	ABU04642	Abj04642 Protein o	216	43	38.4	1551	4	AAAG85026	Aag85026 Shring wh
144	44	39.3	215	3	AAAG54429	Aag54429 Zea mays	217	43	38.4	1673	5	ABP65698	Abp65698 Human pol
145	44	39.3	273	8	ADR04184	Adr04184 E. faecium	218	43	38.4	1690	5	ABP65699	Abp65699 Human pol
146	44	39.3	277	6	ABU29809	Abu29809 Protein e	219	43	38.4	1893	5	AAU84593	Aau84593 HIV Casse
147	44	39.3	282	5	ABP27289	Abp27289 Streptoco	220	43	38.4	1896	5	AAU84590	Aau84590 HIV Casse
148	44	39.3	302	3	AAAG54428	Aag54428 Zea mays	221	43	38.4	3290	6	ADA34199	Ada34199 Acinetoba
149	44	39.3	308	8	ADS44636	AdS44636 Bacterial	222	43	38.4	5245	7	ADJ23931	Adj23931 Streptomy
150	44	39.3	378	3	AAAG46567	Aag46567 Arabidops	223	43	38.4	5245	7	ADJ23897	Adj23897 Streptomy
151	44	39.3	404	3	AAAG46566	Aag46566 Arabidops	224	43	38.4	5746	5	AAU84596	Aau84596 HIV comp1
152	44	39.3	410	5	ABP30521	Abp30521 Streptoco	225	42.5	37.9	226	5	ABP40649	Abp40649 Staphyloc
153	44	39.3	426	6	ABU11528	Abu11528 Human WDD	226	42.5	37.9	226	5	ABU07889	Abu07889 Staphyloc
154	44	39.3	429	5	ABP26315	Abp26315 Streptoco	227	42.5	37.9	227	6	ABW72833	Abw72833 Staphyloc
155	44	39.3	429	5	ABP29714	Abp29714 Streptoco	228	42.5	37.9	429	4	ADN17579	Adn17579 Bacterial
156	44	39.3	463	3	AAAG46565	Aag46565 Arabidops	229	42.5	37.9	429	1	AAAP1958	Aap1958 Peptide e
157	44	39.3	473	7	ADE38435	AdE38435 Human pro	230	42.5	37.9	429	2	AAU51887	Aau51887 DAPA synt
158	44	39.3	476	6	ABP41793	Abp41793 Human ova	231	42.5	37.9	429	4	AAU34505	Aau34505 E. coli c
159	44	39.3	480	6	ADA48242	Ada48242 Rice proc	232	42.5	37.9	429	6	ABU28561	Abu28561 Protein e
160	44	39.3	491	4	AAU34175	Aau34175 Staphyloc	233	42.5	37.9	429	8	ADFO4948	Adfo4948 Bacterial
161	44	39.3	504	4	AAU37099	Aau37099 Staphyloc	234	42.5	37.9	429	8	ADN18117	Adn18117 Bacterial
162	44	39.3	504	6	ABM72813	Abm72813 Staphyloc	235	42.5	37.9	431	2	AAW73903	Aaw73903 E. coli D
163	44	39.3	511	6	ABU16504	Abu16504 Protein e	236	42.5	37.9	435	6	ABU31641	Abu31641 Protein e
164	44	39.3	545	3	AAAB19080	Aab19080 Amino aci	237	42.5	37.9	447	7	ABO66770	AbO66770 Klebsiell
165	44	39.3	553	3	ADG28434	AdG28434 Bacterial	238	42.5	37.9	513	3	ABG63833	AbG63833 Rat Prote
166	44	39.3	560	6	ABM68550	Abm68550 Phototrab	239	42.5	37.9	546	4	AAU23631	Aau23631 Novel hum
167	44	39.3	571	8	ADN17386	Adn17386 Bacterial	240	42.5	37.9	546	4	AAU87604	Aau87604 Novel cen
168	44	39.3	584	4	ABG26094	Abg26094 Novel hum	241	42.5	37.9	546	8	ADJ54919	Adj54919 Novel hum
169	44	39.3	586	4	ABBS8288	Abbs8288 Drosophil	242	42.5	37.9	568	8	AAU87314	Aau87314 Novel cen
170	44	39.3	658	4	ABBS9450	Abbs9450 Drosophil	243	42.5	37.9	568	8	ADJ54629	Adj54629 Novel hum
171	44	39.3	765	7	ADF74168	Adf74168 Human nov	244	42.5	37.9	586	2	AAK49855	Aak49855 Sequence

245	42.5	37.9	624	4	AAU22925	118	41.5	37.1	472	7	ADG33808	Adg33808	Actinomyc
246	42.5	37.9	846	3	AA869345	319	41.5	37.1	489	3	AA853393	AA853393	Arbidiops
247	42.5	37.9	883	4	AA882761	320	41.5	37.1	489	5	AB891098	AB891098	Helicobac
248	42.5	37.9	1300	7	AD863060	321	41.5	37.1	489	8	ADN73091	ADN73091	Thale cre
249	42	37.5	70	3	AA612432	322	41.5	37.1	559	5	AB893132	AB893132	Herbicida
250	42	37.5	78	8	AD841591	323	41.5	37.1	561	5	ABP73469	ABP73469	Candida a
251	42	37.5	82	7	ADCO0634	324	41.5	37.1	639	5	ABP53637	ABP53637	MaiZe cal
252	42	37.5	115	6	ADDA34222	325	41.5	37.1	647	8	ADN72231	ADN72231	Thale cre
253	42	37.5	117	3	AA612617	326	41.5	37.1	846	2	AA808406	AA808406	Sequence
254	42	37.5	120	8	ADOC5051	327	41.5	37.1	854	8	AD195311	AD195311	Human imm
255	42	37.5	127	3	AA612616	328	41	36.6	52	6	ABP76206	ABP76206	Human GEN
256	42	37.5	129	7	ADH86956	329	41	36.6	52	6	ABP76053	ABP76053	Human GEN
257	42	37.5	156	3	AA612615	330	41	36.6	71	2	AAW09412	AAW09412	Human G p
258	42	37.5	178	6	ABM71384	331	41	36.6	71	4	AAE03966	AAE03966	Human gen
259	42	37.5	208	7	ABO60894	332	41	36.6	71	4	AAW39864	AAW39864	Human pol
260	42	37.5	225	6	ABU50105	333	41	36.6	71	5	ABG73049	ABG73049	Human gam
261	42	37.5	244	8	ADN20298	334	41	36.6	71	8	ADM67205	ADM67205	Murine ad
262	42	37.5	268	6	ADA36831	335	41	36.6	82	4	AAW41650	AAW41650	Human pol
263	42	37.5	306	6	ABM69568	336	41	36.6	83	3	AA601243	AA601243	Human sec
264	42	37.5	307	2	AAW93255	337	41	36.6	83	7	ADP59249	ADP59249	Human pol
265	42	37.5	311	7	ADP59532	338	41	36.6	86	2	AAV12896	AAV12896	Human 5'
266	42	37.5	324	6	ABU29166	339	41	36.6	99	5	ABP30099	ABP30099	Streptoco
267	42	37.5	324	6	ADW25910	340	41	36.6	106	7	ADF07525	ADF07525	Bacterial
268	42	37.5	328	7	ADH86358	341	41	36.6	140	2	AAV40111	AAV40111	Amno aci
269	42	37.5	341	8	ADN47212	342	41	36.6	140	6	ABU49843	ABU49843	Protein e
270	42	37.5	351	5	ABP73534	343	41	36.6	144	3	AA607958	AA607958	Arbidiops
271	42	37.5	372	4	AA681063	344	41	36.6	144	3	AA643189	AA643189	Arbidiops
272	42	37.5	423	8	ADN24093	345	41	36.6	149	8	ADN19493	ADN19493	Bacterial
273	42	37.5	450	6	ABU41584	346	41	36.6	158	7	ADU48507	ADU48507	Oll -aeboc
274	42	37.5	451	6	ABU39727	347	41	36.6	160	8	ADW04633	ADW04633	Human pro
275	42	37.5	459	3	AA629591	348	41	36.6	160	8	ADQ67105	ADQ67105	Novel hum
276	42	37.5	460	7	ADG33874	349	41	36.6	161	8	AD843976	AD843976	Bacterial
277	42	37.5	464	3	ADN24352	350	41	36.6	162	4	AAW41792	AAW41792	Human pol
278	42	37.5	467	3	AAV99855	351	41	36.6	162	4	AAW41792	AAW41792	Human pol
279	42	37.5	467	3	AAV99854	352	41	36.6	164	2	AAW04866	AAW04866	Chicken g
280	42	37.5	467	3	AAV99853	353	41	36.6	164	7	ADG31901	ADG31901	Chicken i
281	42	37.5	468	3	AAV99857	354	41	36.6	166	8	ADW67228	ADW67228	Human adi
282	42	37.5	468	3	AAV99856	355	41	36.6	169	3	AA643188	AA643188	Arbidiops
283	42	37.5	468	3	AAV99858	356	41	36.6	169	3	AA607957	AA607957	Arbidiops
284	42	37.5	474	4	AAU46847	357	41	36.6	186	6	ABW72361	ABW72361	Staphyloc
285	42	37.5	474	6	ABM43366	358	41	36.6	188	7	ADP43564	ADP43564	Nocardiol
286	42	37.5	490	6	AD827426	359	41	36.6	188	8	ADW01090	ADW01090	Nocardiol
287	42	37.5	509	5	AB849686	360	41	36.6	188	7	ADR21480	ADR21480	Partial s
288	42	37.5	529	3	AA629590	361	41	36.6	194	7	ABO66351	ABO66351	Klebsiell
289	42	37.5	540	3	AAV75735	362	41	36.6	208	5	ABP39604	ABP39604	Staphyloc
290	42	37.5	542	3	AA629589	363	41	36.6	208	8	ADSO5621	ADSO5621	Staphyloc
291	42	37.5	564	4	AB866319	364	41	36.6	210	5	ABUS1679	ABUS1679	Helicobac
292	42	37.5	564	8	ADQ089714	365	41	36.6	215	3	AA643187	AA643187	Arbidiops
293	42	37.5	574	8	ADK70709	366	41	36.6	215	3	AA607956	AA607956	Arbidiops
294	42	37.5	608	6	ABU43518	367	41	36.6	215	7	ADM25823	ADM25823	Hyperther
295	42	37.5	608	6	ABU39109	368	41	36.6	215	8	ADN73189	ADN73189	Thale cre
296	42	37.5	650	8	ADK70696	369	41	36.6	264	8	ADN47006	ADN47006	Thermococ
297	42	37.5	659	5	AB893561	370	41	36.6	265	6	ABM69559	ABM69559	Photococ
298	42	37.5	684	6	ABU19991	371	41	36.6	280	5	AB891588	AB891588	Herbicida
299	42	37.5	688	8	AD824539	372	41	36.6	299	4	AAW40007	AAW40007	Human pol
300	42	37.5	698	8	AD829165	373	41	36.6	308	4	ABG19573	ABG19573	Human pol
301	42	37.5	747	8	AD866215	374	41	36.6	309	8	AD821870	AD821870	Bacterial
302	42	37.5	1238	7	ADU70644	375	41	36.6	312	3	AAW43035	AAW43035	Human ORF
303	42	37.5	1269	7	ABM81833	376	41	36.6	312	4	AAW40006	AAW40006	Human pol
304	42	37.5	1289	7	AD831527	377	41	36.6	312	7	AD849307	AD849307	Human inh
305	42	37.5	1297	2	AAV13565	378	41	36.6	329	4	AA876662	AA876662	Corynebac
306	42	37.5	1297	2	AAV08403	379	41	36.6	352	4	AAU23088	AAU23088	Novel hum
307	42	37.5	1297	7	AD885337	380	41	36.6	367	3	AA843024	AA843024	Human ORF
308	42	37.5	1409	8	ADN22734	381	41	36.6	376	6	ADA34683	ADA34683	Actinocoba
309	42	37.5	1973	8	AD084852	382	41	36.6	397	7	ABO73973	ABO73973	Pseudomon
310	42	37.5	1973	8	AD084850	383	41	36.6	399	3	AA635778	AA635778	Arbidiops
311	41.5	37.1	203	4	ABG24283	384	41	36.6	401	5	ABUS1332	ABUS1332	Helicobac
312	41.5	37.1	368	4	AAW84128	385	41	36.6	410	4	ABG04922	ABG04922	Novel hum
313	41.5	37.1	368	6	AAE29785	386	41	36.6	415	5	ABUS2179	ABUS2179	Helicobac
314	41.5	37.1	368	6	ADK39716	387	41	36.6	420	2	AAV10965	AAV10965	H. pylori
315	41.5	37.1	425	6	ABU40737	388	41	36.6	426	4	AA862035	AA862035	P. furios
316	41.5	37.1	461	3	AA653395	389	41	36.6	421	2	AAW20369	AAW20369	H. pylori
317	41.5	37.1	462	3	AA653394	390	41	36.6	421	2	AAW20835	AAW20835	H. pylori

391	41	36.6	425	3	AAG35777	Aag35777	Arabidops	464	41	36.6	977	2	AAW03942	Aaw03942	LKT-GnRH
392	41	36.6	430	7	ADB70157	Adb70157	C. neofor	465	41	36.6	977	2	AAW79569	Aaw79569	LKT-GnRH
393	41	36.6	433	4	ABB65475	Abb65475	Drosophi1	466	41	36.6	1069	2	AAE52748	Aae52748	Bovine IF
394	41	36.6	441	5	ABM48633	Abm48633	Listeria	467	41	36.6	1069	2	AAW13867	Aaw13867	Chimeric
395	41	36.6	448	6	ABM68700	Abm68700	phototrab	468	41	36.6	1069	2	AAAB21074	Aab21074	Bovine ga
396	41	36.6	451	7	ADL65455	Adl65455	C. glutam	469	41	36.6	1068	2	AAAR22103	Aar22103	Bovine IL
397	41	36.6	455	8	ADS29127	Ads29127	Bacterial	470	41	36.6	1098	2	AAAR32747	Aar32747	Bovine IL
398	41	36.6	459	4	AAAB76660	Aab76660	Corynebac	471	41	36.6	1098	2	AAAW13866	Aaw13866	Chimeric
399	41	36.6	465	6	ABU38244	Abu38244	Protein e	472	41	36.6	1098	3	AAAB21073	Aab21073	Bovine IL
400	41	36.6	469	7	ABO79123	AbO79123	Pseudomon	473	41	36.6	1100	8	ADP99064	Adp99064	C. albica
401	41	36.6	477	2	AAI10993	Aai10993	H. pylori	474	41	36.6	1133	3	AAAG38914	Aag38914	Arabidops
402	41	36.6	479	4	AAAG90011	Aag90011	C. glutam1	475	41	36.6	1193	3	AAAG38913	Aag38913	Arabidops
403	41	36.6	479	7	ABM73851	Abm73851	DNA clone	476	41	36.6	1256	4	ABBB4133	Abb4133	Drosophi1
404	41	36.6	489	6	ABU17356	Abu17356	Protein e	477	41	36.6	1411	6	ABBR3378	Abbr3378	Protein t
405	41	36.6	490	2	AAV33929	Aav33929	Leukotoxi	478	41	36.6	1411	7	ADK63342	Adk63342	Disease t
406	41	36.6	490	6	ADA28694	Ada28694	Plasmid p	479	41	36.6	1566	4	ABBB4884	Abb4884	Drosophi1
407	41	36.6	494	4	ABBB68783	Abbb68783	Drosophi1	480	41	36.6	2188	6	ADA36476	Ada36476	Acinetoba
408	41	36.6	495	5	AAAM48000	Aam48000	Arabidops	481	41	36.6	3196	5	ABU1611	Abu1611	Protein e
409	41	36.6	495	8	ADN23982	Adn23982	Bacterial	482	40.5	36.2	96	3	ABG26753	Abg26753	Zea mays
410	41	36.6	501	3	AAG35776	Aag35776	Arabidops	483	40.5	36.2	100	7	ADHB6104	Adhb6104	Enterococ
411	41	36.6	501	5	AAAM48001	Aam48001	Arabidops	484	40.5	36.2	163	3	AAAG26752	Aag26752	Zea mays
412	41	36.6	505	6	ABU18461	Abu18461	Protein e	485	40.5	36.2	213	4	ABBR1455	Abbr1455	Drosophi1
413	41	36.6	510	2	AAAR88360	Aar88360	Caenorhab	486	40.5	36.2	243	6	ABBP78956	Abbp78956	N. gonorr
414	41	36.6	544	2	AAAM03943	Aam03943	LKT-GnRH	487	40.5	36.2	248	6	ABM67960	Abm67960	Phototrab
415	41	36.6	544	2	AAW79570	Aaw79570	LKT-GnRH	488	40.5	36.2	251	8	ADSS25182	Adss25182	Bacterial
416	41	36.6	572	4	ABBB1834	Abbb1834	Drosophi1	489	40.5	36.2	251	8	ADSS25911	Adss25911	Bacterial
417	41	36.6	572	8	ADK70707	Adk70707	Collapsin	490	40.5	36.2	252	8	ADSS25556	Adss25556	Bacterial
418	41	36.6	579	2	AAW37874	Aaw37874	Alcohol a	491	40.5	36.2	257	8	ADSS22518	Adss22518	Bacterial
419	41	36.6	585	6	ABU43406	Abu43406	Protein e	492	40.5	36.2	291	7	ADCG6763	Adcg6763	E. faeciu
420	41	36.6	596	4	AAU33748	Aau33748	Staphyloc	493	40.5	36.2	413	6	ABMB68660	Abmb68660	Phototrab
421	41	36.6	604	4	AAU36932	Aau36932	Staphyloc	494	40.5	36.2	459	8	ADN19683	Adn19683	Bacterial
422	41	36.6	604	6	ABU16053	Abu16053	Protein e	495	40.5	36.2	459	8	ADN19681	Adn19681	Bacterial
423	41	36.6	604	6	ABM73224	Abm73224	Staphyloc	496	40.5	36.2	470	5	ADDP74741	Adp74741	HIV-1 iso
424	41	36.6	608	4	AAEO4636	Aae04636	Pasteurel	497	40.5	36.2	479	5	ABBB91096	Abbb91096	Herbicida
425	41	36.6	611	8	ADN22551	Adn22551	Bacterial	498	40.5	36.2	503	4	AAAB83355	Abab83355	HIV-1 gp1
426	41	36.6	630	5	ABBB48390	Abbb48390	Listeria	499	40.5	36.2	571	4	ABBB60235	Abbb60235	Drosophi1
427	41	36.6	630	6	ABU32723	Abu32723	Protein e	500	40.5	36.2	838	2	AAW49078	Aaw49078	Solanum t
428	41	36.6	676	8	ADK70694	Adk70694	Chicken C	501	40.5	36.2	840	2	ABO70815	AbO70815	Pseudomon
429	41	36.6	695	2	AAW79573	Aaw79573	LKT-GnRH	502	40.5	36.2	3768	7	AAAR13753	Aar13753	ACVS. 3/2
430	41	36.6	695	3	AAV58361	Aav58361	Leukotoxi	503	40.5	36.2	3778	2	AAAR13895	Aar13895	ACV synth
431	41	36.6	695	3	AAV58133	Aav58133	Gonadotro	504	40.5	36.2	4644	8	ADP26621	Adp26621	Mouse cyt
432	41	36.6	754	6	ABU38838	Abu38838	Protein e	505	40.5	36.2	4644	8	ADP26623	Adp26623	Mouse cyt
433	41	36.6	754	8	ADH97174	Adh97174	P. aerugi	506	40.5	36.2	4646	8	ADP26625	Adp26625	Human cyt
434	41	36.6	754	8	ADH97176	Adh97176	P. aerugi	507	40.5	36.2	4646	8	ADP26631	Adp26631	Human cyt
435	41	36.6	774	8	ABMB3465	Abmb3465	Human dia	508	40.5	36.2	10	6	ABBP70338	Abbp70338	Tryptic p
436	41	36.6	780	7	ABO84146	AbO84146	Pseudomon	509	40.5	35.7	10	6	ABBP70337	Abbp70337	Tryptic p
437	41	36.6	786	3	AAV70243	Aav70243	Human RNA	510	40.5	35.7	43	5	ABBP30629	Abbp30629	Streptoco
438	41	36.6	831	7	ADCS1486	Adcs1486	Bacterial	511	40.5	35.7	50	2	AAAR71093	Aar71093	C. jejuni
439	41	36.6	831	8	ADSS29643	Adss29643	Bacterial	512	40.5	35.7	52	6	ABBB82557	Abbb82557	Human MAN
440	41	36.6	849	4	AAAB93170	Aab93170	Human pro	513	40.5	35.7	65	5	ABBP39574	Abbp39574	Staphyloc
441	41	36.6	883	6	ABU02533	Abu02533	S. pneumo	514	40.5	35.7	65	8	ADSS05543	Adss05543	Staphyloc
442	41	36.6	887	4	AAU37586	Aau37586	Streptoco	515	40.5	35.7	90	4	AAAG74248	Aag74248	Human col
443	41	36.6	890	6	ABBP1476	Abbp1476	Streptoco	516	40.5	35.7	94	5	ABBB78867	Abbb78867	Tumour ne
444	41	36.6	890	6	ABU46263	Abu46263	Protein e	517	40.5	35.7	94	5	ABBB78866	Abbb78866	Tumour ne
445	41	36.6	890	8	ADK48224	Adk48224	Streptoco	518	40.5	35.7	106	5	ABBP30637	Abbp30637	Streptoco
446	41	36.6	920	4	ABGG29636	Abg29636	Novel hum	519	40.5	35.7	106	5	ABBP30640	Abbp30640	Streptoco
447	41	36.6	924	2	AAAR10889	Aar10889	Leukotoxi	520	40.5	35.7	120	4	AAAG00723	Aag00723	Novel hum
448	41	36.6	924	2	AAAR42378	Aar42378	Recombina	521	40.5	35.7	126	4	AAAG00976	Aag00976	Human imm
449	41	36.6	924	2	AAAR42380	Aar42380	Recombina	522	40.5	35.7	138	2	AAAY36920	Aay36920	Amino aci
450	41	36.6	924	2	AAAR42385	Aar42385	Recombina	523	40.5	35.7	143	3	AAAG29998	Aag29998	Arabidops
451	41	36.6	926	2	AAAR14482	Aar14482	LKT352. 1	524	40.5	35.7	144	1	AAAP91033	Aap91033	Modified
452	41	36.6	926	2	AAAR34545	Aar34545	Leukotoxi	525	40.5	35.7	146	1	AAAP30676	Aap30676	Phes3, Ly
453	41	36.6	926	2	AAAR50291	Aar50291	Recombina	526	40.5	35.7	147	1	AAAP91042	Aap91042	Modified
454	41	36.6	926	2	AAAW03945	Aaw03945	P. haemo1	527	40.5	35.7	147	1	AAAP91035	Aap91035	Modified
455	41	36.6	926	2	AAAW79568	Aaw79568	Leukotoxi	528	40.5	35.7	153	3	AAAG40483	Aag40483	Arabidops
456	41	36.6	936	2	AAAR34547	Aar34547	GnRH-Leuk	529	40.5	35.7	153	4	AAAM38761	Aam38761	Human pol
457	41	36.6	936	2	AAAR34546	Aar34546	Somatosta	530	40.5	35.7	154	3	AAAG29997	Aag29997	Arabidops
458	41	36.6	951	2	AAAR34548	Aar34548	Rotavirius	531	40.5	35.7	158	6	ABBB82550	Abbb82550	Human MAN
459	41	36.6	953	2	AAAR07167	Aar07167	105KD PTX	532	40.5	35.7	158	6	ABBB82553	Abbb82553	Mouse MAN
460	41	36.6	953	2	AAAR15159	Aar15159	Leukotoxi	533	40.5	35.7	158	6	AAO26456	Aao26456	Human ch3
461	41	36.6	953	2	AAAR3865	Aar3865	Leukotoxi	534	40.5	35.7	159	6	ABBB82554	Abbb82554	A synthet
462	41	36.6	953	2	AAAB60072	Aab60072	PKA prot	535	40.5	35.7	159	6	ABBB82551	Abbb82551	A synthet
463	41	36.6	953	4	AAAB04638	Aab04638	Pasteurel	536	40.5	35.7	161	4	ABG00722	Abg00722	Novel hum



537	40	35..7	162	3	AAB43377	AbB43377 Human ORF	610	40	35..7	275	4	ABG07277	Abg07277 Novel hum
538	40	35..7	162	6	ABG99957	ABg99957 Human nov	611	40	35..7	276	7	ABO63141	AbO63141 Klebsiell
539	40	35..7	166	6	ABP97165	ABp97165 Human lys	612	40	35..7	282	6	ABU36887	ABu36887 Protein e
540	40	35..7	166	7	ADJ70254	ADj70254 Human hea	613	40	35..7	282	6	ABU34865	ABu34865 Protein e
541	40	35..7	179	4	ABB62160	ABb62160 Mouse arg	614	40	35..7	291	4	ABB36424	ABb36424 Peptide #
542	40	35..7	179	4	ABAB62159	ABab62159 Mouse arg	615	40	35..7	291	4	AAW29924	AAw29924 Peptide #
543	40	35..7	179	6	ABBB82558	ABbb82558 Bovine pr	616	40	35..7	291	4	ABBB31217	ABbb31217 Peptide #
544	40	35..7	179	6	ABBB82552	ABbb82552 Mouse pro	617	40	35..7	291	4	ABBB21776	ABbb21776 Protein #
545	40	35..7	179	6	ABBB82559	ABbb82559 Human pro	618	40	35..7	291	4	AAW65985	AAw65985 Human bon
546	40	35..7	179	6	ABBB82559	ABbb82559 Pig pro-M	619	40	35..7	291	4	AAW57183	AAw57183 Human bra
547	40	35..7	179	6	AAO26455	AAo26455 Human ch3	620	40	35..7	291	4	ABG51259	ABg51259 Human liv
548	40	35..7	182	4	ABBB5390	ABbb5390 Drosophil	621	40	35..7	291	5	ABG39209	ABg39209 Human pep
549	40	35..7	182	4	ABBB57808	ABbb57808 Drosophil	622	40	35..7	294	5	ABBB54169	ABbb54169 Lactococc
550	40	35..7	182	8	ADQ96544	ADq96544 T cell ac	623	40	35..7	294	8	ADG29357	ADg29357 Bacteri
551	40	35..7	187	4	AAAG65919	AAg65919 Amino aci	624	40	35..7	307	5	AAW49055	AAw49055 Tobacco a
552	40	35..7	198	4	AAAG65920	AAg65920 Amino aci	625	40	35..7	316	4	AAU00818	AAu00818 Human Imm
553	40	35..7	199	6	ABU24475	ABu24475 Protein e	626	40	35..7	319	7	ADC95915	ADc95915 E. faeciu
554	40	35..7	201	4	AAW38762	AAw38762 Human pol	627	40	35..7	324	6	ADW454362	ADw454362 Human pro
555	40	35..7	206	5	ABP51289	ABp51289 Human MDD	628	40	35..7	326	6	ABU25302	ABu25302 Protein e
556	40	35..7	206	7	ADH85557	ADh85557 Enterococ	629	40	35..7	327	5	ABW49937	ABw49937 Listeria
557	40	35..7	207	2	AAW09530	AAw09530 Human lys	630	40	35..7	330	7	ABW74320	ABw74320 DNA clone
558	40	35..7	207	3	AAW40482	AAw40482 Arabidops	631	40	35..7	332	8	ADH56074	ADh56074 Debaromy
559	40	35..7	207	7	ABO82593	ABo82593 Pseudomon	632	40	35..7	336	8	ADU119383	ADu119383 Pyrococc
560	40	35..7	209	3	AAW29996	AAw29996 Arabidops	633	40	35..7	339	4	AAW56053	AAw56053 Putative
561	40	35..7	214	3	AAW69296	AAw69296 A human 1	634	40	35..7	344	3	AAW56782	AAw56782 Human pro
562	40	35..7	214	3	AAW40481	AAw40481 Arabidops	635	40	35..7	344	8	ADG27683	ADg27683 Bacteri
563	40	35..7	214	8	ADG47876	ADg47876 Arabidops	636	40	35..7	345	4	AAW96222	AAw96222 Putative
564	40	35..7	214	8	ADG62901	ADg62901 Transcript	637	40	35..7	345	5	ABP60914	ABp60914 Pyrococc
565	40	35..7	215	8	ADW66301	ADw66301 Human pro	638	40	35..7	345	7	ADFO4255	ADfO4255 Bacteri
566	40	35..7	215	8	ADW66302	ADw66302 Human pro	639	40	35..7	347	4	ABBB61186	ABbb61186 Drosophil
567	40	35..7	217	6	AAE34443	AAe34443 Human lip	640	40	35..7	351	8	ADS28060	ADs28060 Bacteri
568	40	35..7	218	4	AAW25257	AAw25257 Human pro	641	40	35..7	357	6	ABU24898	ABu24898 Protein e
569	40	35..7	219	4	AAW75019	AAw75019 Human col	642	40	35..7	358	6	ADA35088	ADa35088 Actinocba
570	40	35..7	224	4	AAW62621	AAw62621 Human SNA	643	40	35..7	359	7	ADW28205	ADw28205 Human MDD
571	40	35..7	224	6	ABU00236	ABu00236 Human nov	644	40	35..7	360	5	ABP26080	ABp26080 Streptoco
572	40	35..7	230	2	AAW09531	AAw09531 Human lys	645	40	35..7	371	3	AAW21115	AAw21115 Arabidops
573	40	35..7	230	4	AAW82669	AAw82669 Human bra	646	40	35..7	372	3	AAW21114	AAw21114 Arabidops
574	40	35..7	230	5	AAW85136	AAw85136 Mouse lys	647	40	35..7	388	3	AAW43313	AAw43313 Human ORF
575	40	35..7	230	5	AAW85133	AAw85133 Mouse lys	648	40	35..7	389	8	ADW99415	ADw99415 Chlamydia
576	40	35..7	230	5	AAW85134	AAw85134 Human lys	649	40	35..7	390	7	ADC96041	ADc96041 E. faeciu
577	40	35..7	230	5	AAW85132	AAw85132 Human lys	650	40	35..7	391	2	AAW35503	AAw35503 Chlamydia
578	40	35..7	230	6	ABP97164	ABp97164 Human lys	651	40	35..7	394	7	ADW04014	ADw04014 Human pro
579	40	35..7	230	6	ABR54196	ABr54196 Human NOV	652	40	35..7	407	4	AAW93675	AAw93675 Human pol
580	40	35..7	230	6	ABR54198	ABr54198 Human NOV	653	40	35..7	407	8	ADL15531	ADl15531 Human pro
581	40	35..7	230	7	ADW58736	ADw58736 Human pro	654	40	35..7	418	6	ABU27547	ABu27547 Protein e
582	40	35..7	230	7	ADW45662	ADw45662 Human pro	655	40	35..7	443	3	AAW21113	AAw21113 Arabidops
583	40	35..7	230	7	ADW47694	ADw47694 Human NOV	656	40	35..7	444	5	ABG79686	ABg79686 Tumour in
584	40	35..7	230	8	ABW60964	ABw60964 Human NOV	657	40	35..7	450	6	ABU43672	ABu43672 Protein e
585	40	35..7	234	4	ABW60990	ABw60990 Tumour-as	658	40	35..7	455	5	ABW05727	ABw05727 Human sig
586	40	35..7	234	4	ABW82548	ABw82548 Human she	659	40	35..7	463	3	AAW12529	AAw12529 Human Mas
587	40	35..7	234	6	ABBB2548	ABbb2548 Human arg	660	40	35..7	463	3	AAW42315	AAw42315 Human ORF
588	40	35..7	234	6	AAE34881	AAe34881 Human ARP	661	40	35..7	466	7	ADG33792	ADg33792 Actinomy
589	40	35..7	234	8	ADW44586	ADw44586 Human arg	662	40	35..7	469	3	AAW98040	AAw98040 Human ets
590	40	35..7	234	8	ADW05973	ADw05973 Antipepti	663	40	35..7	469	3	AAW90689	AAw90689 Human Ets
591	40	35..7	234	8	ADW019303	ADw019303 Human PRO	664	40	35..7	469	5	ABW878349	ABw878349 Human act
592	40	35..7	234	8	ADW096546	ADw096546 T cell ac	665	40	35..7	469	8	ABW085042	ABw085042 Human can
593	40	35..7	234	8	ADW54366	ADw54366 Human PRO	666	40	35..7	470	6	ADW09370	ADw09370 Alloiococ
594	40	35..7	235	6	ADP23376	ADp23376 PRO polyp	667	40	35..7	472	2	AAW66327	AAw66327 Kidney in
595	40	35..7	235	6	ABW11366	ABw11366 Protein e	668	40	35..7	473	6	ADW09372	ADw09372 Alloiococ
596	40	35..7	238	4	ABW07040	ABw07040 Novel hum	669	40	35..7	476	4	ABW08740	ABw08740 Novel hum
597	40	35..7	247	8	ADN17795	ADn17795 Bacteri	670	40	35..7	478	6	ABW63344	ABw63344 Protein e
598	40	35..7	248	2	AAW64050	AAw64050 Rice OsMA	671	40	35..7	484	6	ABU24912	ABu24912 Protein e
599	40	35..7	248	3	AAO14278	AAo14278 Plant flo	672	40	35..7	486	7	ABO70890	ABo70890 Pseudomon
600	40	35..7	248	8	ADQ37091	ADq37091 Cell prol	673	40	35..7	490	8	ADW72386	ADw72386 A. thaila
601	40	35..7	250	1	AAW70498	AAw70498 Aspergill	674	40	35..7	491	6	ABW20497	ABw20497 Protein e
602	40	35..7	250	4	ABW60023	ABw60023 Drosophil	675	40	35..7	505	6	ADW09374	ADw09374 Alloiococ
603	40	35..7	250	6	ABW41029	ABw41029 Protein e	676	40	35..7	509	6	AAW30011	AAw30011 Tobacco c
604	40	35..7	252	7	ABW082067	ABw082067 Pseudomon	677	40	35..7	513	6	ABW72116	ABw72116 Staphyloc
605	40	35..7	254	8	ADW42533	ADw42533 Bacteri	678	40	35..7	535	4	AAW74327	AAw74327 Human col
606	40	35..7	258	2	AAW37099	AAw37099 Amino aci	679	40	35..7	541	6	ABW49123	ABw49123 Protein e
607	40	35..7	263	3	AAW53451	AAw53451 Human col	680	40	35..7	544	2	AAW13337	AAw13337 HyPB prot
608	40	35..7	272	7	ADFO4631	ADfO4631 Bacteri	681	40	35..7	544	2	AAW67383	AAw67383 C. psittac
609	40	35..7	273	8	ADW23832	ADw23832 Bacteri	682	40	35..7	544	2	AAW10975	AAw10975 Chlamydia

683	40	35.7	544	2	AAW1863	Aw11863	Polypepti	756	40	35.7	1231	7	ADC95523	Adc95523	E. faeciu
684	40	35.7	544	2	AAy34735	Aay34735	Amino aci	757	40	35.7	1253	6	ABO07127	Ab007127	Novel hum
685	40	35.7	544	2	AAE11757	Aae11757	Chlamydo	758	40	35.7	1357	6	ADG42170	Adg42170	Human bra
686	40	35.7	544	5	ABB94272	Abb94272	Chlamydia	759	40	35.7	1394	6	AAg79647	Aag79647	Human pro
687	40	35.7	544	5	ABG31261	Abg31261	Chlamydia	760	40	35.7	1444	6	ADN61347	Adn61347	Penibacti
688	40	35.7	544	5	ADL97984	Adl97984	C. psittca	761	40	35.7	1444	8	ADR21520	Adr21520	Penibacti
689	40	35.7	544	5	ADL97987	Adl97987	C. tiracho	762	40	35.7	1518	7	ADD93660	Add93660	Streptoco
690	40	35.7	544	6	ABU26931	Abu26931	Protein e	763	40	35.7	1600	4	ABG20004	Abg20004	Novel hum
691	40	35.7	544	6	ABU27237	Abu27237	Protein e	764	40	35.7	1600	4	ABG09417	Abg09417	Novel hum
692	40	35.7	549	8	ADI45327	Adi45327	Rice isop	765	40	35.7	1600	4	ABG09473	Abg09473	Novel hum
693	40	35.7	551	8	ADS29961	Ads29961	Bacterial	766	40	35.7	1600	4	ABG12275	Abg12275	Novel hum
694	40	35.7	551	8	ADS11754	Ads11754	Bacterial	767	40	35.7	1600	7	ADP60439	Adp60439	Human con
695	40	35.7	551	5	ABB92269	Abb92269	Herbicide	768	40	35.7	1600	7	ADP60402	Adp60402	Human con
696	40	35.7	572	2	AAW68487	Aaw68487	Mouise Utl	769	40	35.7	1941	5	ABP65509	Abp65509	Bl fidobac
697	40	35.7	572	2	AAW62230	Aaw62230	Human Utl	770	40	35.7	1987	7	ABU63358	Abu63358	Human sin
698	40	35.7	572	5	AAU85553	Aau85553	Clone #50	771	40	35.7	2000	8	ADN04333	Adn04333	Antipseori
699	40	35.7	572	5	ABR42050	Abx42050	Human col	772	40	35.7	2000	8	ADP24104	Adp24104	PRO Poly
700	40	35.7	572	6	ABU69525	Abu69525	Human lun	773	40	35.7	2013	4	ABE62322	Abbe2322	Drosophi
701	40	35.7	572	6	ABU66428	Abu66428	Lung canc	774	40	35.7	2013	7	ABU63356	Abu63356	Human sin
702	40	35.7	572	6	ABP97909	Abp97909	Amino aci	775	40	35.7	2014	7	ABU63356	Abu63356	Human sin
703	40	35.7	572	7	ADE59435	Ades59435	Rat Prote	776	40	35.7	2014	4	AAE24137	Aae24137	Human kin
704	40	35.7	572	7	ADE59437	Ades9437	Rat Prote	777	40	35.7	2014	5	ABP60434	Abp60434	Human ste
705	40	35.7	572	7	ADH47334	Adh47334	Human lun	778	40	35.7	2014	7	ABU63359	Abu63359	Human sin
706	40	35.7	572	7	ADN95176	Adn95176	Human BGC	779	40	35.7	2040	7	ABU63357	Abu63357	Human sin
707	40	35.7	572	8	ADK70705	Adk70705	Collapsin	780	40	35.7	2041	6	ABP60435	Abp60435	Human ste
708	40	35.7	572	8	ADJ21253	Adj21253	Human lun	781	40	35.7	2168	4	ABG09420	Abg09420	Novel hum
709	40	35.7	572	8	ABM60551	Abm60551	Tumour -as	782	40	35.7	2168	4	ABG09420	Abg09420	Novel hum
710	40	35.7	584	6	ABU25339	Abu25339	Human ORF	783	40	35.7	2176	4	ABG12287	Abg12287	Novel hum
711	40	35.7	584	6	ABU00948	Abu00948	S. pneumo	784	40	35.7	2176	4	ABG20022	Abg20022	Novel hum
712	40	35.7	589	4	AAW39712	Aam39712	Human pol	785	40	35.7	2176	7	ADP60184	Adp60184	Human con
713	40	35.7	607	5	ABR52408	Abri52408	Protein r	786	40	35.7	2472	7	ADP60184	Adp60184	Human con
714	40	35.7	609	7	ADM05286	Adm05286	Human pro	787	40	35.7	2472	7	ADP60184	Adp60184	Human con
715	40	35.7	622	5	ABBA8075	Abba8075	Listeria	788	40	35.7	2477	7	ABR84742	Abri84742	Human spe
716	40	35.7	622	6	ABU32903	Abu32903	Protein e	789	40	35.7	2477	7	ADJ68432	Adj68432	Human hea
717	40	35.7	629	6	ABJ25441	Abj25441	Aspergill	790	40	35.7	2509	7	ABO67896	Ab067896	Pseudomon
718	40	35.7	629	8	ADJ75404	Adj75404	Marker ge	791	40	35.7	2541	3	ABA41087	Ab41087	Human ORF
719	40	35.7	631	7	ADH88290	Adh88290	Enterococ	792	40	35.7	2541	3	ABE81459	Ab81459	Human Tal
720	40	35.7	647	8	ADS44610	Ads44610	Bacterial	793	40	35.7	2541	5	ADG90450	Adg90450	Human tal
721	40	35.7	650	8	ADJ76381	Adj76381	Marker ge	794	40	35.7	2541	6	ABR47614	Abri47614	Breast ca
722	40	35.7	651	5	ABP69617	Abp69617	Human pol	795	40	35.7	2541	7	ADDA5522	Adda5522	Human pro
723	40	35.7	651	7	ADJ69772	Adj69772	Human hea	796	40	35.7	2541	7	ADDS8868	Adds8868	Human pro
724	40	35.7	662	5	ABR52423	Abri52423	Protein r	797	40	35.7	2541	7	ADP65318	Adp65318	Human tal
725	40	35.7	666	4	AAW41498	Aaw41498	Human pol	798	40	35.7	2541	8	ADP65745	Adp65745	Human Tal
726	40	35.7	683	8	ADK70692	Adk70692	Chicken C	799	40	35.7	2541	8	ABW81037	Abw81037	Tumour -as
727	40	35.7	684	4	ABR69330	Abbr69330	Drosophi	800	40	35.7	2636	7	ABO77007	Ab077007	Pseudomon
728	40	35.7	685	6	ABJ26041	Abj26041	Aspergill	801	40	35.7	2652	5	ABG31321	Abg31321	Predicted
729	40	35.7	693	5	ABR52422	Abri52422	Protein r	802	40	35.7	2652	8	ADL02250	Adl02250	Human OCP
730	40	35.7	703	6	ABJ26648	Abj26648	Human pro	803	40	35.7	2727	4	ABE61674	Abbe1674	Drosophi
731	40	35.7	703	7	ADC39232	Adc39232	Novel hum	804	40	35.7	2828	5	ABG31332	Abg31332	Human adl
732	40	35.7	704	2	AAW10976	Aaw10976	Dihydrofo	805	40	35.7	2828	5	ABG31319	Abg31319	Human adl
733	40	35.7	704	2	AAW11864	Aaw11864	DHFR/Poly	806	40	35.7	2828	5	ABG32897	Abg32897	Human adl
734	40	35.7	747	5	ABR52421	Abri52421	Protein r	807	40	35.7	2828	5	ADL17071	Adl17071	Human NOV
735	40	35.7	749	7	ADJ22754	Adj22754	Human dis	808	40	35.7	2828	5	ADL17072	Adl17072	Human NOV
736	40	35.7	774	1	AAE60616	Aae60616	Cephalosp	809	40	35.7	2828	6	ABJ37051	Abj37051	Human bre
737	40	35.7	806	5	ABR52420	Abri52420	Protein r	810	40	35.7	2828	6	ABU56609	Abu56609	Lung canc
738	40	35.7	806	8	ADS27497	Ads27497	Bacterial	811	40	35.7	2828	6	ABR47439	Abri47439	Breast ca
739	40	35.7	811	6	ABU17849	Abu17849	Protein e	812	40	35.7	2828	7	ADJ83135	Adj83135	Human adl
740	40	35.7	822	8	ADR39827	Adr39827	Rat NRC i	813	40	35.7	2828	7	ADN39857	Adn39857	Cancer/an
741	40	35.7	829	3	AAE58894	Aae58894	Breast an	814	40	35.7	2828	8	ADN38740	Adn38740	Cancer/an
742	40	35.7	904	8	ADG67715	Adg67715	Novel hum	815	40	35.7	2828	8	ADL02241	Adl02241	Human OCP
743	40	35.7	1002	3	AAE38741	Aae38741	Arabidops	816	40	35.7	2828	8	ADQ17737	Adq17737	Human bot
744	40	35.7	1002	5	ABR92602	Abb92602	Herbicide	817	40	35.7	2828	8	ADP67221	Adp67221	Human bla
745	40	35.7	1019	7	ADP04162	Adp04162	Bacterial	818	40	35.7	2845	8	ABP70049	Abp70049	Human NOV
746	40	35.7	1024	5	ABR04821	Abb04821	LDL recep	819	40	35.7	3432	6	ABU41925	Abu41925	Protein e
747	40	35.7	1024	5	ABR04818	Abb04818	LDL recep	820	40	35.7	5149	6	ABU15709	Abu15709	Protein e
748	40	35.7	1048	8	ABO84803	Ab084803	Marine ca	821	40	35.7	5266	4	ABG08551	Abg08551	Novel hum
749	40	35.7	1052	3	ABE26846	Ab26846	Human WAS	822	40	35.7	5385	4	ABE66487	Abbe6487	Drosophi
750	40	35.7	1052	3	ABA42389	Aab42389	Human ORF	823	40	35.7	5496	4	ABE67161	Abbe67161	Drosophi
751	40	35.7	1052	8	ADJ75447	Adj75447	Marker ge	824	40	35.7	8805	4	ABE67112	Abbe67112	Drosophi
752	40	35.7	1052	8	ADJ75508	Adj75508	Marker ge	825	39.5	35.3	90	4	ABG26817	Abg26817	Novel hum
753	40	35.7	1052	8	ABO84804	Ab084804	Human can	826	39.5	35.3	112	8	ABR78889	Ab78889	C. glutam
754	40	35.7	1053	8	ADN05216	Adn05216	Antipseori	827	39.5	35.3	173	4	ADG45861	Adg45861	Staphyloc
755	40	35.7	1093	8	ADO20339	Ado20339	Human PRO	828	39.5	35.3	202	3	AAI90336	Aai90336	B. subtili

829	39.5	35.3	203	3	AAB39147	Aab39147 Human sec	902	39	34.8	64	4	AAW29753	Aam29753 Peptide #
830	39.5	35.3	205	3	AAB39146	Aab39146 Human sec	903	39	34.8	64	4	ABR31068	Abb31068 Peptide #
831	39.5	35.3	234	3	AAAG8926	Aag58926 Arabidops	904	39	34.8	64	4	ABR21630	Abb21630 Protein #
832	39.5	35.3	247	6	ADA34361	Ada34361 Actinotoba	905	39	34.8	64	4	AAW69432	Aam69432 Human bon
833	39.5	35.3	272	8	ADS24473	Ad24473 Bacteriel	906	39	34.8	64	4	AAW57032	Aam57032 Human bra
834	39.5	35.3	278	6	ABU43379	Abu43379 Protein e	907	39	34.8	64	4	ABG51096	Abg51096 Human liv
835	39.5	35.3	221	8	ADN17501	Adn17501 Bacteriel	908	39	34.8	64	4	AAW04947	Aam04947 Human pep
836	39.5	35.3	329	2	AAV05304	Aav05304 S. aureus	909	39	34.8	64	5	ABG39042	Abg39042 Human pep
837	39.5	35.3	329	6	ABM71215	Abm71215 Staphyloc	910	39	34.8	66	5	ABP35526	Abp35526 Human ORF
838	39.5	35.3	340	6	ABR47442	Ab47442 Breast ca	911	39	34.8	79	6	ABW73464	Abw73464 Staphyloc
839	39.5	35.3	344	8	ADJ35104	Adj35104 Xylanase	912	39	34.8	88	5	ABP34686	Abp34686 Human ORF
840	39.5	35.3	376	6	ABU07702	Abu07702 Viral coa	913	39	34.8	93	8	ADR34497	Adr34497 Novel S.
841	39.5	35.3	474	8	ADP74742	Adp74742 HIV-1 iso	914	39	34.8	100	8	ADL88961	Adl88961 Human mod
842	39.5	35.3	481	5	ABB91095	Abb91095 Herbicida	915	39	34.8	100	8	ADL88965	Adl88965 Human mod
843	39.5	35.3	483	4	AAAB67447	Aa67447 Amino ac1	916	39	34.8	100	8	ADL88956	Adl88956 Human mod
844	39.5	35.3	506	6	ABU07703	Abu07703 Viral coa	917	39	34.8	103	4	AAW33022	Aaw33022 Human pro
845	39.5	35.3	506	6	ABU07700	Abu07700 Viral coa	918	39	34.8	105	5	ABB54361	Abb54361 Lactococc
846	39.5	35.3	528	6	AAE39562	Aae39562 HIV gp120	919	39	34.8	107	4	ABR17941	Abbr17941 Human ner
847	39.5	35.3	528	8	ADK19375	Adk19375 HIV gp120	920	39	34.8	108	5	ABP07717	Abp07717 Human ORF
848	39.5	35.3	552	5	ABBS7060	Abbs7060 Mouse isc	921	39	34.8	119	7	ADB93780	Adb93780 Human sig
849	39.5	35.3	554	4	AAAB92446	Aa92446 Human pro	922	39	34.8	119	8	ADM24664	Adm24664 Novel hum
850	39.5	35.3	554	5	ABBS7251	Abbs7251 Novel hum	922	39	34.8	119	4	AAW43643	Aaw43643 Human pol
851	39.5	35.3	554	8	ADF89891	Adf89891 Human can	923	39	34.8	119	4	AAW87634	Aaw87634 Novel cen
852	39.5	35.3	556	6	ABU07696	Abu07696 Viral coa	924	39	34.8	119	4	ABR17239	Abbr17239 Human ner
853	39.5	35.3	578	7	AAE39560	Aae39560 HIV gp120	925	39	34.8	119	6	ABO27195	Abob27195 Human sig
854	39.5	35.3	579	2	AAW37068	Aaw37068 HIV-1 gp1	927	39	34.8	119	8	ADL54949	Adl54949 Novel hum
855	39.5	35.3	587	2	AAV29900	Aav29900 Human MDC	928	39	34.8	119	8	ADM24664	Adm24664 Human PRO
856	39.5	35.3	590	6	ABU07697	Abu07697 Viral coa	929	39	34.8	120	5	ABP00580	Abp00580 Human ORF
857	39.5	35.3	595	2	AAV29902	Aav29902 Human MCP	930	39	34.8	121	6	ABU21032	Abu21032 Protein e
858	39.5	35.3	601	2	AAV29901	Aav29901 Human IP-	931	39	34.8	122	2	AAE5908	Aae5908 Protein f
859	39.5	35.3	608	4	AAAB78888	Aab78888 C. glutam	932	39	34.8	122	3	AAAB35810	Aab35810 Rice chlo
860	39.5	35.3	608	4	AAAG89855	Aag89855 C. glutam	933	39	34.8	122	5	ABP60740	Abp60740 Oryza sac
861	39.5	35.3	618	7	ABR63526	Ab63526 C. glutam	934	39	34.8	122	7	ADOS9274	Ados9274 Rice thio
862	39.5	35.3	618	7	ADD13252	Ad13252 C. glutam	935	39	34.8	124	6	ABU45547	Abu45547 Protein e
863	39.5	35.3	618	7	ADL65915	Adl65915 C. glutam	936	39	34.8	137	1	AAV70101	Aav70101 Sequence
864	39.5	35.3	625	8	ADS30749	Ads30749 Bacteriel	937	39	34.8	147	4	AAAG1340	Aag1340 Human AFP
865	39.5	35.3	657	8	AAU33784	Aau33784 Staphyloc	938	39	34.8	147	6	ABW70029	Abw70029 Photorhab
866	39.5	35.3	662	3	AAAB08632	Aab08632 Amino ac1	939	39	34.8	151	4	ABE68804	Abbe68804 Drosophill
867	39.5	35.3	662	4	AAU36547	Aau36547 Staphyloc	940	39	34.8	151	5	ABU52093	Abu52093 Helicobac
868	39.5	35.3	662	6	ABU15918	Abu15918 Protein e	941	39	34.8	156	3	AAV82525	Aav82525 Human ade
869	39.5	35.3	662	6	ABU43213	Abu43213 Protein e	942	39	34.8	156	4	AAAB9865	Aab9865 Phycomit
870	39.5	35.3	662	6	ABM71307	Abm71307 Staphyloc	943	39	34.8	156	5	ADG79580	Adg79580 Human sec
871	39.5	35.3	669	6	ABU20985	Abu20985 Protein e	944	39	34.8	163	6	AAO26451	Aao26451 Human chl
872	39.5	35.3	687	6	ADA89613	Ada89613 Staphyloc	945	39	34.8	169	3	ABU16898	Abu16898 Protein e
873	39.5	35.3	720	6	ABU07694	Abu07694 Viral coa	946	39	34.8	170	7	ADH86871	Adh86871 Enterococ
874	39.5	35.3	720	6	ABU07695	Abu07695 Viral coa	947	39	34.8	171	6	ADA33496	Ada33496 Actinotoba
875	39.5	35.3	722	8	ADN22998	Adn22998 Bacteriel	948	39	34.8	182	4	ABBE1187	Abbe1187 Drosophill
876	39.5	35.3	722	2	AAAR1056	Aar1056 Acylamino	949	39	34.8	184	6	ABU62886	Abu62886 Rab-Famil
877	39.5	35.3	748	6	ABU20785	Abu20785 Protein e	950	39	34.8	184	7	ADE59010	Ades9010 Rat Prote
878	39.5	35.3	751	8	ADBS29971	Adbs29971 Bacteriel	951	39	34.8	184	7	ADBS29971	Adbs29971 Human pro
879	39.5	35.3	753	1	AAAP94265	Aap94265 Sequence	952	39	34.8	184	7	ADG31704	Adg31704 Human pro
880	39.5	35.3	844	5	AAE18308	Aae18308 Human Imm	953	39	34.8	184	8	ADOS5215	Ados5215 Human Rab
881	39.5	35.3	854	5	AAAM48950	Aam48950 HIV-1 sub	954	39	34.8	184	8	ABW80954	Abw80954 Tumour-as
882	39.5	35.3	855	2	AAAR4905	Aar4905 HIV-1 BA-	955	39	34.8	184	8	ADP23197	Adp23197 PRO polyp
883	39.5	35.3	855	2	AAW11581	Aaw11581 Human Imm	956	39	34.8	185	8	ADOC21857	Adoc21857 Human ves
884	39.5	35.3	855	2	AAW88113	Aaw88113 Env prote	957	39	34.8	187	5	ABPE69697	Abpe69697 Human pol
885	39.5	35.3	855	2	AAAB9351	Aab9351 HIV-1 non	958	39	34.8	187	5	ADG79480	Adg79480 Human sec
886	39.5	35.3	858	5	AAAM48951	Aam48951 HIV-1 sub	959	39	34.8	187	5	ADG79480	Adg79480 Human sec
887	39.5	35.3	950	4	ABBB60145	Abbb60145 Drosophill	960	39	34.8	187	6	AAO26450	Aao26450 Human chl
888	39.5	35.3	1330	7	ADBE1063	Adbe1063 Rat Prote	961	39	34.8	187	6	ADPM44585	Adpm44585 Novel hum
889	39.5	35.3	1332	7	ADPO9883	Adpo9883 CDKICP1 c	962	39	34.8	190	5	ABP73450	Abp73450 Candida a
890	39.5	35.3	14	3	AAV80978	Aav80978 Bovine 63	963	39	34.8	194	5	ADFP94728	Adfp94728 Hepatictis
891	39.5	35.3	14	3	ABUS8717	Abus8717 Bovine br	964	39	34.8	205	5	ABUS0891	Abus0891 Helicobac
892	39.5	35.3	14	8	ADQ94948	Adq94948 Bovine 63	965	39	34.8	208	4	AAU31549	Aau31549 Novel hum
893	39.5	35.3	46	1	AAAP80509	Aap80509 Polypept1	966	39	34.8	210	2	AAV31641	Aav31641 Human tra
894	39.5	35.3	46	1	AAO26454	Aao26454 Human chl	967	39	34.8	210	8	ADOC23725	Adoc23725 COP1 coat
895	39.5	35.3	48	6	AAO26465	Aao26465 Human chl	968	39	34.8	214	4	AAAM3569	Aam3569 Human pol
896	39.5	35.3	52	4	AAW92022	Aaw92022 Human dig	969	39	34.8	214	4	AAU87352	Aau87352 Novel cen
897	39.5	35.3	52	4	AAU20000	Aau20000 Human liv	970	39	34.8	214	8	ADIS4667	Adis4667 Novel hum
898	39.5	35.3	52	5	ABP40861	Abp40861 Human liv	971	39	34.8	214	8	ADM24550	Adm24550 Human PRO
899	39.5	35.3	52	7	ADJ14979	Adj14979 Human liv	972	39	34.8	215	4	ABBB63890	Abbb63890 Drosophill
900	39.5	35.3	64	4	AAAM17258	Aam17258 Peptide #	973	39	34.8	216	5	ABUS1709	Abus1709 Helicobac
901	39.5	35.3	64	4	ABBB6257	Abbb6257 Peptide #	974	39	34.8	230	3	AAV96099	Aav96099 Human ald

```
975 39 34.8 230 3 AAY90353 Aay90353 Human gly
976 39 34.8 230 4 AAB84681 Aab84681 Amino aci
977 39 34.8 230 5 ABP65425 Abp65425 Bifidobac
978 39 34.8 230 6 AAO26544 Aao26544 Human ald
979 39 34.8 238 6 ABU5159 Abu5159 Protein e
980 39 34.8 239 8 ADS42137 Adas42137 Bacterial
981 39 34.8 241 5 ABUS2152 Abus2152 Helicobac
982 39 34.8 242 2 AAR45020 Aar45020 Staphyloc
983 39 34.8 242 4 AAB67347 Aab67347 Staphyloc
984 39 34.8 242 5 ABB76243 Abb76243 Staphyloc
985 39 34.8 242 8 ABM83829 Abm83829 Human dia
986 39 34.8 244 4 AAG81950 Aag81950 S. epider
987 39 34.8 256 3 AAG42482 Aag42482 Arabidops
988 39 34.8 256 3 AAG44055 Aag44055 Arabidops
989 39 34.8 256 6 ABM69042 Abm69042 Photorhab
990 39 34.8 260 3 AAG42130 Aag42130 Arabidops
991 39 34.8 260 5 AAE16385 Aae16385 Human dec
992 39 34.8 260 6 AAO26448 Aao26448 Deoxycytl
993 39 34.8 260 6 AAO26449 Aao26449 Deoxycytl
994 39 34.8 260 6 AAO26446 Aao26446 Deoxycytl
995 39 34.8 260 6 AAO26447 Aao26447 Deoxycytl
996 39 34.8 260 6 ABU48008 Abu48008 Protein e
997 39 34.8 260 7 ADJ68602 Adj68602 Human hea
998 39 34.8 260 7 ADN95414 Adn95414 Human BEC
999 39 34.8 260 8 ADR73958 Adr73958 Human dec
1000 39 34.8 260 8 ADR73962 Adr73962 Human dec
```

## ALIGNMENTS

```
RESULT 1
AD195325
ID AD195325 standard; protein; 221 AA.
```

```
XX AD195325;
```

```
DT 04-NOV-2004 (first entry)
```

```
XX OSPF-related SARS coronavirus matrix protein.
```

```
XX immune response; overlapping synthetic peptide formulation; OSPF;
KM immunostimulant; virucide; antibacterial; antiparasitic; cytostatic;
KW vaccine; viral; bacterial; parasitic infection; prion disease;
KM neoplastic; toxin; matrix.
```

```
XX SARS coronavirus.
```

```
XX WO2004002415-A2.
```

```
XX 08-JAN-2004.
```

```
XX 27-JUN-2003; 2003WO-US020322.
```

```
XX 27-JUN-2002; 2002US-0392718P.
```

```
XX (DAND ) DANA FARBER CANCER INST INC.
```

```
XX Ruprecht RM, Jiang S;
```

```
XX WPI; 2004-082868/08.
```

```
XX Modulating an immune response, useful for treating immune disorders, e.g.,
PT viral, bacterial and parasitic infections, prion diseases, or neoplastic
PT diseases, administering to a subject an overlapping synthetic peptide
PT formulation.
```

```
XX Claim 13; SEQ ID NO 233; 175bp; English.
```

```
XX The invention relates to a novel method for modulating an immune response
CC comprising administering to a subject an overlapping synthetic peptide
CC formulation (OSPF) which comprises a combination of single chain peptides
CC corresponding to the amino acid sequence of a protein of interest. The
```

```
CC method of the invention has immunostimulant, virucide, antibacterial,
CC antiparasitic and cytostatic applications and may be useful during
CC vaccine production and for treating immune disorders including viral,
CC bacterial and parasitic infections, prion diseases, neoplastic diseases,
CC as well as providing protection against toxins. The current sequence is
CC that of the OSPF-related SARS coronavirus matrix protein of the
CC invention.
```

```
XX SQ Sequence 221 AA;
```

```
Query Match 100.0%; Score 112; DB 8; Length 221;
Best Local Similarity 100.0%; Pred.No.2.7e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MADNGTITVEELKQLLEQNNLV 22
1 MADNGTITVEELKQLLEQNNLV 22
Db 1 MADNGTITVEELKQLLEQNNLV 22
```

```
RESULT 2
ABM67171
ID ABM67171 standard; protein; 16368 AA.
```

```
XX ABM67171;
```

```
XX 20-NOV-2003 (first entry)
```

```
XX Photorhabdus luminescens protein sequence #268.
```

```
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KM detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; bioplastic; virulence factor; disease model; plague;
KM whooping cough.
```

```
XX Photorhabdus luminescens.
```

```
XX WO200294867-A2.
```

```
XX 28-NOV-2002.
```

```
XX 07-FEB-2002; 2002WO-1B003040.
```

```
XX 07-FEB-2001; 2001FR-00001659.
```

```
XX (INSP ) INST PASTEUR.
```

```
XX (CNRS ) CNRS CENT NAT RECH SCI.
```

```
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
```

```
XX Buchrieser C;
```

```
XX WPI; 2003-148459/14.
```

```
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
```

```
XX Claim 2; SEQ ID NO 268; 1205bp; French.
```

```
XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
```



```

XX Peptide#086 encoded by probe for measuring placental gene expression.
XX Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder.
XX Homo sapiens.
OS
PN WO200157272-A2.
PD
XX 09-AUG-2001.
PF
XX 30-JAN-2001; 2001WO-US000663.
PR 04-FEB-2000; 2000US--0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US--00608408.
PR 03-AUG-2000; 2000US--00632366.
PR 21-SEP-2000; 2000US--0234687P.
PR 27-SEP-2000; 2000US--0236359P.
PR 04-OCT-2000; 2000GB--00024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488897/53.
DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
PS Claim 27; SEQ ID NO 32318; 654bp; English.
XX The present invention relates to single exon nucleic acid probes (SENP;
CC see A13115-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders
SQ Sequence 54 AA;
Query Match 45.5%; Score 51; DB 4; Length 54;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0
QY      1 MADNGTIVEELKQLLEBOMLT 21
       : | ::||| | |||:
Db     23 LEDKKQVSVEAKNRABEQMNV 43
RESULT 6
ABB23710
ID ABB23710 standard; protein; 54 AA.
XX
AC ABB23710;
XX
DT 23-JAN-2002 (first entry)
XX
XX Protein #5709 encoded by probe for measuring heart cell gene expression.
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US--0180312P.

```

XX	PR	26-MAY-2000;	2000US-0207456P.
XX	PR	30-JUN-2000;	2000US-0060840B.
XX	PR	03-AUG-2000;	2000US-00632356.
XX	PR	21-SEP-2000;	2000US-0234687P.
XX	PR	27-SEP-2000;	2000US-0236359P.
XX	PR	04-OCT-2000;	2000GB-00024263.
PA	(MOLE-)	MOLECULAR DYNAMICS INC.	
XX	PT	Penn SG, Hanzel DK, Chen W, Rank DR;	
XX	DR	WPI; 2001-488899/53.	
XX	PT	Single exon nucleic acid probes for analyzing gene expression in human hearts.	
XX	PS	Claim 15; SEQ ID NO 25480; 530bp; English.	
XX	CC	The present invention relates to single exon nucleic acid probes for	
XX	CC	measuring human gene expression in a sample derived from human heart (see	
XX	CC	AB21555-ABA41305). The present sequence is a protein encoded by one such	
XX	CC	probe. The probe may be used for predicting, measuring and displaying	
XX	CC	gene expression in samples derived from the human heart via microarrays.	
XX	CC	By measuring gene expression, the probes are useful for predicting,	
XX	CC	diagnosing, grading, staging, monitoring and prognosing diseases of the	
XX	CC	human heart and vascular system e.g. cardiovascular disease,	
XX	CC	hypertension, cardiac arrhythmias and congenital heart disease. Note: The	
XX	CC	sequence data for this patent did not form part of the printed	
XX	CC	specification, but was obtained in electronic format directly from WIPO	
XX	CC	at ftp.wipo.int/pub/published_pct_sequences	
XX	Sequence	54 AA;	
QY	Query Match	45.5%; Score 51; DB 4; Length 54;	
DB	Best Local Similarity	42.9%; Pred. No. 15;	
	Matches	9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;	
	1	MADNGITVEELKOLEQNL 21	
	:	:::	
	23	LEDKROVSVEAKNRARQMN 43	
RESULT 7			
AA071757	ID	AA071757 standard; protein; 54 AA.	
AA071757;	AC		
06-NOV-2001	DT	(first entry)	
Human bone marrow expressed probe encoded protein SEQ ID NO: 32063.	DE		
Human; bone marrow expressed exon; gene expression analysis; probe;	KW		
microarray; cancer; leukaemia; lymphoma; myeloma.	XX		
Homo sapiens.	OS		
MO200157276-A2.	XX		
09-AUG-2001.	PD		
30-JAN-2001; 2001WO-US000668.	PF		
04-FEB-2000; 2000US-0180312P.	PR		
26-MAY-2000; 2000US-0207456P.	PR		
30-JUN-2000; 2000US-0060840B.	PR		
03-AUG-2000; 2000US-00632356.	PR		
21-SEP-2000; 2000US-0234687P.	PR		
27-SEP-2000; 2000US-0236359P.	PR		
04-OCT-2000; 2000GB-00024263.	PR		
(MOLE-)	PA	MOLECULAR DYNAMICS INC.	

XX	PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	DR	WPI; 2001-488900/53.
XX	PT	Human genome-derived single exon nucleic acid probes useful for analyzing
XX	PT	gene expression in human bone marrow.
XX	PS	Example 4; SEQ ID NO 32063; 658bp + Sequence Listing; English.
XX	CC	The present invention provides a number of single exon nucleic acid
XX	CC	probes which are derived from genomic sequences expressed in the human
XX	CC	bone marrow. They can be used to measure gene expression in bone marrow
XX	CC	samples, which may enable the improved diagnosis and treatment of cancers
XX	CC	such as lymphoma, leukemia and myeloma. The present sequence is a
XX	CC	protein encoded by one of the probes of the invention
SO		Sequence 54 AA;
OY		Query Match 45.5%; Score 51; DB 4; Length 54;
		Best Local Similarity 42.9%; Pred. NO. 15;
Db		Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0
		1 MADNGTIVEELKQULEQWNL 21
		23 LEDKROVSVEEAKRAEQMNV 43
RESULT 8		
AAM59222	ID	AAM59222 standard; protein; 54 AA.
XX	AC	AAM59222;
XX	DT	05-NOV-2001 (first entry)
DE		Human brain expressed single exon probe encoded protein SEQ ID NO: 31327.
XX	XX	Human; brain expressed exon; gene expression analysis; probe; microarray;
XX	KM	Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
OS		Homo sapiens.
XX		WO200157275-A2.
XX		09-AUG-2001.
XX		30-JAN-2001; 2001WO-US000667.
XX		04-FEB-2000; 2000US-0180312P.
XX		26-MAY-2000; 2000US-0207456P.
XX		30-JUN-2000; 2000US-00608408.
XX		03-AUG-2000; 2000US-00632366.
XX		21-SEP-2000; 2000US-0234687P.
XX		27-SEP-2000; 2000US-0236359P.
XX		04-OCT-2000; 2000GB-00024263.
XX		(MOLE-) MOLECULAR DYNAMICS INC.
XX		Penn SG, Hanzel DK, Chen W, Rank DR;
XX		WPI; 2001-483446/52.
XX		Single exon nucleic acid probes for analyzing gene expression in human
XX		brain.
XX		Example 4; SEQ ID NO 31327; 650bp + Sequence Listing; English.
XX		The present invention provides a number of single exon nucleic acid
XX		probes which are derived from genomic sequences expressed in the human
XX		brain. They can be used to measure gene expression in brain cell samples,
XX		which may enable the diagnosis and improved treatment of nervous system
XX		diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX		epilepsy and cancer. The present sequence is a protein encoded by one of

CC	the probes of the invention
XX	
SQ	Sequence 54 AA;
Query Match	45.5%; Score 51; DB 4; Length 54;
Best Local Similarity	42.9%; Pred.No. 15;
Matches	9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
DG	1 MADNGTTVEELKQLLEQWNL 21 ::                  :
Db	23 LEDRKGVSVBEAKRRAEQMNV 43
RESULT 9	
ABG53442	
ID	ABG53442 standard; peptide; 54 AA.
XX	
AC	ABG53442;
XX	
DT	25-FEB-2003 (first entry)
XX	
DE	Human liver peptide, SEQ ID NO 32090.
XX	
KM	Human; liver: cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
XX	
OS	Homo sapiens.
PX	WO200157273-A2.
PN	
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US000664.
PE	
PR	04-FEB-2000; 2000US-0180312P. 26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-00608408. PR 03-AUG-2000; 2000US-0063236P. PR 21-SEP-2000; 2000US-0234687P. PR 27-SEP-2000; 2000US-0236359P. PR 04-OCT-2000; 2000GB-00024263.
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
P1	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-488898/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
XX	
PS	Claim 27; SEQ ID NO 32090; 658bp; English.
CC	
XX	The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at <a href="http://wipo.int/pub/published_pct_sequences">ftp.wipo.int/pub/published_pct_sequences</a>
CC	
XX	
SQ	Sequence 54 AA;
Query Match	45.5%; Score 51; DB 4; Length 54;
Best Local Similarity	42.9%; Pred.No. 15;
Matches	9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY	I	MADNGRTTVELKQLEQNTL	21
DB	23	LEDRQVSVSEAKRAEOMNV	43
RESULT 10			
ABG41571			
ID	ABG41571	standard; peptide; 54 AA.	
XX	ABG41571;		
AC	19-AUG-2002	(first entry)	
XX			
DE	Human peptide encoded by genome-derived single exon probe SEQ ID 31236.		
XX			
KW	Human; single exon probe; asthma; lung cancer; COPD; ILD;		
KW	chronic obstructive pulmonary disease; interstitial lung disease;		
KW	familial idiopathic pulmonary fibrosis; neurofibromatosis;		
KW	tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;		
KW	Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;		
KW	pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome;		
KW	pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;		
KW	primary ciliary dyskinesia; pulmonary hypertension;		
KW	hyaline membrane disease.		
XX			
OS	Homo sapiens.		
XX			
PN	MO200186003-A2.		
XX			
PD	15-NOV-2001.		
XX			
PF	30-JAN-2001; 2001MO-US000665.		
XX			
PR	04-FEB-2000; 2000US-0180312P.		
PR	26-MAY-2000; 2000US-0207456P.		
PR	30-JUN-2000; 2000US-00608408.		
PR	03-AUG-2000; 2000US-00632366.		
PR	21-SEP-2000; 2000US-0234687P.		
PR	27-SEP-2000; 2000US-0236359P.		
PR	04-OCT-2000; 2000GB-00024263.		
XX			
PA	(MOLE-) MOLECULAR DYNAMICS INC.		
XX			
PI	Penn SG, Hanzel DK, Chen W, Rank DR;		
XX			
DR	WPI; 2002-114183/15.		
XX			
PT	Spatially-addressable set of single exon nucleic acid probes, used to		
XX	measure gene expression in human lung samples.		
XX			
PS	Claim 27; SEQ ID NO 31236; 634pp; English.		
XX			
CC	The invention relates to a spatially-addressable set of single exon		
CC	nucleic acid probes for measuring gene expression in a sample derived		
CC	from human lung comprising single exon nucleic acid probes having one of		
CC	12614 nucleic acid sequences mentioned in the specification, or their		
CC	complements or the 12387 open reading frames derived from the 12614		
CC	probes. Also included are a microarray comprising the novel set of probes		
CC	; the novel set of probes which hybridise at high stringency to a nucleic		
CC	acid expressed in the human lung; measuring gene expression in a sample		
CC	derived from human lung, comprising (a) contacting the array with a		
CC	collection of detectably labeled nucleic acids derived from human lung		
CC	mRNA, and (b) measuring the label detectably bound to each probe of the		
CC	array; identifying exons in a eukaryotic genome, comprising (a)		
CC	algorithmically predicting at least one exon from genomic sequences of		
CC	the eukaryotic acids; and (b) detecting specific hybridisation of detectably		
CC	labeled nucleic acids from eukaryotic lung mRNA, to a single exon probe,		
CC	having a fragment identical to the predicted exon, the probe is included		
CC	in the above mentioned microarray; assigning exons to a single gene,		
CC	comprising (a) identifying exons from genomic sequence by the method		
CC	above and (b) measuring the expression of each of the exons in several		
CC	tissues and/or cell types using hybridisation to a single exon		

CC	microarrays having a probe with the exon, where a common pattern of
CC	expression of the exons in the tissues and/or cell types indicates that
CC	the exons should be assigned to a single gene; a peptide comprising one
CC	of 12011 sequences, mentioned in the specification, or encoded by the
CC	probes/open reading frames (ORF). The probes are used for gene expression
CC	analysis and for identifying exons in a gene, particularly using human
CC	lung derived mRNA and for the study of lung diseases such as asthma, lung
CC	cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC	disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC	tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC	Pulak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC	histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC	Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC	dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC	present sequence is a peptide/protein encoded by a single exon probe of
CC	the invention. Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic format
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 54 AA;
XX	
XX	Query Match 45.5%; Score 51; DB 5; Length 54;
XX	Best Local Similarity 42.9%; Pred. No. 15;
XX	Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY	1 MADNGTTFVEELKQLLEQWNL 21
DB	:   ::
DB	23 LEDRKQVSVVEAKRRAEQWNV 43
RESULT 11	
ABU03494	ABU03494 standard; protein; 206 AA.
XX	
XX	ABU03494;
XX	
XX	21-JAN-2003 (first entry)
DE	Angiogenesis-associated human protein sequence #39.
XX	
XX	Human; angiogenesis-associated transcript; angiogenesis;
KW	angiogenesis-associated disease; cancer; cyrostatic.
OS	
XX	Homo sapiens.
XX	
XX	WO200279492-A2.
XX	
XX	10-OCT-2002.
XX	
XX	14-FEB-2002; 2002WO-US004915.
XX	
XX	14-FEB-2001; 2001US-00784356.
XX	22-FEB-2001; 2001US-00791390.
XX	19-APR-2001; 2001US-0285475P.
XX	03-AUG-2001; 2001US-0310025P.
XX	13-NOV-2001; 2001US-0350666P.
XX	29-NOV-2001; 2001US-0334244P.
XX	
XX	(EOSB-) EOS BIOTECHNOLOGY INC.
XX	
XX	Murray R, Glynn R, Watson SR, Aziz N;
XX	
XX	WPI; 2003-040681/03.
XX	
XX	N-PSDB; ABX08778.
XX	
XX	Detecting angiogenesis-associated transcript in a cell for diagnosing and
XX	treating cancer by contacting a sample with a polynucleotide that
XX	exhibits changes in expression level as a function of time in tissue
XX	undergoing angiogenesis.
XX	
XX	Example 2; Page 217; 291pp; English.
XX	
XX	The present invention relates to methods and compositions for detecting







DT 02-DEC-2004 (first entry)  
 XX POSH protein associated protein #53.  
 XX  
 XX cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant;  
 KW antiviral; neuroleptic; central nervous system; POSH polypeptide;  
 KW POSH-associated protein; POSH-AP; HERPDL; ubiquitin ligase;  
 KW antiviral agent; anti-apoptotic agent; anti-cancer agent;  
 KW secretory pathway trafficking inhibitor;  
 KW neurological disorder progression disorder; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; schizophrenia;  
 KW Niemann-Pick's disease.  
 XX Homo sapiens.  
 XX MO2004078130-A2.  
 XX  
 PD 16-SEP-2004.  
 XX  
 PF 02-MAR-2004; 2004WO-US006308.  
 XX  
 XX 03-MAR-2003; 2003US-0451437P.  
 PR 05-MAR-2003; 2003US-0452284P.  
 PR 19-MAR-2003; 2003US-0455760P.  
 PR 20-MAR-2003; 2003US-0456640P.  
 PR 03-APR-2003; 2003US-0460526P.  
 PR 04-APR-2003; 2003US-0460792P.  
 PR 21-APR-2003; 2003US-0464285P.  
 PR 09-MAY-2003; 2003US-0469462P.  
 PR 15-MAY-2003; 2003US-0471378P.  
 PR 20-MAY-2003; 2003US-0472327P.  
 PR 30-MAY-2003; 2003US-0474706P.  
 PR 03-JUN-2003; 2003US-0475825P.  
 PR 17-JUN-2003; 2003US-0479317P.  
 PR 19-JUN-2003; 2003US-0480215P.  
 PR 19-JUN-2003; 2003US-0480376P.  
 PR 08-AUG-2003; 2003US-0493860P.  
 PR 28-AUG-2003; 2003US-0498634P.  
 PR 16-SEP-2003; 2003US-0503931P.  
 PR 10-NOV-2003; 2003WO-US035712.  
 PR 05-FEB-2004; 2004WO-US003600.  
 PR 02-MAR-2004; 2004US-0549896P.  
 XX  
 XX (PROT-) PROTEOLOGICS INC.  
 XX  
 XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;  
 PI Greener T;  
 XX  
 DR WPI; 2004-662346/64.  
 XX  
 PT Isolated, purified or recombinant complex, useful for identifying an  
 PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and  
 PT POSH-associated protein (POSH-AP).  
 XX  
 XX Disclosure; SEQ ID NO 253; 374pp; English.  
 XX  
 XX The invention relates to an isolated, purified or recombinant complex (1)  
 CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)  
 CC or HERPDL and a ubiquitin ligase (b). Methods using (1), (a) or (b) are  
 CC useful for identifying an agent that modulates an activity of a POSH  
 CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-  
 CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking  
 CC of a protein through the secretory pathway, an agent that inhibits the  
 CC progression of a neurological disorder, an agent that modulates a POSH  
 CC function, an agent that modulates a HERPDL function. The methods can be  
 CC used for treating a viral infection, for inhibiting an activity of a POSH  
 CC -AP in a cell, for treating a POSH-associated disease in a subject. The  
 CC POSH-associated disease is viral infection, POSH-associated cancer or  
 CC POSH-associated neurological disorder. The methods are useful for  
 CC treating or preventing POSH-associated neurological disorder in a subject  
 CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,  
 CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a  
 CC protein of the invention.

XX SQ Sequence 206 AA;  
 XX  
 XX Query Match 45.5%; Score 51; DB 8; Length 206;  
 XX Best Local Similarity 42.9%; Pred. No. 61;  
 XX Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 XX  
 XX 1 MADNGTITVEELKQLEONNL 21  
 XX :|||:|||||:  
 XX Db 131 LEDKQVSVBEAKNRALQNNV 151  
 XX  
 XX RESULT 17  
 XX ADD14139  
 XX ID ADD14139 standard; protein; 209 AA.  
 XX  
 XX ADD14139;  
 XX  
 XX 01-JAN-2004 (first entry)  
 XX  
 XX Human src biomarker polypeptide SEQ ID NO:328.  
 XX  
 XX predictor set; protein tyrosine kinase activity modulator;  
 KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;  
 KW gene therapy; drug sensitivity; genetic profile; cancer; human.  
 XX  
 XX Homo sapiens.  
 XX  
 XX MO2003062395-A2.  
 XX  
 XX 31-JUL-2003.  
 XX  
 XX 17-JAN-2003; 2003WO-US001981.  
 XX  
 XX 18-JAN-2002; 2002US-0350061P.  
 XX  
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.  
 XX  
 XX Huang F, Fairchild CR, Lee FY, Shaw P;  
 PI WPI; 2003-636735/60.  
 DR N-PSDB; ADD14741.  
 XX  
 XX New polynucleotides and polypeptides for predicting the activity of  
 PT compounds that interact with protein tyrosine kinases and/or protein  
 PT tyrosine kinase pathways.  
 XX  
 XX Claim 10; SEQ ID NO 328; 139pp; English.  
 XX  
 XX The present invention describes a predictor set comprising a plurality of  
 CC polynucleotides or polypeptides whose expression pattern is predictive of  
 CC the response of cells to treatment with a compound that modulates protein  
 CC tyrosine kinase activity or members of the protein tyrosine kinase  
 CC pathway. Also described: (1) predicting whether a compound is capable of  
 CC modulating the activity of cells, comprising obtaining a sample of cells,  
 CC determining whether the cells express a plurality of markers, and  
 CC correlating the expression of the markers to the compound's ability to  
 CC modulate the activity of the cells; (2) a plurality of cell lines for  
 CC identifying polynucleotides and polypeptides whose expression levels  
 CC correlate with compound sensitivity or resistance of cells associated  
 CC with a disease state; and (3) identifying polynucleotides and  
 CC polypeptides that predict compound sensitivity or resistance of cells  
 CC associated with a disease state, comprising subjecting the plurality of  
 CC cell lines to one or more compounds, analysing the expression pattern of  
 CC a microarray of polynucleotides or polypeptides, and selecting  
 CC polynucleotides or polypeptides that predict the sensitivity or  
 CC resistance of cells associated with a disease state by using the  
 CC expression pattern of the microarray. The polynucleotides and  
 CC polypeptides have cytostatic activities, and can be used in gene therapy.  
 CC The polynucleotides and polypeptides are useful in predicting the  
 CC activity of compounds that interact with protein tyrosine kinases and/or  
 CC protein tyrosine kinase pathways. These may be used in determining drug  
 CC sensitivity in patients to allow the development of individualized

CC genetic profiles which aid in treating diseases and disorders (e.g.  
CC cancer) based on patient response at a molecular level. The present  
CC sequence is used in the exemplification of the present invention.  
XX

SO Sequence 209 AA;

Query Match 45.5%; Score 51; DB 7; Length 209;  
Best Local Similarity 42.9%; Pred. No. 62;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQWNL 21  
DB 134 LEDKQVSYBEAKNRABQMN 154

RESULT 18  
ADP24705  
ID ADP24705 standard; protein; 209 AA.

XX ADP24705;

DT 18-NOV-2004 (first entry)

XX PRO polypeptide SEQ ID NO:1883.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;  
XX osteopathic; antidiabetic; dermatological; antiporiatic; antiallergic;  
XX antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

OS Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH ) GENENTECH INC.

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

XX WI ID;

XX WPI; 2004-419628/39.

XX N-PSDB; ADP24704.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
XX renal disease, or demyelinating diseases of the central or peripheral  
XX nervous system.

XX Claim 7; SEQ ID NO 1883; 2940bp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO  
XX polypeptide encoded by it. A protein of the invention has  
XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
XX osteopathic, antidiabetic, dermatological, antiporiatic, antiallergic,  
XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
XX of the invention may have a use in gene therapy. The PRO polypeptide, its  
XX agonist, antagonist, or antibody that specifically binds to the  
XX polypeptide is useful for treating an immune related disorder such as  
XX systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,  
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
XX disease, a demyelinating disease of the central or peripheral nervous  
XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
XX disease, infectious or autoimmune chronic active hepatitis, primary  
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
CC hypersensitivity, urticaria, an immunologic disease of the lung,  
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence represents a PRO protein  
CC of the invention.

SO Sequence 209 AA;

Query Match 45.5%; Score 51; DB 8; Length 209;  
Best Local Similarity 42.9%; Pred. No. 62;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQWNL 21  
DB 134 LEDKQVSYBEAKNRABQMN 154

RESULT 19  
ADS34490  
ID ADS34490 standard; protein; 209 AA.

XX ADS34490;

DT 02-DEC-2004 (first entry)

XX POSH protein associated protein #54.

XX cyostatic; noctropic; neuroprotective; antiparkinsonian; anticonvulsant;  
XX antiviral; neuroleptic; central nervous system; POSH polypeptide;  
XX POSH-associated protein; POSH-AP; HERPUD1; Ubiquitin ligase;  
XX antiviral agent; anti-apoptotic agent; anti-cancer agent;  
XX secretory pathway trafficking inhibitor;  
XX neurological disorder progression disorder; Alzheimer's disease;  
XX Parkinson's disease; Huntington's disease; schizophrenia;  
XX Niemann-Pick's disease.

XX Homo sapiens.

XX PN WO2004078130-A2.

XX 16-SEP-2004.

XX 02-MAR-2004; 2004WO-US006308.

XX 03-MAR-2003; 2003US-0451437P.

XX 05-MAR-2003; 2003US-0452284P.

XX 19-MAR-2003; 2003US-0455760P.

XX 20-MAR-2003; 2003US-0456640P.

XX 03-APR-2003; 2003US-0460526P.

XX 21-APR-2003; 2003US-0460792P.

XX 09-MAY-2003; 2003US-0469482P.

XX 15-MAY-2003; 2003US-0471378P.

XX 20-MAY-2003; 2003US-0472327P.

XX 30-MAY-2003; 2003US-0474706P.

XX 03-JUN-2003; 2003US-0475825P.

XX 17-JUN-2003; 2003US-0479317P.

XX 19-JUN-2003; 2003US-0480215P.

XX 19-JUN-2003; 2003US-0480376P.

XX 08-AUG-2003; 2003US-0493860P.

XX 28-AUG-2003; 2003US-0498634P.

XX 16-SEP-2003; 2003US-0503931P.

XX 10-NOV-2003; 2003WO-US035712.

XX 05-FEB-2004; 2004WO-US003600.

XX 02-MAR-2004; 2004US-0549896P.

XX (PROT-) PROTEOLOGICS INC.

XX Taglicht DN, Alroy I, Reies Y, Yaar L, Ben-Avraham D, Tuvia S;

XX Greener T;

XX WPI; 2004-662346/64.  
DR Isolated, purified or recombinant complex, useful for identifying an  
XX antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and  
PT POSH-associated protein (POSH-AP).  
XX  
PS Disclosure; SEQ ID NO 254; 374pp; English.  
XX  
XX The invention relates to an isolated, purified or recombinant complex (1)  
CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)  
CC or HERPUD1 and a ubiquitin ligase (b). Methods using (1), (a) or (b) are  
CC useful for identifying an agent that modulates an activity of a POSH  
CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-  
CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking  
CC of a protein through the secretory pathway, an agent that inhibits the  
CC progression of a neurological disorder, an agent that modulates a POSH  
CC function, an agent that modulates a HERPUD1 function. The methods can be  
CC used for treating a viral infection, for inhibiting an activity of a POSH  
CC -AP in a cell, for treating a POSH-associated disease in a subject. The  
CC POSH-associated disease is viral infection, POSH-associated cancer or  
CC POSH-associated neurological disorder. The methods are useful for  
CC treating or preventing POSH-associated neurological disorder in a subject  
CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,  
CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a  
CC protein of the invention.  
XX  
SQ Sequence 209 AA;  
XX  
Query Match 45.5%; Score 51; DB 8; Length 209;  
Best Local Similarity 42.9%; Pred. No. 62;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MADNGTITVEBELKQLLEQNL 21  
DB 134 LEDKQVSVBEAKNRAEQNMV 154  
XX  
RESULT 20  
MAU31548  
ID MAU31548 standard; protein; 246 AA.  
XX  
AC MAU31548;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Novel human secreted protein #2039.  
XX  
KW Human; vaccination; gene therapy; nutritional supplement;  
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN MO200179449-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 16-APR-2001; 2001WO-US008656.  
XX  
PR 18-APR-2000; 2000US-00552929.  
XX  
PR 26-JAN-2001; 2001US-00770160.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI; 2001-611725/70.  
XX  
PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
XX vaccination, testing and therapy.  
XX  
PS Claim 20; Page 457; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The  
CC polypeptides and antibodies to the polypeptides are useful for  
CC determining the presence of or predisposition to a disease associated  
CC with altered levels of polypeptide. The polypeptides are also useful for  
CC identifying agents (agonists and antagonists) that bind to them. Cells  
CC expressing the proteins are useful for identifying a therapeutic agent  
CC for use in treatment of a pathology related to aberrant expression or  
CC physiological interactions of the polypeptide. Vectors comprising the  
CC nucleic acids encoding the polypeptides and cells genetically engineered  
CC to express them are also useful for producing the proteins. The proteins  
CC are useful in genetic vaccination, testing and therapy, and can be used  
CC as nutritional supplements. They may be used to increase stem cell  
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon  
CC and/or nerve tissue growth or regeneration; immune suppression and/or  
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.  
CC MAU2510-MAU3304 represent the amino acid sequences of novel human  
CC secreted proteins of the invention  
XX  
SQ Sequence 246 AA;  
XX  
Query Match 45.5%; Score 51; DB 4; Length 246;  
Best Local Similarity 42.9%; Pred. No. 74;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MADNGTITVEBELKQLLEQNL 21  
DB 136 LEDKQVSVBEAKNRAEQNMV 156  
XX  
RESULT 21  
ABU23669  
ID ABU23669 standard; protein; 351 AA.  
XX  
AC ABU23669;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by prokaryotic essential gene #9196.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Clostridium acetobutylicum.  
XX  
PN MO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
XX  
PR 06-SEP-2001; 2001US-00948993.  
XX  
PR 25-OCT-2001; 2001US-0342923P.  
XX  
PR 08-FEB-2002; 2002US-00072851.  
XX  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KU, Zyekind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR N-PSDB; ACA27539.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 51593; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SO Sequence 351 AA;

Query Match 45.5%; Score 51; DB 6; Length 351;  
 Best Local Similarity 42.1%; Pred. No. 1.1e+02;  
 Matches 8; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTTTVEELKQLLEQNNLV 22  
 ||:|||||:|:|:  
 DB 132 NGELISIELKQWMDASNIY 150

RESULT 22

AAW68488  
 ID AAW68488 standard; protein; 572 AA.

AC AAW68488;

DT 08-DEC-1998 (first entry)

XX Mouse UIIP-4 protein.

XX Mouse; Unc-33-like phospho-protein; UIIP; rat; neoplasm; tumorigenesis;  
 XX neurodegenerative disorder; diagnosis.

OS Mus musculus.

PN FR2759701-A1.

PD 21-AUG-1998.

PF 19-FEB-1997; 97FR-00001961.

PR 19-FEB-1997; 97FR-00001961.

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PI Aguera M, Belin MF, Hommorat J, Kolatukudy P, Quach TT, Byk T;  
 PI Sobel A;

XX WPI; 1998-449610/39.

DR N-PSDB; AAW60817.

XX Mouse and human UIIP poly:peptide(s) - useful in detection of para-  
 PT neoplastic neurological syndromes.

XX Claim 1; Fig 11; 90pp; French.

PS This sequence represents the mouse unc-33-like phospho-protein (UIIP)-4.  
 CC The coding sequence was isolated based on similarity to the rat UIIP  
 CC sequence. Proteins of the UIIP family or their corresponding nucleic  
 CC acids can be used in compositions for treating neurodegenerative  
 CC disorders and neoplasms, especially for para-neoplastic neurological  
 CC syndromes and/or for the early diagnosis of tumorigenesis

SO Sequence 572 AA;

Query Match 45.5%; Score 51; DB 2; Length 572;  
 Best Local Similarity 64.7%; Pred. No. 1.8e+02;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ADNGTTTVEELKQLLEQ 18  
 ||:|||||:|:|:  
 DB 199 AENGDIIVEEQKRLLEQ 215

RESULT 23

ID ADG33790  
 ADG33790 standard; protein; 469 AA.

AC ADG33790;

DT 26-FEB-2004 (first entry)

DE Actinomycetes dual condensation/epimerisation NRPS domain protein ID 49.

XX non-ribosomal peptide synthetase; NRPS; dual condensation; epimerisation;  
 XX ramoplanin; complestatin; actinomycetes taxon.

OS Pseudomonas syringae pv. syringae.

PN WO2003089641-A2.

PD 30-OCT-2003.

PF 17-APR-2003; 2003WO-CA000575.

PR 17-APR-2002; 2002US-0372790P.

PA (ECOP-) ECOPIA BIOSCIENCES INC.

PI Farnet CM, Scaffa A;

XX WPI; 2003-854123/79.

DR N-PSDB; ADG33791.

PT New dual condensation/epimerization non-ribosomal peptide synthetase  
 PT domain and encoding polynucleotide, useful for modifying the  
 PT stereochemistry of synthesized peptides (e.g. ramoplanin or complestatin)  
 PT in vitro or in vivo.

PS Claim 9; SEQ ID NO 49; 245pp; English.

XX This invention relates to novel domains of non-ribosomal peptide  
 CC synthetases (NRPSs) that exhibit dual condensation and epimerisation  
 CC activities. Specifically, these domains allow incorporation of non-  
 CC proteinogenic substrates (e.g. D-amino acids) into peptide products.  
 CC Furthermore, they can be used in vivo to modify the stereochemistry of  
 CC synthesised peptides (e.g. ramoplanin or complestatin) at selected amino  
 CC acid sites by the addition of non-chiral residues. The present invention  
 CC describes the identification of isolated polynucleotide NRPS domains in  
 CC various organisms from the actinomycetes taxon, and the encoded  
 CC polypeptides thereof, as well as suitable expression vectors. This  
 CC polypeptide sequence is a dual condensation/ epimerisation NRPS domain  
 CC protein of the invention.

SO Sequence 469 AA;

Query Match 44.6%; Score 50; DB 7; Length 469;  
Best Local Similarity 64.3%; Pred. No. 2e+02;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 ITVEELKOLLEQWN 20  
: | | | | | | | | | |  
Db 432 LPLNERKOLLEQWN 445

## RESULT 24

ABU48797  
ID ABU48797 standard; protein; 673 AA.

XX  
XX  
AC ABU48797;

XX  
XX  
DT 19-JUN-2003 (first entry)

XX  
XX  
DE Protein encoded by Prokaryotic essential gene #34324.

XX  
XX  
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX  
XX  
OS Ureaplasma urealyticum.

XX  
XX  
PN WO200277183-A2.

XX  
XX  
PD 03-OCT-2002.

XX  
XX  
PF 21-MAR-2002; 2002WO-US009107.

XX  
XX  
PR 21-MAR-2001; 2001US-00815242.

XX  
XX  
PR 06-SEP-2001; 2001US-00948993.

XX  
XX  
PR 25-OCT-2001; 2001US-0342923P.

XX  
XX  
PR 08-FEB-2002; 2002US-00072851.

XX  
XX  
PR 06-MAR-2002; 2002US-0362699P.

XX  
XX  
PA (ELIT-) ELITRA PHARM INC.

XX  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX  
XX  
DR N-PSDB; ACAS2667.

XX  
XX  
PS WPI; 2003-029926/02.

XX  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

XX  
XX  
PS Claim 25; SEQ ID NO 76721; 1766bp; English.

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-regulated gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
XX  
SQ Sequence 673 AA;

Query Match 44.6%; Score 50; DB 6; Length 673;  
Best Local Similarity 66.7%; Pred. No. 3e+02;  
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEELKOLLEQWN 20  
: | | | | | | | | | |  
Db 8 IDELKOLLEQWN 19

## RESULT 25

AAB32530  
ID AAB32530 standard; protein; 123 AA.

XX  
XX  
AC AAB32530;

XX  
XX  
DT 19-JAN-2001 (first entry)

XX  
XX  
DE *S. lavendulae* MmcQ encoded protein sequence.

XX  
XX  
KM Mitomycin; biosynthesis; mitosome ring system; antibiotic; anti-cancer;

XX  
XX  
KM anti-inflammatory; immune-enhancer; immunosuppressant; asthma;

XX  
XX  
KM chronic obstructive pulmonary disease; respiratory inflammation;

XX  
XX  
KM fungicide; pesticide.

XX  
XX  
OS Streptomyces lavendulae.

XX  
XX  
PN WO200053737-A2.

XX  
XX  
PD 14-SEP-2000.

XX  
XX  
PF 10-MAR-2000; 2000WO-US006394.

XX  
XX  
PR 12-MAR-1999; 99US-00266965.

XX  
XX  
PA (MINU) UNIV MINNESOTA.

XX  
XX  
PA (SHER) SHERMAN D H.

XX  
XX  
PA (MAOY) MAO Y.

XX  
XX  
PA (VARO) VAROGU M.

XX  
XX  
PA (HEMM) HE M.

XX  
XX  
PA (SHEL) SHELTON P C.

XX  
XX  
PI Sherman DH, Mao Y, Varoglu M, He M, Sheldon PC;

XX  
XX  
DR N-PSDB; AAC55831.

XX  
XX  
PS WPI; 2000-601980/57.

XX  
XX  
PT Novel nucleic acid molecule comprising mitomycin biosynthetic gene  
PT cluster useful for cloning mitomycin biosynthetic genes for elucidating  
PT the molecular basis of mitosome ring system biosynthesis.

XX  
XX  
PS Disclosure; Page 382; 399pp; English.

CC This invention relates to isolated and purified nucleic acid molecules  
CC from the mitomycin biosynthetic gene cluster. Mitomycins are a group of  
CC natural products that contain a variety of functional groups, including  
CC amino benzoguanone and axiridine ring systems. The *S. lavendulae*  
CC mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning  
CC 55kb of DNA. The invention includes an expression cassette comprising a  
CC mitomycin biosynthetic gene operably linked to a promoter, and host cells  
CC transformed with the cassette. The nucleotide, and protein sequences and  
CC the transformed host cells of the invention result in antitastmatic,  
CC antiinflammatory, cytostatic, immunomodulatory, and antibiotic  
CC activities. The nucleotide sequences are used to elucidate the molecular

CC basis for the biosynthesis of the mitosome ring system, as well as to  
CC engineer the biosynthesis of novel natural products, e.g. antibiotics,  
CC anti-inflammatory agents, anti-cancer agents, immune-enhancers,  
CC immunosuppressants, agents to treat asthma, chronic obstructive pulmonary  
CC disease as well as other disease involving respiratory inflammation, or  
CC cholesterol-lowering agents or as crop protection agents (e.g. fungicides  
CC or insecticides) as well as biopolymers, e.g., in packaging or biomedical  
CC applications, or to engineer PHA monomer synthases. Sequences AAC55782-  
CC C55881, AAC55815-C55849 and AAB32485-832542 represent mitomycin  
CC biosynthetic gene cluster DNA sequences and encoded proteins. Sequences  
CC AAC55812-C55814, AAC55850-C55856 and AAC55862-C55863 represent PCR  
CC primers used in the cloning of the mitomycin biosynthetic genes  
XX

Sequence 123 AA:

Query Match 43.8%; Score 49; DB 3; Length 123;  
Best Local Similarity 57.1%; Pred. No. 67;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NGTIVBELKQLE 17  
|||:||||:|  
Db 86 NGTVPVELREMYE 99

RESULT 26  
ADE10302  
ID ADE10302 standard; protein; 123 AA.  
XX  
AC ADE10302;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE S. lavendulae mitomycin biosynthetic protein MmcQ.  
XX

KM Mitomycin biosynthetic protein; mitomycin C; antibiotic; MC; apoptosis;  
KW tumour hypoxia; cytosol; anti-tumour agent; cancer.  
XX  
OS Streptomyces lavendulae.  
XX  
PN US2003134398-A1.  
XX  
PD 17-JUL-2003.  
XX  
PF 12-SEP-2001; 2001US-00953348.  
XX  
PR 12-SEP-2001; 2001US-00953348.

PA (SHER/) SHERMAN D H.  
PA (MAOY/) MAO Y.  
PA (VARO/) VAROGILU M.  
PA (HEMM/) HE M.  
PA (SHEL/) SHELDON P.  
XX

PI Sherman DH, Mao Y, Varoglu M, He M, Sheldon P;  
XX  
XX WPI: 2003-863498/80.  
DR N-PSDB; ADE10250.  
XX

PT New nucleic acid molecule comprising a sequence having mitomycin  
XX  
XX biosynthetic gene cluster, useful for enhancing production of  
XX  
XX antibiotics.  
XX

Disclousure; SEQ ID NO 132; 308bp; English.

CC The invention relates to an isolated and purified nucleic acid molecule  
CC comprising a sequence having mitomycin biosynthetic gene cluster, or its  
CC variant or fragment. Also included are an expression cassette comprising  
CC the novel nucleic acid molecule (operably linked to a promoter functional  
CC in a host cell), a recombinant bacterial host cell in which at least a  
CC portion of a nucleic acid molecule comprising mitomycin biosynthetic gene  
CC cluster is disrupted (resulting in a recombinant host cell that produces  
CC altered levels of mitomycin relative to a corresponding nonrecombinant  
CC bacterial host cell), introducing exogenous DNA into a refractory

CC Streptomycin strain, identifying a nucleic acid molecule that is related  
CC to at least a portion of a nucleic acid molecule comprising a mitomycin  
CC gene cluster, preparing a compound or its salt from the recombinant host  
CC cell and a product produced by the recombinant host cell. The nucleic  
CC acid encodes a MitT, MitS, MitR, MitQ, MitP, MitO, MitN, MitM, MitL,  
CC MitK, MitJ, MitI, MitH, MitG, MitF, MitE, MitD, MitC, MitB, MitA and/or  
CC MmcA-MmcY. The nucleic acid is useful for enhancing production of  
CC mitomycin antibiotics, which induce apoptosis and hence are useful as  
CC anti-tumour (via tumour hypoxia) agents and are useful in treating  
CC cancer. The gene cluster was isolated from Streptomyces lavendulae. The  
CC present sequence is a mitomycin biosynthetic protein of the invention.  
XX

Sequence 123 AA:

Query Match 43.8%; Score 49; DB 7; Length 123;  
Best Local Similarity 57.1%; Pred. No. 67;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NGTIVBELKQLE 17  
|||:||||:|  
Db 86 NGTVPVELREMYE 99

RESULT 27  
AAB69350  
ID AAB69350 standard; protein; 842 AA.  
XX  
AC AAB69350;  
XX  
DT 12-SEP-2003 (revised)  
DT 20-APR-2001 (first entry)  
XX  
DE HIV-1 non-subtype B clone 93BR029-4 env protein.  
XX

KM HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env; vpu;  
KW vif; vpr; tat; rev; nef; vaccine.  
XX  
XX Human immunodeficiency virus 1.  
XX  
PN WO200026416-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 25-OCT-1999; 99WO-US024837.  
XX  
PR 02-NOV-1998; 98US-00184418.

PA (UABR-) UAB RES FOUND.  
XX

PI Hahn BH, Shaw GM, Gao F;  
XX

DR WPI: 2000-365651/31.  
XX

PT Novel genomic nucleic acids of non-subtype B human immunodeficiency virus  
XX  
XX type 1 useful for detecting and treating AIDS comprises a specific  
XX  
XX nucleotide sequence.  
XX

Claim 41; Fig 21; 131bp; English.

CC The present invention provides the protein and coding sequences for a  
CC number of human immunodeficiency virus (HIV) type 1 non-subtype B  
CC isolates. The sequences shown include the near full-length coding  
CC sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat,  
CC rev and nef proteins. These can be used to detect the presence of HIV-1  
CC in a sample and to produce antibodies against non-subtype B HIV-1 virus.  
CC These antibodies can be used in vaccines to prevent and treat HIV  
CC infection. (Updated on 12-SEP-2003 to standardise OS field)  
XX

Sequence 842 AA;

Query Match 43.3%; Score 48.5; DB 3; Length 842;  
Best Local Similarity 47.6%; Pred. No. 66+02;  
Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;



Oy	3	DNNGTTFVEELKOLLEQNNLV	22	:~:	
Db	396	DNNGTTFVEELKOLLEQNNLV	416		
RESULT 28					
ADP07641					
ADF07641		standard; protein; 300 AA.			
AC	ADP07641;				
XX	12-FEB-2004	(first entry)			
XX	Bacterial polypeptide #3754.				
DE	Proteus mirabilis infection; bacterial infection; antibacterial;				
XX	immunostimulant.				
XX	Proteus mirabilis.				
OS	US6605709-B1.				
XX	12-AUG-2003.				
PD	05-APR-2000; 2000US-00543681.				
PF	09-APR-1999; 99US-0128706P.				
XX	(GENO-) GENOME THERAPEUTICS CORP.				
PA	Breton GL;				
XX	WPI; 2003-095291/82.				
DR	N-PSDB; ADP03469.				
XX	New Proteus mirabilis polypeptides and polynucleotides, useful as				
XX	reagents for diagnosis of bacterial disease, as components of				
PT	antibacterial vaccines, as targets for antibacterial drugs, or as				
PT	biocontrol agents for plants.				
XX	Disclosure; SEQ ID NO 7926; 870pp; English.				
PS	The invention relates to new Proteus mirabilis polypeptides and				
XX	polynucleotides. The invention also relates to antibodies against the				
CC	polynucleotides, methods for producing the polypeptides, a method of				
CC	generating vaccines for immunising an individual against P. mirabilis, a				
CC	method for evaluating a compound for the ability to bind a P. mirabilis				
CC	polypeptide and a method for screening test compounds for anti-bacterial				
CC	activity. The polypeptides and polynucleotides are useful as molecular				
CC	targets for diagnosing, preventing and treating pathological conditions				
CC	resulting from bacterial infection, as reagents for diagnosis of				
CC	bacterial diseases, as components of antibacterial vaccines, as targets				
CC	for antibacterial drugs or as bio-control agents for plants. This				
CC	sequence represents a Proteus mirabilis polypeptide of the invention.				
XX	Sequence 300 AA;				
SO					
Query Match	42.9%;	Score 48;	DB 7;	Length 300;	
Best Local Similarity	45.0%;	Pred. No. 2.4e+02;			
Matches	9;	Conservative	4;	Mismatches	7;
				Indels	0;
				Gaps	0;
Oy	1	MADNGTTFVEELKOLLEQNNLV	20	: : : : : : : : :	
Db	60	LTDGQALTYEHAKQILAQFN	79		
RESULT 29					
ADP21407					
ID	ADP21407	standard; protein; 401 AA.			
XX	ADP21407;				
XX					

DT		02-DEC-2004 (first entry)	
XX		Bacterial polypeptide #10440.	
DE			
XX		Recombinant DNA construct; transformed plant; improved plant property;	
KM		cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;	
KM		pathogen tolerance; pest tolerance; plant disease resistance;	
KM		cell cycle pathway modification; plant growth regulator;	
KM		homologous recombination; seed oil yield; protein yield; carbohydrate;	
KM		nitrogen; phosphorus; photosynthesis; lignin; galactomannan;	
XX		bacterial polypeptide.	
OS		Bacteria.	
XX			
PN		US200323675-A1.	
XX			
PD		18-DEC-2003.	
XX			
PF		20-FEB-2003; 2003US-00369493.	
PR		21-FEB-2002; 2002US-0360039P.	
XX			
PA	(CAOY//	CAO Y.	
PA	(HINK//	HINKLE G J.	
PA	(SLAT//	SLATER S C.	
PA	(CHEN//	CHEN X.	
PA	(GOLD//	GOLDMAN B S.	
PI		Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;	
DR		WPI; 2004-061375/06.	
PT		New recombinant DNA construct comprising a promoter positioned to provide	
XX		for expression of a polynucleotide encoding a polypeptide from a	
PT		microbial source, useful for producing plants with improved properties.	
PS		Claim 1; SEQ ID NO 10440; 122pp; English.	
XX			
CC		The invention relates to a recombinant DNA construct comprising a	
CC		promoter functional in a plant cell, where the promoter is positioned to	
CC		provide for expression of a polynucleotide encoding a polypeptide from a	
CC		microbial source. The invention also relates to a transformed plant	
CC		comprising the recombinant DNA construct and a method of producing a	
CC		transformed plant having an improved property. The plant is a crop plant	
CC		such as maize or soybean. The method of producing a transformed plant	
CC		having an improved property comprises transforming a plant with the	
CC		recombinant DNA construct and growing the transforming plant, where the	
CC		polynucleotide or polypeptide is useful for improving plant properties.	
CC		The recombinant DNA construct is useful for producing plants with	
CC		improved plant properties, e.g. improved cold, heat or drought tolerance,	
CC		tolerance to herbicides, extreme osmotic conditions, pathogens or pests,	
CC		increased resistance to plant disease, better growth rate by modification	
CC		of the cell cycle pathway with plant growth regulators, increased rate of	
CC		homologous recombination, modified seed oil or protein yield and/or	
CC		content, improved yield by modification of carbohydrate, nitrogen or	
CC		phosphorus use and/or uptake, by modification of photosynthesis or by	
CC		providing improved plant growth and development under at least one stress	
CC		condition, improved lignin production or improved galactomannan	
CC		production. This sequence represents a bacterial polypeptide used in the	
CC		scope of the invention. Note: The sequence date for this patent did not	
CC		form part of the printed specification but was obtained in electronic	
CC		format from USPTO at seqdata.uspto.gov/sequence.html.	
XX			
SQ		Sequence 401 AA:	
Query Match	42.9%; Score 48; DB 8; Length 401;		
Best Local Similarity	46.7%; Pred. No. 3.2e+02;		
Matches	7; Conservative	6; Mismatches	2; Indels
			0; Gaps
07	5 GTTVEELKQLLEQW 19		
	:: :: :: :: ::		
DB	184 GNVTLEOVKKLSERK 198		

RESULT 30  
ABU11364  
ID ABU11364 standard; protein; 4437 AA.  
XX  
AC ABU11364;  
XX  
DT 11-FEB-2003 (first entry)  
XX  
DE Protein encoded by S. atroolivaceus leinamycin gene cluster ORF 1m1.  
XX  
KM leinamycin biosynthesis gene cluster; lmm; open reading frame; ORF;  
KM anti-tumour antibiotic; broad spectrum antimicrobial activity;  
KM Gram-positive; Gram-negative bacteria; chemical modification; metabolite  
KM apo-carrier protein; holo-carrier protein; tumour; polypeptide;  
KM hybrid polypeptide/polypeptide metabolite; lmm production; cytosolic.  
XX  
OS Streptomyces atroolivaceus.  
XX  
PN MO20027179-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 22-MAR-2002; 2002MO-US008937.  
XX  
PR 26-MAR-2001; 2001US-0278935P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
PA (KYO ) KYOMA HAKKO KOGYO KK.  
XX  
PI Shen B, Cheng Y, Tang G;  
XX  
WP1; 2003-018907/01.  
DR N-PSDB; ABX34289.  
XX  
PT Novel gene cluster responsible for synthesis of leinamycin in  
PT Streptomyces atroolivaceus useful for making various peptide and/or  
PT polypeptide, and/or hybrid polypeptide/polypeptide metabolites.  
XX  
PS Claim 13; Page 143-145; 185pp; English.  
XX  
XX The present invention relates to the isolation of the Streptomyces  
CC atroolivaceus leinamycin (lmm) biosynthesis gene cluster containing 71  
CC open reading frames (ORFs) (ORFs -35 through -1, ORFs lmmA through lmmZ,  
CC and ORFs +1 through +9). Leinamycin is a novel anti-tumour antibiotic  
CC produced by several Streptomyces species. It exhibits broad spectrum  
CC antimicrobial activity against Gram-positive and Gram-negative bacteria,  
CC but not against fungi. The polypeptides encoded by the lmm biosynthesis  
CC gene cluster ORFs are useful for chemically modifying a molecule in a  
CC host cell. The host cell is a bacterium or eukaryotic cell, including a  
CC mammalian, yeast, plant, fungal, or insect cell. The molecule is an  
CC endogenous metabolite produced by the host cell or exogenously supplied  
CC metabolite, or an amino acid, and the polypeptide is a peptide synthetase  
CC or amino transferase. The polypeptides encoded by the lmm gene cluster  
CC are useful for converting an apo-carrier protein to a holo-carrier  
CC protein. lmm shows potent antitumour activity in tumour models in vivo.  
CC The lmm gene cluster modules and/or catalytic domains are useful for  
CC making various peptide and/or polypeptide, and/or hybrid  
CC polypeptide/polypeptide metabolites. The proteins encoded by the ORFs are  
CC useful alone, or in combination with other active domains to modify  
CC various target substrates. The lmm gene cluster is useful to upregulate  
CC endogenous lmm production to permit lmm production in cells and/or to  
CC make various modified lmm. lmm, its analogue, or other polypeptide,  
CC peptide or hybrid polypeptide/peptide metabolites are useful as  
CC therapeutic agents, to treat a number of disorders, depending upon the  
CC type of metabolite. ABU11341-ABU11411 represent the proteins encoded by  
CC ORFs of the S. atroolivaceus leinamycin biosynthesis gene cluster  
XX  
XX Sequence 4437 AA;  
XX

```
QY      2 ADNGTITVEELKQ̄LLEQ̄WN 20
        ||:|: ||:|: ||
Db      949 ADDGEVRGBAEHLKILHEWN 96
```

RESULT 31  
 ID ADI38885 standard; protein; 159 AA.  
 XX ADI38885;  
 AC  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Glucosamine-6-phosphate acetyltransferase, GNA1, SEQ ID 30.  
 XX  
 KW Glucosamine; N-acetylglucosamine; fermentation;  
 KW glucosamine-6-phosphate acetyltransferase;  
 KW glucosamine-6-phosphate synthase; glucosamine-6-phosphate deaminase;  
 KW glucosamine-1-phosphate N-acetyltransferase; glucosamine-6-phosphate;  
 KW glucosamine-1-phosphate; N-acetylglucosamine-1-phosphate;  
 KW N-acetylglucosamine-6-phosphate; enzyme.  
 XX  
 OS Saccharomycetes cerevisiae.  
 OS  
 XX  
 PN WO2004003175-A2.  
 PN  
 XX  
 PD 08-JAN-2004.  
 PD  
 XX  
 PF 01-JUL-2003; 2003WO-US020925.  
 PF  
 XX  
 PR 01-JUL-2002; 2002US-0393348P.  
 PR  
 XX  
 PA (ARKT-) ARKION LIFE SCI LLC.  
 PA  
 XX  
 PI Deng M, Angerer JD, Cyron D, Grund AD, Jerrell TA, Leanna C,  
 PI Mathre O, Rosson R, Running J, Severson D, Song L, Wassink S;  
 XX  
 DR WPI: 2004-203380/19.  
 DR  
 XX  
 DR N-PSDB; ADI38884.  
 DR  
 XX  
 PT Producing glucosamine or N-acetylglucosamine by fermentation involves  
 PT culturing microorganism comprising glucosamine-6-phosphate  
 PT acetyltransferase, in fermentation medium, and collecting product.  
 PT  
 XX  
 PS Claim 5; SEQ ID NO 30; 327bp; English.  
 PS  
 XX  
 CC The present invention relates to a method (M1) for producing glucosamine  
 CC and N-acetylglucosamine by fermentation. The method comprises (a)  
 CC culturing in a fermentation medium a microorganism (I) which comprises  
 CC endogenous glucosamine-6-phosphate acetyltransferase (II) and a genetic  
 CC modification that increases the activity of (II), glucosamine-6-phosphate  
 CC synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases  
 CC the activity of (IV) and increases the activity of glucosamine-1-  
 CC phosphate N-acetyltransferase (V), and (b) and collecting the product,  
 CC which is chosen from the group consisting of glucosamine-6-phosphate,  
 CC acetylglucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate, N-  
 CC acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present  
 CC sequence was used to illustrate the method of the invention.  
 CC  
 XX  
 XX Sequence 159 AA;  
 XX

Query Match	42.0%;	Score 47;	DB 8;	Length 159;
Best Local Similarity	50.0%;	Pred. NO.	1.7e+02;	
Matches	8;	Conservative	3;	Mismatches 5;
				Indels 0;
				Gaps 0;
QY	5	GTITVEELKOLLEQWN	20	
		: : : :		
b	31	GTITPESFSPKILIKYMN	46	

Query Match	42.9%	Score 48;	DB 6;	Length 4437;
Best Local Similarity	42.1%;	Pred. No. 4.1e+03;		
Matches	8;	Conservative	5;	Mismatches 6;
				Indels 0;
				Gaps 0;

RESULT 32  
ADJ64176

ID ADJ64176 standard; protein; 159 AA.  
 XX  
 AC ADJ64176;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE S. cerevisiae glucosamine phosphate N-acetyltransferase.  
 XX  
 KM Hexosamine; arthritis; osteoarthritis; rheumatoid arthritis; pain;  
 KM inflammation; articular joint disease; spondyloarthritis;  
 KM gouty arthritis; systemic lupus erythematosus; juvenile arthritis;  
 KM tendinitis; bursitis; connective tissue injury; psoriasis; eczema; burn;  
 KM dermatitis; transgenic plant; glucosamine phosphate N-acetyltransferase;  
 KM yeast; enzyme; EC 2.3.1.4.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN US2004003432-A1.  
 XX  
 PD 01-JAN-2004.  
 XX  
 PP 05-MAY-2003; 2003US-00423912.  
 XX  
 PR 06-MAY-2002; 2002US-0378297P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Obukowicz MG;  
 XX  
 DR WPI; 2004-061704/06.  
 XX  
 DR N-PSDB; ADJ64175.  
 XX  
 PT Producing hexosamine useful for treating arthritis by culturing cell  
 PT comprising heterologous polynucleotide sequences which encode for enzymes  
 PT required for biosynthetic pathway capable of synthesizing hexosamine.  
 XX  
 PS Disclosure; SEQ ID NO 4; 35pp; English.  
 XX  
 CC The invention relates to a method of producing a hexosamine that involves  
 CC providing a cell comprising polynucleotide sequences which code for  
 CC enzymes required for a biosynthetic pathway capable of synthesizing the  
 CC hexosamine, where at least one of the polynucleotide sequences comprises  
 CC a recombinant polynucleotide. The method involves transforming a cell  
 CC with at least one heterologous polynucleotide coding for a polypeptide in  
 CC a biosynthetic pathway that is capable of producing hexosamine, culturing  
 CC the transformed cell under conditions that permit the cell to translate  
 CC the polynucleotide into a polypeptide comprising an enzyme which is part  
 CC of the biosynthetic pathway. The hexosamine produced by the method of  
 CC invention is useful for treating arthritis, preferably osteoarthritis and  
 CC rheumatoid arthritis in humans and pet animals. The hexosamines are also  
 CC useful for treating pain, inflammation or inflammation-associated  
 CC disorder. The hexosamines are also useful for treating other articular  
 CC joint damage or diseases such as spondyloarthritis, gouty arthritis,  
 CC systemic lupus erythematosus and juvenile arthritis and other joint  
 CC damage disease conditions such as tendinitis, bursitis, connective tissue  
 CC injuries or disorders, and skin related conditions such as psoriasis,  
 CC eczema, burns and dermatitis. The method provides improved production of  
 CC hexosamine without compromising its clinical effectiveness and in a form  
 CC that is acceptable for delivery to a broad class of patients. Consumption  
 CC of edible portions of transgenic plants containing hexosamines provide a  
 CC supply of hexosamine to the subject in a conventional and easily  
 CC consumable form. The present sequence is Saccharomyces cerevisiae  
 CC glucosamine phosphate N-acetyltransferase (EC 2.3.1.4).  
 XX  
 XX  
 SQ Sequence 159 AA;  
 XX  
 Query Match 42.0%; Score 47; DB 8; Length 159;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 GTTVEELKQLLEQWV 20  
 DB 31 GTTPSPFSKLKRYWN 46

RESULT 33  
 ADN10653  
 ID ADN10681 standard; protein; 508 AA.  
 XX  
 AC ADN10681;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Nicotiana p450 enzyme amino acid sequence SEQ ID NO:266.  
 XX  
 KM plant; p450; enzyme; Nicotiana; plant growth regulant; gene therapy;  
 KM phenotype.  
 XX  
 OS Nicotiana sp.  
 XX  
 PN WO2004035745-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PP 16-OCT-2003; 2003WO-US032722.  
 XX  
 PR 16-OCT-2002; 2002US-0418933P.  
 XX  
 PR 08-JUL-2003; 2003US-0485168P.  
 XX  
 PR 18-SEP-2003; 2003US-0503989P.  
 XX  
 PA (USSM-) US SMOKELESS TOBACCO CO.  
 XX  
 PI Xu D;  
 XX  
 DR WPI; 2004-348441/32.  
 XX  
 DR N-PSDB; ADN10680.  
 XX  
 PT New isolated nucleic acid molecules and encoded cytochrome P450 enzymes  
 PT from Nicotiana plants, useful for altering plant phenotypes.  
 XX  
 PS Claim 3; SEQ ID NO 266; 198pp; English.  
 XX  
 CC The present invention describes a plant p450 enzyme nucleic acid molecule  
 CC isolated from Nicotiana. Also described: (i) an isolated p450 protein  
 CC from Nicotiana; (2) a transgenic plant comprising the nucleic acid  
 CC molecule described above; (3) a method of producing the transgenic plant,  
 CC comprising: (i) operably linking the above nucleic acid molecule with a  
 CC promoter functional in the plant to create a plant transformational  
 CC vector; (ii) transforming the plant with the vector; (iii) selecting a  
 CC plant cell transformed with the transformation vector; and (iv)  
 CC regenerating a transformation plant from the transformed plant cell; and  
 CC (4) a method of selecting a plant containing the above nucleic acid  
 CC molecule, where the plant is analysed for the presence of the above  
 CC nucleic acid sequences. The p450 sequences have plant growth regulant  
 CC activity, and can be used in gene therapy. Compositions and methods from  
 CC the present invention are useful for altering plant phenotypes. The  
 CC present sequence represents a Nicotiana p450 enzyme amino acid sequence  
 CC from the present invention.  
 XX  
 XX  
 SQ Sequence 508 AA;  
 XX  
 Query Match 42.0%; Score 47; DB 8; Length 508;  
 Best Local Similarity 47.1%; Pred. No. 5.7e+02;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 TTTVEELKQLLEQWV 22  
 DB 196 TVRVEDLYLVDPQWFL 212  
 RESULT 34  
 ADN10653  
 ID ADN10653 standard; protein; 508 AA.  
 XX  
 AC ADN10653;  
 XX

DT	15-JUL-2004	(first entry)
XX	Nicotiana p450 enzyme amino acid sequence SEQ ID NO:238.	
DE	Nicotiana p450 enzyme; Nicotiana; plant growth regulant; gene therapy;	
KW	plant; p450; enzyme; Nicotiana; plant growth regulant; gene therapy;	
KM	phenotype.	
XX	Nicotiana sp.	
OS	Nicotiana sp.	
PN	WO2004035745-A2.	
PD	29-APR-2004.	
PF	16-OCT-2003; 2003WO-US032722.	
PR	16-OCT-2002; 2002US-0418933P.	
PR	08-JUL-2003; 2003US-0485368P.	
XX	18-SEP-2003; 2003US-0503989P.	
PA	(USSM-) US SMOKELESS TOBACCO CO.	
XX	Xu D;	
P1	WIPI; 2004-348441/32.	
DR	N-P5DB; ADN10652.	
XX	New isolated nucleic acid molecules and encoded cytochrome P450 enzymes from Nicotiana plants, useful for altering plant phenotypes.	
PS	Claim 3; SEQ ID NO 238; 198pp; English.	
CC	The present invention describes a plant p450 enzyme nucleic acid molecule isolated from Nicotiana. Also described: (i) an isolated p450 protein from Nicotiana; (2) a transgenic plant comprising the nucleic acid molecule described above; (3) a method of producing the transgenic plant, comprising: (i) operably linking the above nucleic acid molecule with a promoter functional in the plant to create a plant transformational vector; (ii) transforming the plant with the vector; (iii) selecting a plant cell transformed with the transformation vector; and (iv) regenerating a transformation plant from the transformed plant cell; and (4) a method of selecting a plant containing the above nucleic acid molecule, where the plant is analysed for the presence of the above nucleic acid sequences. The p450 sequences have plant growth regulant activity, and can be used in gene therapy. Compositions and methods from the present invention are useful for altering plant phenotypes. The present sequence represents a Nicotiana p450 enzyme amino acid sequence from the present invention.	
SQ	Sequence 508 AA:	
QY	Query Match 42.0%; Score 47; DB 8; Length 508; Best Local Similarity 47.1%; Pred.No. 5.7e+02; Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;	
Dd	6 TTTVEELKQLLEFONMLV 22   :   :   :   :   :   : 196 TVRVEDLQYLVDQWFLL 212	
RESULT 35		
ID	ADN10655 standard; protein; 509 AA.	
AC	ADN10655;	
XX	15-JUL-2004 (first entry)	
DE	Nicotiana p450 enzyme amino acid sequence SEQ ID NO:240.	
KW	plant; p450; enzyme; Nicotiana; plant growth regulant; gene therapy;	
KM	phenotype.	
XX	Nicotiana sp	

[illegible]

PD 18-DEC-2003.  
 XX  
 XX 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX  
 DR WPI; 2004-061375/06.  
 XX  
 PT New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 PS Claim 1; SEQ ID NO 2600; 122pp; English.  
 XX  
 CC The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomanan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 CC  
 XX  
 SQ Sequence 659 AA;  
 XX  
 Query Match 42.0%; Score 47; DB 8; Length 659;  
 Best Local Similarity 56.2%; Pred. No. 7.5e+02;  
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 OY 4 NGTIVYELDKQLLEQW 19  
 Db 633 NGQITLESRRLLLEDY 648  
 XX  
 RESULT 37  
 ABU49306  
 ID ABU49306 standard; protein; 428 AA;  
 XX  
 AC ABU49306;  
 XX  
 XX 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by prokaryotic essential gene #34833.  
 XX  
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Vibrio cholerae.  
 XX  
 PN WO200277183-A2.

XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haeelbeck R, Ohlsen KL, Zyckind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 XX  
 DR N-PDB; ACAS3176.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 77230; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 623 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the antisense  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 CC  
 XX  
 SQ Sequence 428 AA;  
 XX  
 Query Match 41.5%; Score 46.5; DB 6; Length 428;  
 Best Local Similarity 42.9%; Pred. No. 5.5e+02;  
 Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;  
 OY 1 MADNGTIVE-ELKQLLEQW 20  
 Db 107 LADSGVAIVEVSLKVALQYTM 127  
 XX  
 RESULT 38  
 AA96945  
 ID AA96945 standard; protein; 849 AA.  
 XX  
 AC AA96945;

```

XX 31-OCT-2000 (first entry)
DT
XX HIV sythetic Env containing polypeptide.
DE
XX Gag; expression cassette; antigenic; type C; HIV; Env; sythetic;
KW DNA immunization; packaging cell line; antigen presentation.
XX
XX Human immunodeficiency virus; type C strain AF110968.
OS
XX Synthetic.
PN WO200039304-A2.
XX
XX 06-JUL-2000.
PD
XX
XX 30-DEC-1999; 99WO-US031273.
PE
XX
XX 31-DEC-1998; 98US-0114495P.
PR
XX 01-SEP-1999; 99US-0152195P.
XX
XX (CHIR ) CHIRON CORP.
PA
XX
XX Barnett S, Zur Megede J;
PI
XX
XX WPI; 2000-452401/39.
DR
XX
XX Polypeptide encoding antigenic type C HIV Gag polypeptide or a HIV Env
PT polypeptide and the polypeptide useful for immunizing a mammal especially
PT human against HIV.
XX
XX Example 1; Page 106-109; 113pp; English.
PS
XX
XX Expression cassettes comprising a polynucleotide encoding antigenic type
CC C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful
CC in DNA immunization, generation of packaging cell lines and production of
CC Gag- and/or Env-containing proteins. Synthetic Env and Gag expression
CC cassettes exhibit increased potency for induction of cytotoxic T-
CC lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-
CC assemble into non-infectious virus-like particles which are used as a
CC matrix for the proper presentation of an antigen entrapped or associated
CC to the immune system of the host
XX
XX
SQ Sequence 849 AA;

Query Match 41.5%; Score 46.5; DB 3; Length 849;
Best Local Similarity 45.0%; Pred. No. 1.1e+03;
Matches 9; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

OY 4 NGTITVE-ELKOLLEQWNLV 22
DB 403 NGTITTCRKQITIMWQKV 422

RESULT 39
AAAG02044
ID AAG02044 standard; protein; 100 AA.
XX
XX AAG02044;
AC
XX
XX 06-OCT-2000 (first entry)
DT
XX
XX Human secreted protein, SEQ ID NO: 6125.
DE
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
XX Homo sapiens.
OS
XX
XX EP1033401-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 21-FEB-2000; 2000EP-00200610.
PF

```

```

XX 26-FEB-1999; 99US-0122487P.
PR XX
XX (GBST ) GENSET.
PA XX
PI Dunas Milne Edwards J, Nuclert A, Giordano J;
XX
XX DR WPI; 2000-500381/45.
XX N-PSDB; AAC02050.
DR XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX PS Claim 13; SEQ ID NO 6125; 71pp + Sequence Listing; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNA or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
XX SQ Sequence 100 AA;
XX
OY Query Match 41.1%; Score 46; DB 3; Length 100;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
DB 47 ENGNIIEELKQLE 61
3 DNGTIVEELKQLE 17
: |||: |||: ||
OY 47 ENGNIIEELKQLE 61
DB 47 ENGNIIEELKQLE 61
RESULT 40
ABB70970
ID ABB70970 standard; protein: 114 AA.
XX
XX AC ABB70970;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster polypeptide SEQ ID NO 39702.
XX
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX OS Drosophila melanogaster.
XX
XX PN WO200171042-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX
XX PR 23-MAR-2000; 2000US-0191637P.
XX
XX PR 11-JUL-2000; 2000US-00614150.
XX
XX PA (PEKE ) PE CORP NY.
XX
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX DR WPI; 2001-656860/75.
XX
XX DR N-PSDB; AB115073.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more

```

PT genes from *Drosophila* and for elucidating cell signaling and cell-cell interactions.  
 XX  
 XX  
 PS Disclosure; SEQ ID NO 39702; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (AB57737-AB572072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIGO at ftp.wigo.int/pub/published\_pct\_sequences  
 CC  
 XX  
 SQ Sequence 114 AA;  
 Query Match 41.1%; Score 46; DB 4; Length 114;  
 Best Local Similarity 41.2%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 DNGTIVEELKQLEQM 19  
 Db 57 NKGTISARQLRNLIQNW 73  
 RESULT 41  
 ABG59978 standard; protein; 189 AA.  
 XX  
 AC ABG59978;  
 XX  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE Human DITHP polypeptide #36.  
 XX  
 KW Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin; cell proliferative disorder; cancer; tumour; autoimmune disorder; brain; inflammatory disorder; viral infection; bacterial infection; seizure; fungal infection; parasitic infections; developmental disorder; breast; endocrine disorder; metabolic disorders; neurological disorder; cervix; gastrointestinal disorder; transport disorder; gene therapy; kidney; adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen; thymus.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220754-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 29-AUG-2001; 2001WO-US027127.  
 XX  
 PR 05-SEP-2000; 2000US-0229747P.  
 PR 05-SEP-2000; 2000US-0229748P.  
 PR 05-SEP-2000; 2000US-0229749P.  
 PR 05-SEP-2000; 2000US-0229750P.  
 PR 05-SEP-2000; 2000US-0229751P.  
 PR 05-SEP-2000; 2000US-0230583P.  
 PR 06-SEP-2000; 2000US-0230585P.  
 PR 06-SEP-2000; 2000US-0230514P.  
 PR 06-SEP-2000; 2000US-0230515P.  
 PR 06-SEP-2000; 2000US-0230517P.  
 PR 06-SEP-2000; 2000US-0230518P.  
 PR 06-SEP-2000; 2000US-0230519P.  
 PR 06-SEP-2000; 2000US-0230595P.  
 PR 06-SEP-2000; 2000US-0230597P.  
 PR 06-SEP-2000; 2000US-0230598P.  
 PR 06-SEP-2000; 2000US-0230599P.  
 PR 06-SEP-2000; 2000US-0230610P.  
 PR 06-SEP-2000; 2000US-0230655P.  
 PR 06-SEP-2000; 2000US-0230988P.

PR 07-SEP-2000; 2000US-0230951P.  
 PR 07-SEP-2000; 2000US-0231163P.  
 PR 07-SEP-2000; 2000US-0231167P.  
 XX  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR; Momiya MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM; Gerstein EH, Peralta CH, David MH, Panzer SR, Flores V, Dafio A; Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;  
 PI  
 XX  
 DR WPI; 2002-383054/41.  
 DR N-PSDB; ABK71570.  
 XX  
 PT An isolated polynucleotide useful in diagnostics and therapeutics.  
 PS  
 PS Claim 29; Page 553; 686pp; English.  
 XX  
 CC The invention relates to human diagnostic and therapeutic (dithp) polynucleotides and their associated polypeptides (DITHP polypeptides).  
 CC The sequences of the invention are used in the treatment and diagnosis of cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis), viral infections, bacterial infections, fungal infections, parasitic infections, developmental disorders (e.g. anaemia, epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal disorders (e.g. ulcerative colitis, lysinuria) and transport disorders (e.g. myotonic dys trophy, cataracts, peripheral neuropathy). Sequences ABG59943-ABG60220 represent human DITHP polypeptides of the invention  
 CC  
 XX  
 SQ Sequence 189 AA;  
 Query Match 41.1%; Score 46; DB 5; Length 189;  
 Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 4 NGTIVEELKQLEQNL 21  
 Db 113 SGRTIDELSGACEQFGL 130  
 RESULT 42  
 AAG82765 standard; protein; 216 AA.  
 ID AAG82765  
 XX  
 AC AAG82765;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:2624.  
 XX  
 KW Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination; endocarditis.  
 KW  
 OS Staphylococcus epidermidis.  
 XX  
 PN WO200134809-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PR 09-NOV-2000; 2000WO-US030782.  
 XX  
 PR 09-NOV-1999; 99US-0164258P.  
 XX  
 PA (GLAXO) GLAXO GROUP LTD.  
 XX  
 PI kimmerly WJ;

XX WPI; 2001-316495/33.  
 DR N-PSDB; AAH53615.  
 XX  
 PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,  
 PT useful for vaccinating against infections, e.g. endocarditis.  
 XX  
 PS Claim 18; Page 688; 2188pp; English.  
 XX  
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*, (I)  
 CC and (II) can have antibacterial activity and therefore can be used in  
 CC vaccination. The nucleic acids (I) may be used to produce the S.  
 CC epidermidis polypeptides (II) via the production of vectors containing  
 CC them which are used to produce hosts cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to AAH55098  
 CC represent oligonucleotide sequences and primers which are used in the  
 CC exemplification of the present invention. N.B. The present invention  
 CC specifically claims all the polynucleotide sequences given in the  
 CC sequence listing of the present specification, however the sequence  
 CC listing only goes up to SEQ ID NO:4454 so even though sequences are given  
 CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present  
 CC for SEQ ID NO:4455 to 4464  
 CC  
 SQ Sequence 216 AA;  
 XX  
 Query Match 41.1%; Score 46; DB 4; Length 216;  
 Best Local Similarity 60.0%; Pred. No. 3.1e+02;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NGTITVEELKQLLEQ 18  
 DB 59 NGMTLLEAKYQLE 73  
 XX  
 RESULT 43  
 ABJ19037  
 ID ABJ19037 standard; protein; 216 AA.  
 AC  
 XX ABJ19037;  
 XX  
 DT 06-MAR-2003 (first entry)  
 XX  
 DE Pathogen specific antigen related staphylococcal protein SEQ ID No 286.  
 XX  
 KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;  
 KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;  
 KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;  
 KW autoimmune disease; HIV; hepatitis.  
 XX  
 OS Staphylococcus sp.  
 OS  
 XX  
 PN WO200259148-A2.  
 PN  
 PD 01-AUG-2002.  
 PD  
 PF 21-JAN-2002; 2002WO-EP000546.  
 PF  
 PR 26-JAN-2001; 2001AT-00000130.  
 PR  
 XX  
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
 PA  
 XX Meinke A, Nagy E, Von Ahesen U, Klade C, Henics T, Zauner W;  
 PI Meinke DB, Vytvytska O, Eltz H, Dryla A, Weichardt T, Hafner M;  
 PI Tempelmeier B;  
 PI  
 XX WPI; 2003-075410/07.

XX identifying, isolating and producing hyperimmune serum-reactive antigens  
 PT from a pathogen, for preparing vaccine or medicament for treating or  
 PT preventing e.g. staphylococcal infections, comprises providing antibody  
 PT preparation.  
 XX  
 PS Example 7; Page 201; 252pp; English.  
 XX  
 CC The invention relates to a novel method for identifying, isolating and  
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,  
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are  
 CC used in a vaccine, comprises providing antibody preparation from a plasma  
 CC pool of a type of animal, or individual sera with antibodies against the  
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-  
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the  
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,  
 CC or their hyperimmune fragments are useful for the manufacture of a  
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal  
 CC infections or colonisation against S. aureus or S. epidermidis. The  
 CC preparation of antibodies is useful for the manufacture of a medicament  
 CC for treating or preventing staphylococcal infections or colonisation  
 CC against S. aureus or S. epidermidis. The antibody preparations may also  
 CC be used for diagnostic and imaging purposes. Other conditions that can be  
 CC treated include cancer, autoimmune diseases or infections caused by viral  
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This  
 CC sequence represents a staphylococcal protein relating to the method for  
 CC identifying and producing pathogen specific antigens of the invention  
 CC  
 SQ Sequence 216 AA;  
 XX  
 Query Match 41.1%; Score 46; DB 6; Length 216;  
 Best Local Similarity 60.0%; Pred. No. 3.1e+02;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NGTITVEELKQLLEQ 18  
 DB 59 NGMTLLEAKYQLE 73  
 XX  
 RESULT 44  
 ADQ37007  
 ID ADQ37007 standard; protein; 253 AA.  
 AC  
 XX ADQ37007;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Cell proliferation-related polypeptide #81.  
 XX  
 KW cell proliferation related polypeptide; cell proliferation; senescence;  
 KW differentiation; stress response.  
 XX  
 OS Oryza sativa.  
 OS  
 XX  
 PN WO2004061122-A2.  
 PN  
 PD 22-JUL-2004.  
 PD  
 PF 23-DEC-2003; 2003WO-US041200.  
 PF  
 PR 26-DEC-2002; 2002US-0436565P.  
 PR  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 PA  
 PI Cooper B;  
 PI  
 XX WPI; 2004-534389/51.  
 DR  
 XX  
 XX New nucleic acid molecule encoding a cell proliferation-related  
 PT polypeptide, useful for modulating cell proliferation, senescence,  
 PT differentiation, development, and stress response in plants, and for  
 PT producing enhanced food crops.



PS Claim 28; SEQ ID NO 166; 408bp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a cell proliferation-related polypeptide. The nucleic acid  
CC molecule and the encoded polypeptide, and methods are useful for  
CC modulating cell proliferation, senescence, differentiation, development,  
CC and stress response in plants, and for producing enhanced food crops. The  
CC present sequence represents a cell proliferation-related polypeptide. The  
CC present sequence is published separately from the main body of the  
CC specification as EPO data.  
XX  
SQ Sequence 253 AA;  
XX  
QY 4 NGTITVEELKQLLEQWNL 21  
: |||::|||::|||:  
Db 186 SGFTITDELSQLACEQFGL 203  
XX  
RESULT 45  
ADQ15677  
ID ADQ15677 standard; protein; 253 AA.  
XX  
XX ADQ15677;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
XX Rice stress-related protein #43.  
XX  
XX Rice; stress-related protein; plant maturation; plant development;  
XX plant proliferation; plant senescence; plant disease-resistance;  
XX plant stress response; transgenic plant; pest tolerance;  
XX herbicide tolerance; biotic stress tolerance; abiotic stress tolerance;  
XX improved nutritional value; increased yield; increased proliferation.  
XX  
XX Oryza sativa.  
XX  
XX WO2004061080-A2.  
XX  
XX 22-JUL-2004.  
XX  
XX 23-DEC-2003; 2003MO-US041098.  
XX  
XX 26-DEC-2002; 2002US-0436564P.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Cooper B;  
XX  
XX MPI; 2004-534374/51.  
XX N-PSDB; ADQ15676.  
XX  
XX New isolated nucleic acids and proteins, useful for producing transgenic  
XX plants having improved properties, e.g. tolerance to pests, herbicides,  
XX or biotic or abiotic stresses, improved nutritional value, or increased  
XX yield or proliferation.  
XX  
XX Claim 28; SEQ ID NO 86; 551pp; English.  
XX  
XX The invention comprises the amino acid and coding sequences of rice  
XX stress-related proteins. The DNA and protein sequences of the invention  
XX are useful for regulating and controlling plant maturation and  
XX development, including proliferation, senescence, disease-resistance, or  
XX stress response. They are also useful for producing transgenic plants  
XX having improved properties, e.g. tolerance to pests, herbicides, or  
XX biotic or abiotic stresses, improved nutritional value, increased yield  
XX or proliferation, or improved structure causing less loss from lodging or  
XX shattering. The present amino acid sequence represents a rice stress-  
XX related protein of the invention.

SQ Sequence 253 AA;  
XX  
QY 4 NGTITVEELKQLLEQWNL 21  
: |||::|||::|||:  
Db 186 SGFTITDELSQLACEQFGL 203  
XX  
RESULT 46  
ABP40434  
ID ABP40434 standard; protein; 274 AA.  
XX  
XX ABP40434;  
XX  
XX 24-JUL-2002 (first entry)  
XX  
XX Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5279.  
XX  
XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
XX antibacterial; gene therapy.  
XX  
XX Staphylococcus epidermidis.  
XX  
XX US6380370-B1.  
XX  
XX 30-APR-2002.  
XX  
XX 13-AUG-1998; 98US-00134001.  
XX  
XX 14-AUG-1997; 97US-0055779P.  
XX 08-NOV-1997; 97US-0064964P.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Doucette-Stamm LA, Bush D;  
XX  
XX MPI; 2002-381255/41.  
XX N-PSDB; ABN92979.  
XX  
XX Novel isolated nucleic acid encoding a Staphylococcus epidermis  
XX polypeptide, useful for diagnosing and treating bacterial infections.  
XX  
XX Disclosure; SEQ ID NO 5279; 267pp; English.  
XX  
XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
XX frame (ORF) nucleic acid sequences which encode the amino acid sequences  
XX given in ABP35124 to ABP37960. The S. epidermidis sequences have  
XX antibacterial activity and can be used in gene therapy. The sequences can  
XX also be used in the diagnosis and treatment of bacterial infections,  
XX particularly S. epidermidis infections. The sequences can be used to  
XX screen for compounds able to interfere with the S. epidermidis life cycle  
XX or inhibit S. epidermidis infection. N.B. The sequence data for this  
XX patent did not form part of the printed specification, but was obtained  
XX in electronic format directly from the USPTO web site  
XX  
SQ Sequence 274 AA;  
XX  
QY 4 NGTITVEELKQLLEQ 18  
: |||::|||::|||:  
Db 117 NGMTLEBAKYGQEE 131  
XX  
RESULT 47  
ADS05966  
ID ADS05966 standard; protein; 274 AA.  
XX

AC ADS05966;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Staphylococcus epidermis polypeptide seqid 5261.  
 XX  
 XX antibacterial; vaccine; antiense therapy; Staphylococcus epidermidis;  
 KM recombinant expression vector; infection; computer readable medium;  
 KM computer based system.  
 XX  
 OS Staphylococcus epidermidis.  
 XX  
 PN US2004147734-A1.  
 XX  
 PD 29-JUL-2004.  
 XX  
 PF 01-DEC-2003; 2003US-00724972.  
 XX  
 PR 08-NOV-1997; 97US-0064964P.  
 PR 13-AUG-1998; 98US-00134001.  
 PR 29-NOV-1999; 99US-00450969.  
 XX  
 PA (DOUC/) DOUCETTE-STAMM L.  
 PA (BUSH/) BUSH D.  
 PI Doucette-Stamm L, Bush D;  
 PI WPI; 2004-580138/56.  
 DR N-PSDB; ADS02194.  
 XX  
 PT New isolated polypeptide and encoding nucleic acid derived from  
 PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or  
 PT treating an S. epidermidis bacterial infection.  
 XX  
 PS Claim 17; SEQ ID NO 5261; 741pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid comprising a nucleotide  
 CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
 CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
 CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
 CC given in the specification. Also described are: a recombinant expression  
 CC vector; a cell comprising a recombinant expression vector of (1);  
 CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
 CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
 CC vaccine composition for prevention or treatment of an S. epidermidis  
 CC infection, comprising a nucleic acid cited above and a carrier; treating  
 CC a subject for S. epidermidis infection; a recombinant or substantially  
 CC pure preparation of an S. epidermidis polypeptide or its fragment; a  
 CC vaccine composition for prevention or treatment of an S. epidermidis  
 CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
 CC sample; a computer readable medium having recorded in it the nucleotide  
 CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
 CC system for identifying fragments of the Staphylococcus genome of  
 CC commercial importance; a computer based system for identifying fragments  
 CC of the Staphylococcus plasmids of commercial importance; identifying  
 CC commercially important nucleic acid fragments of the Staphylococcus  
 CC genome and/or plasmids; and identifying an expression modulating fragment  
 CC of the Staphylococcus genome and/or plasmids. The methods and  
 CC compositions of the present invention are useful for the diagnosis,  
 CC prevention and/or treatment of an Staphylococcal epidermidis bacterial  
 CC infection. This is the amino acid sequence of a S. epidermis protein of  
 CC the invention.  
 CC  
 XX  
 XX  
 SQ Sequence 274 AA;  
 XX  
 XX  
 Query Match 41.1%; Score 46; DB 8; Length 274;  
 Best Local Similarity 60.0%; Pred. No. 4e+02;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NGTTTVEELKQLLEQ 18  
 DB 117 NGMTTLEAKYQLDE 131

RESULT 48  
 ID ADA12194  
 XX ADA12194 standard; protein; 300 AA.  
 XX  
 AC ADA12194;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Acinetobacter sp. hydrolase.  
 XX  
 XX adipic acid synthesis; cyclohexanone monooxygenase;  
 KM 6-aldehyde hexanoic dehydrogenase; cyclohexanol dehydrogenase;  
 KM cyclohexanol; adipic acid; hydrolase; enzyme.  
 XX  
 OS Acinetobacter sp.  
 XX  
 PN US6498242-B1.  
 XX  
 PD 24-DEC-2002.  
 XX  
 PF 14-JUL-1999; 99US-00648004.  
 XX  
 PR 19-FEB-1999; 99US-00252553.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E. I.  
 PA Cheng Q, Nagarajan V, Thomas SM;  
 PI WPI; 2003-605313/57.  
 DR N-PSDB; ADA12193.  
 XX  
 PT New nucleic acid fragment isolated from Acinetobacter for converting  
 PT cyclohexanol to adipic acid. encodes adipic acid synthesizing enzymes  
 PT e.g. cyclohexanone monooxygenase and caprolactone hydrolase.  
 XX  
 XX Example 2; Col 57-58; 43pp; English.  
 PS  
 XX  
 CC The invention relates to an isolated nucleic acid fragment from  
 CC Acinetobacter sp. encoding adipic acid synthesizing enzymes where the  
 CC nucleic acid comprises open reading frames encoding e.g. cyclohexanone  
 CC monooxygenase, 6-aldehyde hexanoic dehydrogenase and cyclohexanol  
 CC dehydrogenase. The nucleic acid fragment is useful for isolating cDNAs  
 CC and genes encoding homologous enzymes from the same or other bacterial  
 CC species, and for the conversion of cyclohexanol to adipic acid. The  
 CC nucleic acid fragment is also useful in immunological screening cDNA  
 CC expression libraries, and as probes for genetically and physically  
 CC mapping the genes that they are a part of, and as markers for traits  
 CC linked to expression of the enzymes. The nucleic acid fragment is useful  
 CC to design and produce primer pairs for use in the amplification reaction  
 CC or in primer extension reactions, and for the creation of recombinant  
 CC organisms that have the ability to produce adipic acid while growing on  
 CC cyclohexanol. The present sequence represents the amino acid sequence of  
 CC the Acinetobacter sp. hydrolase.  
 CC  
 XX  
 XX  
 SQ Sequence 300 AA;  
 XX  
 XX  
 Query Match 41.1%; Score 46; DB 6; Length 300;  
 Best Local Similarity 25.0%; Pred. No. 4.5e+02;  
 Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MADNGTIVTEELKQLLEQWN 20  
 DB 22 MOENPNMTIEDFRSMDEWH 41  
 XX  
 RESULT 49  
 AAE39415  
 ID AAE39415 standard; protein; 300 AA.  
 XX  
 AC AAE39415;  
 XX  
 DT 18-DEC-2003 (first entry)

XX Acinetobacter sp. caprolactone hydrolase.  
DE Adipic acid, nylon-6,6; lubricant; plasticizer; food acidulant; enzyme;  
XX caprolactone hydrolase.  
KW Acinetobacter sp.  
XX US2003087403-A1.  
PN 08-MAY-2003.  
PD 16-OCT-2002; 2002US-00272419.  
PF 19-FEB-1999; 99US-00252553.  
PR 14-JUL-1999; 99US-00648004.  
XX (CHEN/) CHENG Q.  
PA (NAGA/) NAGARAJAN V.  
PA (THOM/) THOMAS S M.  
PI Cheng Q, Nagarajan V, Thomas SM;  
XX MPI; 2003-755145/71.  
DR N-PSDB; AAD59830.  
XX New nucleic acid fragment encoding an adipic acid synthesizing enzyme,  
PT useful for producing nylon-6,6, lubricants and plasticizers, or as food  
PT acidulant.  
XX Claim 4; Page 31-32; 45pp; English.  
PS The present invention provides novel nucleic acid molecules derived from  
CC Acinetobacter sp. encoding adipic acid synthesizing enzymes, useful for  
CC producing nylon-6,6, lubricants and plasticizers. The invention is also  
CC useful as food acidulant. The present sequence is Acinetobacter sp.  
CC caprolactone hydrolase enzyme. This enzyme is involved in the synthesis  
CC of adipic acid  
SQ Sequence 300 AA;  
QY Query Match 41.1%; Score 46; DB 7; Length 300;  
Best Local Similarity 25.0%; Pred. No. 4.5e+02;  
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;  
Db 1 MADNGTTVEELKQLEQWN 20  
22 MQENPMWTTEDFRSMFDEWH 41  
RESULT 50  
AAG34981  
ID AAG34981 standard; protein; 385 AA.  
XX AAG34981;  
AC 18-OCT-2000 (first entry)  
DT Arabidopsis thaliana protein fragment SEQ ID NO: 42658.  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 42658.  
DE Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridization assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS EP1033405-A2.  
PN 06-SEP-2000.  
PD 25-FEB-2000; 2000EP-00301439.  
PF 25-FEB-1999; 99US-0121825P.  
XX

PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 28-APR-1999; 99US-0130891P.  
PR 30-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 04-MAY-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140911P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141482P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 30-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.

PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 14-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160742P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161044P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 25-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161820P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 41.1%; Score 46; DB 3; Length 385;  
Best Local Similarity 44.4%; Pred. No. 5.8e+02;  
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;  
Qy 2 ADNGTIT-----VEELKOLLEQWN 20  
Db 92 SDNGTIVEDIYENDLHLLQLLEVCN 118

Search completed: May 11, 2005, 21:22:33  
Job time : 160.489 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 21:13:14 : Search time 22 Seconds  
(without alignments)  
96.217 Million cell updates/sec

Title: US-10-712-812-5

Perfect score: 112

Sequence: 1 MADNGTITVEELKQLEQMNLV 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR 79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	51.8	376	2	TS1170
2	51	45.5	206	1	TVH00A
3	51	45.5	344	2	D83694
4	51	45.5	351	2	E97225
5	50	44.6	323	2	C64087
6	50	44.6	673	2	P82930
7	50	44.6	882	2	S41034
8	49	43.8	218	2	S50566
9	49	43.8	462	2	B32840
10	48	42.9	206	1	TVU00A
11	48	42.9	206	2	JN0622
12	48	42.9	309	2	T23021
13	48	42.9	462	2	S52528
14	47.5	42.4	294	2	S60545
15	47.5	42.4	294	2	S60524
16	47	42.0	159	1	S56237
17	47	42.0	312	2	AC0897
18	47	42.0	335	2	AG2311
19	47	42.0	627	2	B83692
20	47	42.0	659	2	S74435
21	47	42.0	1067	2	T06312
22	46.5	41.5	201	2	E97339
23	46.5	41.5	428	2	G82338
24	46	41.1	118	2	E90178
25	46	41.1	340	2	E69527
26	46	41.1	420	2	C71407
27	46	41.1	472	2	H90563
28	46	41.1	474	2	H72403
29	46	41.1	506	2	AC0845

30	46	41.1	529	2	A65051	YgaA protein - Ec
31	46	41.1	529	2	E91074	probable 2-compone
32	46	41.1	529	2	D85919	probable 2-compone
33	46	41.1	536	1	JC6129	3',5'-cyclic-nucle
34	46	41.1	545	2	G81328	60 kD chaperonin (
35	46	41.1	594	2	A82913	hypothetical prote
36	45.5	40.6	88	2	AB2591	conserved hypotet
37	45.5	40.6	88	2	B97373	hypothetical prote
38	45.5	40.6	422	2	AD0141	adenosylmethionine
39	45	40.2	104	2	P90183	hypothetical prote
40	45	40.2	128	2	C69183	hypothetical prote
41	45	40.2	226	2	S37434	membrane glycopro
42	45	40.2	226	2	D49591	membrane protein M
43	45	40.2	264	2	T38795	conserved uncharac
44	45	40.2	318	2	T43492	hypothetical prote
45	45	40.2	335	2	F72404	flagellar motor sw
46	45	40.2	468	2	F82012	hypothetical prote
47	45	40.2	514	2	T10938	calcium-dependent
48	45	40.2	534	1	A44162	3',5'-cyclic-nucle
49	45	40.2	535	1	A44161	3',5'-cyclic-nucle
50	45	40.2	535	1	A46378	3',5'-cyclic-nucle
51	45	40.2	626	2	AC1619	DNA primase [import
52	45	40.2	626	2	AG1256	DNA primase [import
53	45	40.2	643	2	H64119	threonine-tRNA lig
54	45	40.2	644	2	T02366	hypothetical prote
55	45	40.2	755	2	T47806	hypothetical prote
56	45	40.2	897	2	AC2001	hypothetical prote
57	45	40.2	1052	2	T17093	intraluminal subu
58	45	40.2	1696	2	T00057	hypothetical prote
59	44.5	39.7	146	2	G90201	conserved hypotet
60	44.5	39.7	536	2	T05500	calcium-dependent
61	44.5	39.7	852	2	T12016	envelope glycoproc
62	44	39.3	100	2	T49043	hypothetical prote
63	44	39.3	258	2	A59369	ubiquinol-cytochro
64	44	39.3	308	1	F69752	5-dehydro-4-deoxyg
65	44	39.3	401	2	E72213	probable 2,3-bisph
66	44	39.3	447	2	F90248	hypothetical prote
67	44	39.3	511	2	H89758	histidine ammonia-
68	44	39.3	553	2	H84133	exo-alpha-1,4-gluc
69	44	39.3	571	2	C70353	succinate dehydrog
70	44	39.3	603	2	G82738	gamma-glutamyltran
71	44	39.3	750	2	S34683	hypothetical prote
72	44	39.3	919	2	E83212	probable sensor/re
73	44	39.3	1019	2	F70342	cation efflux syst
74	44	39.3	1577	2	T30858	glucosyltransferas
75	44	39.3	1505	2	E15553	Plexin - African c
76	44	39.3	5369	2	T44807	mycosubtilin synth
77	43.5	38.8	209	2	H69901	general stress pro
78	43.5	38.8	355	2	S74678	hypothetical prote
79	43.5	38.8	429	1	JC5005	adenosylmethionine
80	43.5	38.8	429	2	AG0596	adenosylmethionine
81	43.5	38.8	571	2	T00835	calcium-dependent
82	43	38.4	80	2	B82267	exodeoxyribonuclea
83	43	38.4	145	2	A56085	regulatory protein
84	43	38.4	178	2	AG0049	hypothetical prote
85	43	38.4	199	2	A44033	ubiquinol-cytochro
86	43	38.4	206	1	E64317	hypothetical prote
87	43	38.4	237	2	D97801	hypothetical prote
88	43	38.4	267	2	H69373	hypothetical prote
89	43	38.4	278	2	T24444	hypothetical prote
90	43	38.4	279	2	B72255	dimethyladenosine
91	43	38.4	292	2	D85863	probable regulator
92	43	38.4	292	2	B91019	probable transcrip
93	43	38.4	322	2	S52032	triase-phosphate 1
94	43	38.4	336	2	S74424	sphx protein - Syn
95	43	38.4	353	2	T15429	hypothetical prote
96	43	38.4	420	2	AH2225	two-component sens
97	43	38.4	429	2	D70763	chroonine ammonia-
98	43	38.4	469	2	A72377	6-phosphogluconate
99	43	38.4	481	2	UQ1147	N-acetylmutamoyl-L
100	43	38.4	490	2	T08873	calcium-dependent
101	43	38.4	499	2	AH0485	probable insulinas
102	43	38.4	500	2	A71874	hypothetical prote

103	43	38.4	510	2	B70368	L-aspartate oxidase	176	41.5	37.1	236	2	A86075	probable transcrip
104	43	38.4	521	2	B71717	hypothetical prote	177	41.5	37.1	236	2	S40817	hypothetical prote
105	43	38.4	532	2	S22262	transcription fact	178	41.5	37.1	236	2	B91228	probable transcrip
106	43	38.4	577	2	TS1264	calcium-dependent	179	41.5	37.1	239	2	D70359	conserved hypothet
107	43	38.4	602	2	S60052	calcium-dependent	180	41.5	37.1	239	2	B84964	adenosylmethionine
108	43	38.4	642	2	C81345	hypothetical prote	181	41.5	37.1	450	2	D86356	hypothetical prote
109	43	38.4	759	2	D89946	protein-export mem	182	41.5	37.1	489	2	H86356	probable UDP-gluc
110	43	38.4	1245	2	G88104	protein F40B12.2 [	183	41.5	37.1	559	2	T09038	NADH dehydrogenase
111	43	38.4	1245	2	T31953	hypothetical prote	184	41.5	37.1	639	1	T02784	calcium-dependent
112	43	38.4	1493	2	S61023	hypothetical prote	185	41.5	37.1	678	2	S56284	hypothetical prote
113	42.5	37.9	224	2	D89836	hypothetical prote	186	41.5	37.1	846	1	VCLJND	env. polyprotein pr
114	42.5	37.9	321	2	D89088	conserved hypothet	187	41.5	37.1	886	1	F83862	penicillin-binding
115	42.5	37.9	340	2	PH0217	reverse transcript	188	41	36.6	71	1	RGBOG2	GTP-binding regula
116	42.5	37.9	428	2	S09134	gene ND4L, intcon 1	189	41	36.6	71	2	UC7290	guanine nucleotide
117	42.5	37.9	429	1	XNECDP	adenosylmethionine	190	41	36.6	118	2	G70478	hypothetical prote
118	42.5	37.9	429	2	E85585	7,8-diaminopelargo	191	41	36.6	138	2	H90461	hypothetical prote
119	42.5	37.9	429	2	D90735	7,8-diaminopelargo	192	41	36.6	140	2	A10114	conserved hypothet
120	42.5	37.9	513	2	S21976	probable RNA-direc	193	41	36.6	147	2	A29910	myosin calcium-bln
121	42.5	37.9	556	2	S21347	hypothetical prote	194	41	36.6	150	1	MC2P	calmodulin - f1sbl
122	42.5	37.9	666	2	S71032	flagellar hook-ass	195	41	36.6	150	2	S18394	troponin C isoform
123	42.5	37.9	685	2	S16783	probable RNA-direc	196	41	36.6	152	2	A11018	SoxR protein (limp
124	42.5	37.9	821	2	T24728	hypothetical prote	197	41	36.6	154	2	E91259	SoxR protein (limp
125	42.5	37.9	932	2	H86325	hypothetical prote	198	41	36.6	154	2	A86100	redox-sensing acti
126	42.5	37.9	1601	2	AE2011	hypothetical prote	199	41	36.6	154	2	US0577	soxR protein - Esc
127	42	37.5	58	2	T04616	hypothetical prote	200	41	36.6	156	2	T32236	hypothetical prote
128	42	37.5	82	2	A99836	hypothetical prote	201	41	36.6	159	2	T32233	hypothetical prote
129	42	37.5	82	2	C85694	unknown protein en	202	41	36.6	161	2	S47549	cell division cont
130	42	37.5	103	2	P69110	hypothetical prote	203	41	36.6	169	2	D84864	probable calcium b
131	42	37.5	134	2	AE2496	transposase alt714	204	41	36.6	169	2	H75387	hypothetical prote
132	42	37.5	135	2	T29428	hypothetical prote	205	41	36.6	186	2	F89831	hypothetical prote
133	42	37.5	158	2	A72562	hypothetical prote	206	41	36.6	207	2	A69349	conserved hypothet
134	42	37.5	172	2	G69087	conserved hypothet	207	41	36.6	211	2	T32591	hypothetical prote
135	42	37.5	186	2	F82508	hypothetical prote	208	41	36.6	240	2	T22210	hypothetical prote
136	42	37.5	189	2	B69044	conserved hypothet	209	41	36.6	280	2	F66768	hypothetical prote
137	42	37.5	191	2	T10620	probable calcium-b	210	41	36.6	292	2	AC0791	probable transcrip
138	42	37.5	225	2	AF0219	basal-body rod mod	211	41	36.6	307	2	B69837	hypothetical prote
139	42	37.5	229	1	B43685	nonstructural prot	212	41	36.6	312	1	Q0ECRG	tdcA protein - Esc
140	42	37.5	244	2	E72364	ABC transporter, A	213	41	36.6	312	2	E85973	transcription acti
141	42	37.5	314	2	G70750	DNA-methyltransfer	214	41	36.6	312	2	F91128	transcription acti
142	42	37.5	368	2	B97198	probable enzyme wi	215	41	36.6	325	2	T32838	hypothetical prote
143	42	37.5	377	2	A38862	crRNA-splicing endo	216	41	36.6	325	2	E83165	hypothetical prote
144	42	37.5	389	1	A48329	histidinol-phospha	217	41	36.6	338	2	G71220	hypothetical prote
145	42	37.5	399	1	A43685	polymerase-associ	218	41	36.6	344	2	G75260	response regulator
146	42	37.5	423	2	T29549	hypothetical prote	219	41	36.6	344	2	T48827	hypothetical prote
147	42	37.5	427	2	C87060	phosphogluconate d	220	41	36.6	407	2	S27774	transforming prote
148	42	37.5	451	2	S56717	threonine deaminase	221	41	36.6	408	2	AG1745	amino transferase h
149	42	37.5	464	2	T22087	calcium-dependent	222	41	36.6	416	2	F71869	hypothetical prote
150	42	37.5	468	2	D85828	hypothetical prote	223	41	36.6	420	2	T43932	cell division cont
151	42	37.5	468	2	F90982	gluconate-6-phosph	224	41	36.6	441	2	AB1290	ATP-dependent RNA
152	42	37.5	482	2	T01659	phosphogluconate d	225	41	36.6	442	2	AH1661	ATP-dependent RNA
153	42	37.5	484	2	T01658	phosphogluconate d	226	41	36.6	455	2	H71028	hypothetical prote
154	42	37.5	509	2	AB1295	Bifunctional phosph	227	41	36.6	461	2	S50864	avermectin-sensiti
155	42	37.5	509	2	AC1667	Bifunctional phosph	228	41	36.6	465	2	D83598	probable zinc prot
156	42	37.5	521	2	G96543	calcium-dependent	229	41	36.6	472	1	B53236	transcription fact
157	42	37.5	529	1	S71774	calcium-dependent	230	41	36.6	472	2	AD1889	adenylate cyclase
158	42	37.5	540	2	D81192	hypothetical prote	231	41	36.6	477	2	E64595	hypothetical prote
159	42	37.5	553	1	T02139	calcium-dependent	232	41	36.6	477	2	F71918	phosphogluconate d
160	42	37.5	554	1	T03263	calcium-dependent	233	41	36.6	486	2	S57786	phosphogluconate d
161	42	37.5	601	2	C81044	hypothetical prote	234	41	36.6	492	2	S50554	hypothetical prote
162	42	37.5	674	2	S74506	ribonuclease E - S	235	41	36.6	494	2	S75398	lysine-tRNA ligase
163	42	37.5	750	2	AG3008	polyketide synthet	236	41	36.6	495	1	S46284	calcium-dependent
164	42	37.5	770	2	F98275	saframycin mxi syn	237	41	36.6	495	2	T20754	hypothetical prote
165	42	37.5	979	2	E72236	clostridial-relate	238	41	36.6	501	2	G85097	hypothetical prote
166	42	37.5	1125	2	T30298	dynamin heavy chain	239	41	36.6	510	2	JC7886	cytochrome P450 92
167	42	37.5	1203	2	B55094	chromosomal protei	240	41	36.6	520	2	C84774	probable calcium-d
168	42	37.5	1268	2	A49674	flitchless-I homol	241	41	36.6	526	2	E86149	TlN6.20 protein -
169	42	37.5	1273	2	T42405	sax-3 protein - Ca	242	41	36.6	534	2	H82244	sensor histidine k
170	42	37.5	1286	2	A88396	protein M0E10.2 [	243	41	36.6	538	2	A70485	single-strand-DNA-
171	42	37.5	1386	1	RNLWC2	DNA-directed RNA p	244	41	36.6	546	2	S35311	heat shock cognate
172	42	37.5	1409	2	T29594	hypothetical prote	245	41	36.6	557	2	AC3137	ABC transporter AT
173	42	37.5	1415	2	C86438	hypothetical prote	246	41	36.6	572	2	S58889	collapsin response
174	42	37.5	1733	2	D70887	probable polyketid	247	41	36.6	604	2	G89864	hypothetical prote
175	42	37.5	4488	1	RR1HM2	genome polyprotein	248	41	36.6	611	2	T21747	hypothetical prote

249	41	36.6	627	2	C98148	acetoin catabolism	322	40	35.7	188	2	E82370	Sua5/Ycd10/Yrdc fam
250	41	36.6	627	2	A13139	transcription regu	323	40	35.7	190	2	A90354	conserved hypotet
251	41	36.6	630	2	AC1309	probable ABC trans	324	40	35.7	192	2	T17331	hypothetical prote
252	41	36.6	654	2	T17959	hypothetical prote	325	40	35.7	198	2	T20305	hypothetical prote
253	41	36.6	692	1	S46953	phosphotransferase	326	40	35.7	214	2	T00879	MADS-box protein A
254	41	36.6	695	2	T13639	probable tail-host	327	40	35.7	226	1	H69474	conserved hypotet
255	41	36.6	712	1	A47331	ribonucleoside-tri	328	40	35.7	229	1	D43685	nonstructural prot
256	41	36.6	712	1	AC1058	ribonucleoside-tri	329	40	35.7	231	1	D64170	hypothetical prote
257	41	36.6	712	2	G91280	anaerobic ribonuc	330	40	35.7	231	2	H70157	hypothetical prote
258	41	36.6	712	2	G86121	anaerobic ribonuc	331	40	35.7	231	2	B83060	hypothetical prote
259	41	36.6	712	2	G86121	anaerobic ribonuc	332	40	35.7	234	2	S27956	arginine-rich prot
260	41	36.6	754	2	A82123	topoisomerase IV s	333	40	35.7	235	2	AB1515	probable phosphor
261	41	36.6	785	2	G83025	chemotaxis protein	334	40	35.7	248	2	T04170	MADS box protein -
262	41	36.6	818	2	H83904	hypothetical prote	335	40	35.7	250	2	G81365	probable ABC-type
263	41	36.6	821	2	H84600	probable vacuolar	336	40	35.7	260	2	A90330	hypothetical prote
264	41	36.6	831	2	H84368	MCM / cell divisio	337	40	35.7	270	2	A42882	motility protein (
265	41	36.6	831	2	UC7880	glucosylceramidase	338	40	35.7	282	2	H70571	probable oxidoredu
266	41	36.6	843	2	T13334	probable tail-host	339	40	35.7	294	2	E86731	hypothetical prote
267	41	36.6	847	2	AG1949	hypothetical prote	340	40	35.7	307	2	S16390	auxin-induced prot
268	41	36.6	883	2	B95237	alcohol dehydrogen	341	40	35.7	315	2	AH0897	probable carbohydr
269	41	36.6	890	2	C98101	alcohol-acetaldehy	342	40	35.7	327	2	AI1422	hypothetical prote
270	41	36.6	953	1	B30169	leukotoxin A - Ras	343	40	35.7	328	2	C90196	conserved hypotet
271	41	36.6	1271	2	T43269	microcystin synthe	344	40	35.7	332	2	AF3265	asparaginase (EC 3
272	41	36.6	1411	2	S55123	hypothetical prote	345	40	35.7	333	2	H82245	glyceraldhyde 3-P
273	41	36.6	1557	2	T29132	hypothetical prote	346	40	35.7	336	2	D71016	probable thioredox
274	41	36.6	1795	2	T30332	avirulence protein	347	40	35.7	339	2	H75187	hypothetical prote
275	41	36.6	1819	2	D97033	uncharacterized pr	348	40	35.7	345	2	D75116	thioredoxin reduct
276	41	36.6	3026	2	T28431	variant surface pr	349	40	35.7	351	2	A87716	uroporphyrinogen d
277	40.5	36.2	98	2	D95371	hypothetical prote	350	40	35.7	364	2	T44672	H+-transporting At
278	40.5	36.2	243	2	S43887	restriction endonu	351	40	35.7	367	1	D70395	conserved hypotet
279	40.5	36.2	243	2	F81130	type II restructio	352	40	35.7	372	2	S76448	translational releas
280	40.5	36.2	243	2	H86487	hypothetical prote	353	40	35.7	374	1	E70346	mannosyltransferas
281	40.5	36.2	261	2	B97589	hypothetical prote	354	40	35.7	379	2	H84398	phosphate ABC tran
282	40.5	36.2	291	2	AG2810	1-2,3-butanediol d	355	40	35.7	379	2	S42543	hypothetical prote
283	40.5	36.2	299	2	S60521	envelope chain dehyd	356	40	35.7	383	2	AB1567	hypothetical prote
284	40.5	36.2	299	2	S60552	envelope polypyrte	357	40	35.7	389	2	G72027	conserved hypotet
285	40.5	36.2	299	2	S60551	envelope polypyrte	358	40	35.7	389	2	G86597	CT12 hypotetrical
286	40.5	36.2	299	2	S60523	envelope polypyrte	359	40	35.7	399	1	A43685	polymerase-associ
287	40.5	36.2	299	2	S60554	envelope polypyrte	360	40	35.7	427	2	A53964	carboxyl-terminal
288	40.5	36.2	299	2	S60553	envelope polypyrte	361	40	35.7	443	2	H96841	hypothetical prote
289	40.5	36.2	376	2	T16050	hypothetical prote	362	40	35.7	445	2	T36069	hypothetical prote
290	40.5	36.2	427	2	F87465	GTP-binding protei	363	40	35.7	459	2	F75049	hypothetical prote
291	40.5	36.2	452	2	S10840	gene ND4L intron p	364	40	35.7	462	2	G96506	phosphogluconate d
292	40.5	36.2	459	2	T39668	amino transferase -	365	40	35.7	468	2	I41250	phosphogluconate d
293	40.5	36.2	479	2	F83356	T16R15.2 protein -	366	40	35.7	469	1	TVHHE2	transcription fact
294	40.5	36.2	516	2	T33061	hypothetical prote	367	40	35.7	470	1	S55565	hypothetical 53X p
295	40.5	36.2	523	2	C82289	exopolysphosphate	368	40	35.7	470	2	F91291	probable regulator
296	40.5	36.2	614	2	T33149	hypothetical prote	369	40	35.7	473	2	H86132	probable regulator
297	40.5	36.2	685	2	S65974	conserved hypotet	370	40	35.7	473	2	D83508	two-component resp
298	40.5	36.2	836	2	B84417	cell surface glyco	371	40	35.7	478	1	S73919	pet112 protein hom
299	40.5	36.2	858	1	A40995	starch phosphoryla	372	40	35.7	479	2	T49871	peroxisomal Ca-dep
300	40.5	36.2	852	2	A28459	cell surface glyco	373	40	35.7	487	1	S71770	calcium-dependent
301	40.5	36.2	897	2	G02529	dynein heavy chain	374	40	35.7	490	1	S71776	calcium-dependent
302	40.5	36.2	1481	2	S78373	DNA-directed RNA p	375	40	35.7	511	1	E89775	2',3'-cyclic-nucle
303	40.5	36.2	3746	1	YGPLV3	alpha-aminoadipyl-	376	40	35.7	511	2	T05363	phosphogluconate d
304	40.5	36.2	3770	2	A40889	delta-(L)-alpha-aml	377	40	35.7	513	1	T02259	calcium-dependent
305	40.5	36.2	3791	1	YGPLV8	alpha-aminoadipyl-	378	40	35.7	513	2	S48981	hypothetical prote
306	40.5	36.2	4644	1	A38905	dynein heavy chain	379	40	35.7	530	2	S53392	probable membrane
307	40.5	36.2	4767	2	T31345	hypothetical prote	380	40	35.7	531	1	T02993	calcium-dependent
308	40	35.7	86	2	D69774	PEB1 3'-region hyp	381	40	35.7	533	1	S56652	calcium-dependent
309	40	35.7	105	2	T22980	hypothetical prote	382	40	35.7	536	2	T23346	hypothetical prote
310	40	35.7	126	2	E82184	hypothetical prote	383	40	35.7	538	2	T08874	calcium-dependent
311	40	35.7	134	2	T22275	hypothetical prote	384	40	35.7	540	1	T01989	calcium-dependent
312	40	35.7	146	2	F72638	transcription regu	385	40	35.7	541	2	A82320	methyl-accepting c
313	40	35.7	146	2	D83676	transcription regu	386	40	35.7	543	2	S70013	chaperonin-like pr
314	40	35.7	150	2	H86194	transcriptional prote	387	40	35.7	544	2	I40731	heat shock protein
315	40	35.7	151	2	A97008	transcriptional regu	388	40	35.7	544	2	B41479	60K heat shock pro
316	40	35.7	152	2	G85041	probable calmodul	389	40	35.7	544	2	JL0117	hybp protein - Ch1
317	40	35.7	155	2	G83774	hypothetical prote	390	40	35.7	544	2	B81556	60 kDa chaperonin
318	40	35.7	156	2	T16066	hypothetical prote	391	40	35.7	544	2	F86507	heat shock protein
319	40	35.7	172	2	G69432	hypothetical prote	392	40	35.7	544	2	S19023	chaperonin groEL -
320	40	35.7	177	2	H83323	hypothetical prote	393	40	35.7	544	2	D81709	60 kDa chaperonin
321	40	35.7	177	2	H83323	hypothetical prote	394	40	35.7	544	2	A71555	probable hep-60 -

395	40	35.7	548	2	H95066	helicase, probable
396	40	35.7	550	2	S35309	heat shock protein
397	40	35.7	550	2	T10393	chitinase (EC 3.2.
398	40	35.7	554	2	T25902	hypothetical prote
399	40	35.7	560	2	AB2043	chaperonin GroEL (
400	40	35.7	572	2	UC5316	dihydropyrimidinase
401	40	35.7	573	2	T40474	hypothetical prote
402	40	35.7	584	2	T08678	hypothetical prote
403	40	35.7	606	2	B69805	conserved hypothet
404	40	35.7	608	2	H72292	hypothetical prote
405	40	35.7	622	2	AC1236	acyltransferase (c
406	40	35.7	629	2	AE5536	placatin, intestina
407	40	35.7	642	2	SS9306	probable membrane
408	40	35.7	647	2	C71534	probable transglyc
409	40	35.7	650	2	I49523	tumor necrosis fac
410	40	35.7	680	2	H90558	hypothetical prote
411	40	35.7	757	2	T24266	hypothetical prote
412	40	35.7	774	2	A28392	penicillin amidase
413	40	35.7	777	2	T21048	hypothetical prote
414	40	35.7	819	2	S61217	spectrin alpha II
415	40	35.7	844	2	S77383	hypothetical prote
416	40	35.7	880	2	AC2108	alanyl-tRNA synthe
417	40	35.7	976	2	T40697	processing endopro
418	40	35.7	1002	2	T46033	receptor protein K
419	40	35.7	1013	2	A69226	type I restriction
420	40	35.7	1021	2	AC2202	hypothetical prote
421	40	35.7	1030	2	A32612	spectrin alpha cha
422	40	35.7	1054	2	T07425	conserved hypothet
423	40	35.7	1097	2	AD2572	hypothetical prote
424	40	35.7	1154	2	S69206	regulator protein
425	40	35.7	1247	2	C89583	protein K07E3.1 [1
426	40	35.7	1335	2	T14790	hypothetical prote
427	40	35.7	1441	1	GNVUSV	M polypeptide prec
428	40	35.7	1518	2	A44811	glucosyltransferase
429	40	35.7	1690	2	T35694	ATP dependent DNA
430	40	35.7	2339	2	A45597	DNA-directed RNA p
431	40	35.7	2396	2	T13714	kakapo gene proteol
432	40	35.7	2472	2	A35715	fodrin alpha chain
433	40	35.7	2477	1	SJCHA	spectrin alpha cha
434	40	35.7	3228	2	T21381	hypothetical prote
435	40	35.7	5149	2	P83345	probable non-ribos
436	39.5	35.3	135	2	A81429	hypothetical prote
437	39.5	35.3	165	2	AG2184	hypothetical prote
438	39.5	35.3	202	2	H69902	nitroreductase hom
439	39.5	35.3	206	2	AD1898	urease accessory p
440	39.5	35.3	291	2	A70475	H+-transporting tw
441	39.5	35.3	301	2	S60532	envelope polypept
442	39.5	35.3	301	2	S60531	envelope polypept
443	39.5	35.3	314	2	D89958	catabolite control
444	39.5	35.3	368	2	S54575	hypothetical prote
445	39.5	35.3	481	2	E86356	hypothetical prote
446	39.5	35.3	548	2	AC0871	probable integrase
447	39.5	35.3	552	2	JC4030	DnaJ-like protein
448	39.5	35.3	662	2	G89909	transketolase (imp
449	39.5	35.3	707	2	T42239	probable phosphopr
450	39.5	35.3	722	2	T34072	hypothetical prote
451	39.5	35.3	732	1	JU0132	acylaminoacyl-pept
452	39.5	35.3	732	1	S07624	acylaminoacyl-pept
453	39.5	35.3	751	2	AD2168	phycochrome-like p
454	39.5	35.3	877	2	S76394	hypothetical prote
455	39.5	35.3	888	2	S78288	preprotein translo
456	39.5	35.3	1281	2	I48123	p-glycoprotein iso
457	39.5	35.3	1331	1	XORTDH	xanthine dehydroge
458	39.5	35.3	1343	2	T20718	hypothetical prote
459	39	34.8	36	2	S16552	hypothetical prote
460	39	34.8	40	2	I39944	regulatory extrace
461	39	34.8	46	2	A26929	sacQ protein - Bac
462	39	34.8	81	2	F90454	hypothetical prote
463	39	34.8	89	2	E47758	retrovirus-related
464	39	34.8	92	2	E69408	transcription regu
465	39	34.8	103	2	D83678	hypothetical prote
466	39	34.8	105	2	E86755	prophage p12 prote
467	39	34.8	122	2	T04090	probable thioresox
468	39	34.8	122	2	A45385	translation repres
469	39	34.8	132	2	S76503	hypothetical prote
470	39	34.8	149	2	A33353	calcium-binding pr
471	39	34.8	151	2	S62426	hypothetical prote
472	39	34.8	158	2	JC5434	larva muscle tropo
473	39	34.8	158	2	A38397	tropomyosin C-1 - g
474	39	34.8	161	2	E70381	glycine cleavage s
475	39	34.8	167	2	T43621	hypothetical prote
476	39	34.8	178	2	T22802	hypothetical prote
477	39	34.8	184	2	S41960	ras-related GTP-bi
478	39	34.8	184	2	I55401	Ras-related protei
479	39	34.8	184	2	S16509	DNA-invertase - St
480	39	34.8	192	2	S11781	DNA-invertase - St
481	39	34.8	204	2	C84122	thymidine kinase (
482	39	34.8	208	2	B70208	conserved hypothet
483	39	34.8	209	2	S09885	hypothetical prote
484	39	34.8	219	2	F70474	conserved hypothet
485	39	34.8	229	2	T18629	hypothetical prote
486	39	34.8	233	2	T41263	hypothetical prote
487	39	34.8	238	2	F91221	probable phosphata
488	39	34.8	238	2	A86068	hypothetical phosph
489	39	34.8	238	2	D37841	hypothetical 27.1k
490	39	34.8	240	2	AC1921	hypothetical prote
491	39	34.8	247	2	C71229	hypothetical prote
492	39	34.8	248	2	T20027	hypothetical prote
493	39	34.8	248	2	E90295	hypothetical prote
494	39	34.8	249	2	C90468	hypothetical prote
495	39	34.8	260	1	A38585	deoxycytidine kina
496	39	34.8	260	2	A10934	glutamate racemase
497	39	34.8	269	2	C82080	dihydrodipicolinat
498	39	34.8	270	2	S67389	conserved hypothet
499	39	34.8	278	2	A81266	probable biotin sy
500	39	34.8	280	1	PRSMEA	epidermolytic toxi
501	39	34.8	286	2	C82143	conserved hypothet
502	39	34.8	303	2	S34966	rfbO protein - Shi
503	39	34.8	314	2	C90038	hypothetical prote
504	39	34.8	315	2	A84598	probable triosepho
505	39	34.8	316	2	E90401	hypothetical prote
506	39	34.8	316	2	A99307	hypothetical prote
507	39	34.8	316	2	H90426	hypothetical prote
508	39	34.8	325	2	AC1333	conjugated bile ac
509	39	34.8	334	2	P86226	hypothetical prote
510	39	34.8	338	2	D72327	heat shock operon
511	39	34.8	340	2	I51547	probable RNA-bind
512	39	34.8	342	2	S14432	heterogeneous rbo
513	39	34.8	344	2	B84204	hypothetical prote
514	39	34.8	345	2	AH3131	maleate dehydrogena
515	39	34.8	346	2	C98156	probable L-malate
516	39	34.8	347	2	I51546	probable RNA-bind
517	39	34.8	356	2	A12317	two-component hydr
518	39	34.8	369	2	F81125	glutamate 5-kinase
519	39	34.8	369	2	B81895	probable glutamate
520	39	34.8	371	2	T02284	hypothetical prote
521	39	34.8	387	1	ERADY4	41k fiber protein
522	39	34.8	391	2	T20752	hypothetical prote
523	39	34.8	393	2	S04408	hydroxyneurosporen
524	39	34.8	393	2	E81438	helicase-like prot
525	39	34.8	394	2	H97825	elongation factor
526	39	34.8	398	2	A19371	Ig V-region-like B
527	39	34.8	408	2	AE0103	probable regulator
528	39	34.8	413	2	AE2163	hypothetical prote
529	39	34.8	417	2	S58193	adenosylhomocystei
530	39	34.8	424	2	E64450	hypothetical prote
531	39	34.8	425	2	S17759	protein kinase, ca
532	39	34.8	431	2	A81150	histidyl-tRNA synt
533	39	34.8	442	2	C90224	s-adenosyl-L-homoc
534	39	34.8	445	2	H64067	hypothetical prote
535	39	34.8	446	2	C64205	signal recognition
536	39	34.8	448	2	C82936	signal recognition
537	39	34.8	452	2	JC4100	hydroxyindole O-me
538	39	34.8	453	2	F82702	conserved hypothet
539	39	34.8	465	1	T03024	calcium-dependent
540	39	34.8	465	1	DBECGC	phosphogluconate d



541	39	34.8	468	2	162465	614	38.5	34.4	261	2	A84128	hypothetical prote
542	39	34.8	468	2	162463	615	38.5	34.4	299	2	S60529	envelope polypept
543	39	34.8	469	2	B70486	616	38.5	34.4	299	2	S60528	envelope polypept
544	39	34.8	472	1	A53336	617	38.5	34.4	319	2	H69043	conserved hypochet
545	39	34.8	472	2	AH1246	618	38.5	34.4	327	2	H64155	conserved hypochet
546	39	34.8	472	2	AD1609	619	38.5	34.4	338	2	S45908	hypothetical prote
547	39	34.8	475	2	B27671	620	38.5	34.4	430	2	AB2646	flagellin protein
548	39	34.8	485	2	A84859	621	38.5	34.4	436	2	A97428	flad protein (U951
549	39	34.8	485	2	C97022	622	38.5	34.4	436	2	A13381	selenocysteine lya
550	39	34.8	485	2	P90192	623	38.5	34.4	443	2	B75165	signal recognition
551	39	34.8	494	2	E70352	624	38.5	34.4	459	2	G70672	probable transpos
552	39	34.8	508	1	A43713	625	38.5	34.4	474	2	E83392	probable transcrip
553	39	34.8	508	1	D70747	626	38.5	34.4	502	1	P1WL42	li protein - human
554	39	34.8	530	2	D82412	627	38.5	34.4	533	2	S62489	hypothetical prote
555	39	34.8	531	2	D85059	628	38.5	34.4	563	2	AH2187	DNA mismatch repa
556	39	34.8	532	2	T14335	629	38.5	34.4	634	2	T17232	hypothetical prote
557	39	34.8	532	2	PN0108	630	38.5	34.4	650	2	A11974	ferredoxin-sulfite
558	39	34.8	534	2	T23425	631	38.5	34.4	767	1	S50594	5-methyltetrahydro
559	39	34.8	536	2	S62110	632	38.5	34.4	855	1	VCLJZR	env polypept
560	39	34.8	545	2	D69679	633	38.5	34.4	977	2	E86349	hypothetical prote
561	39	34.8	546	2	S36237	634	38.5	34.4	996	2	T18717	hypothetical prote
562	39	34.8	546	2	B71986	635	38.5	34.4	1032	2	A11697	alpha-mannosidase
563	39	34.8	554	2	T03476	636	38.5	34.4	1048	1	BVBCSC	exonuclease (EC 3.
564	39	34.8	554	2	T43466	637	38.5	34.4	1238	2	A64596	hypothetical prote
565	39	34.8	581	2	S71597	638	38.5	34.4	1562	2	T07323	DNA-directed RNA p
566	39	34.8	583	2	H84810	639	38.5	34.4	1809	2	S57329	tuberous sclerosis
567	39	34.8	583	2	S57721	640	38.5	34.4	2374	2	T21052	hypothetical prote
568	39	34.8	583	2	G64333	641	38.5	33.9	77	2	AH1947	hypothetical prote
569	39	34.8	585	2	G64333	642	38.5	33.9	95	1	LUP610	calpactin I light
570	39	34.8	595	2	S73733	643	38.5	33.9	97	2	UC1139	calpactin I light
571	39	34.8	601	2	T46084	644	38.5	33.9	99	2	D97747	calpactin I light
572	39	34.8	606	2	T11909	645	38.5	33.9	99	2	D97747	hypothetical prote
573	39	34.8	611	1	S62811	646	38.5	33.9	119	2	E84085	arsenate reductase
574	39	34.8	619	2	E81117	647	38.5	33.9	121	2	G75604	hypothetical prote
575	39	34.8	619	2	S67067	648	38.5	33.9	128	2	S75264	hypothetical prote
576	39	34.8	624	2	A55220	649	38.5	33.9	134	2	E85629	hypothetical prote
577	39	34.8	633	2	T47346	650	38.5	33.9	139	2	B86144	transcription term
578	39	34.8	633	2	AH1598	651	38.5	33.9	147	2	D64346	tropoin C isoform
579	39	34.8	633	2	T33940	652	38.5	33.9	150	2	S18435	tropoin C isoform
580	39	34.8	650	2	TC7093	653	38.5	33.9	150	2	S18434	tropoin C isoform
581	39	34.8	657	2	S43415	654	38.5	33.9	150	2	S22208	hypothetical prote
582	39	34.8	664	2	B75532	655	38.5	33.9	151	2	A10635	major curlin chain
583	39	34.8	689	2	H70451	656	38.5	33.9	151	2	JC6039	fimbria protein ag
584	39	34.8	707	2	T20440	657	38.5	33.9	152	2	PT0433	progesterone 11alp
585	39	34.8	717	2	H84057	658	38.5	33.9	159	2	AD2738	conserved hypochet
586	39	34.8	743	2	A97021	659	38.5	33.9	159	2	B97519	hypothetical 17.1k
587	39	34.8	765	2	T22800	660	38.5	33.9	169	1	BCKM	caltractin - Chlam
588	39	34.8	770	2	PN0105	661	38.5	33.9	174	2	AB1443	gp43 (Bacteriophag
589	39	34.8	785	2	T01025	662	38.5	33.9	175	2	A71227	probable cob(I)ala
590	39	34.8	823	2	G89007	663	38.5	33.9	177	2	AC1365	gp43 (Bacteriophag
591	39	34.8	836	2	B96716	664	38.5	33.9	179	2	AG1994	hypothetical prote
592	39	34.8	861	2	T23810	665	38.5	33.9	186	2	F86379	protein P2109.28 l
593	39	34.8	861	2	T23810	666	38.5	33.9	186	2	H64031	hypothetical prote
594	39	34.8	969	2	T23256	667	38.5	33.9	207	2	E38625	GTP-binding prote
595	39	34.8	978	2	T16948	668	38.5	33.9	219	2	S32157	RNA-directed DNA p
596	39	34.8	984	2	F81299	669	38.5	33.9	219	2	S32160	RNA-directed DNA p
597	39	34.8	1057	2	AH2198	670	38.5	33.9	219	2	S32159	RNA-directed DNA p
598	39	34.8	1165	2	S58236	671	38.5	33.9	222	2	H82169	phage shock prote
599	39	34.8	1229	2	F86155	672	38.5	33.9	222	1	VG1HE1	li membrane glycop
600	39	34.8	1353	2	T27404	673	38.5	33.9	228	1	VG1HJH	conserved hypochet
601	39	34.8	1431	2	A45866	674	38.5	33.9	232	2	B86698	H+-transporting AT
602	39	34.8	1441	1	GNVJLC	675	38.5	33.9	234	2	G85098	hypothetical prote
603	39	34.8	1462	2	T06819	676	38.5	33.9	234	2	D84075	hypothetical prote
604	39	34.8	1535	2	T14961	677	38.5	33.9	238	2	AH0918	conserved hypochet
605	39	34.8	1597	2	F71607	678	38.5	33.9	239	2	A97358	glucose-inhibited
606	39	34.8	2059	2	D82671	679	38.5	33.9	241	2	D87547	3-oxoacidate CoA-t
607	39	34.8	2059	2	D82671	680	38.5	33.9	241	2	JX0290	galactose-specific
608	39	34.8	2059	2	D82671	681	38.5	33.9	250	2	T04167	MADS box protein -
609	39	34.8	2059	2	D82671	682	38.5	33.9	254	2	F82151	conserved hypochet
610	39	34.8	2059	2	D82671	683	38.5	33.9	254	2	T03408	MADS box protein -
611	39	34.8	2059	2	D82671	684	38.5	33.9	259	2	AB3750	transcription regu
612	39	34.8	2059	2	D82671	685	38.5	33.9	259	2	AF1102	conserved hypochet
613	39	34.8	2059	2	D82671	686	38.5	33.9	264	2	C84028	septom site-determ

687	38	33.9	265	2	S73334	probable lipoprote	760	38	33.9	431	2	E89829	conserved hypotet
688	38	33.9	265	2	T26442	hypothetical prote	761	38	33.9	433	2	T02157	hypothetical prote
689	38	33.9	269	2	B97113	protein serine/thr	762	38	33.9	436	2	C84743	probable tyrosine-
690	38	33.9	275	2	B64977	hypothetical prote	763	38	33.9	440	1	T06837	protochlorophyllid
691	38	33.9	275	2	A90992	hypothetical prote	764	38	33.9	442	2	G86294	T24D18.11 protein
692	38	33.9	275	2	C85837	hypothetical prote	765	38	33.9	443	2	S65963	flavastacin (EC 3.
693	38	33.9	276	2	T43541	purine nucleotide	766	38	33.9	449	2	H81835	probable glutamate
694	38	33.9	283	2	B81288	hypothetical prote	767	38	33.9	449	2	H81128	probable glutamate
695	38	33.9	285	2	D95095	hypothetical prote	768	38	33.9	457	2	T44879	acetyltransferase
696	38	33.9	287	2	H69067	ATP phosphoribosyl	769	38	33.9	459	2	E86640	argininosuccinate
697	38	33.9	287	2	AC0476	probable glutamate	770	38	33.9	460	2	D70435	hypothetical prote
698	38	33.9	292	2	S60950	probable membrane	771	38	33.9	461	2	A32008	site-specific DNA-
699	38	33.9	294	2	C97774	dihydrodipicolinat	772	38	33.9	465	2	H90508	cobryic acid synth
700	38	33.9	295	2	T25085	hypothetical prote	773	38	33.9	469	2	AD1926	hypothetical prote
701	38	33.9	295	2	H91117	probable transcrip	774	38	33.9	471	2	A28568	pneumolysin - Stre
702	38	33.9	295	2	G85962	probable transcrip	775	38	33.9	471	2	F95224	pneumolysin (impor
703	38	33.9	298	2	F70714	hypothetical prote	776	38	33.9	471	2	A99089	hypothetical prote
704	38	33.9	299	2	B83979	3-hydroxyisobutyla	777	38	33.9	475	1	Z4BPT4	helicase (EC 3.6.1
705	38	33.9	299	2	D83010	probable binding p	778	38	33.9	486	2	AF1575	acetaldehyde dehyd
706	38	33.9	300	2	S73402	1-phosphofructokin	779	38	33.9	486	2	AC1222	hypothetical prote
707	38	33.9	300	2	AC1088	transcription regu	780	38	33.9	490	2	D84592	hypothetical prote
708	38	33.9	300	2	S60558	envelope polypote	781	38	33.9	492	2	S64588	phosphoglucanate d
709	38	33.9	300	2	S60526	envelope polypote	782	38	33.9	504	2	S74034	amidase (EC 3.5.1.
710	38	33.9	301	2	A70731	probable glycerolp	783	38	33.9	505	1	E69417	probable thymidine
711	38	33.9	304	2	T22697	hypothetical prote	784	38	33.9	506	2	C70468	phosphoribosylamin
712	38	33.9	306	2	A97963	methenyltetrahydro	785	38	33.9	509	2	B84643	hypothetical prote
713	38	33.9	309	2	S46684	killer toxin insen	786	38	33.9	516	2	S44191	carboxypeptidase D
714	38	33.9	311	2	T13548	hypothetical prote	787	38	33.9	518	2	AH1211	GMP synthetase hom
715	38	33.9	311	2	C83493	hypothetical prote	788	38	33.9	518	2	AH1567	GMP synthetase hom
716	38	33.9	312	2	T20932	hypothetical prote	789	38	33.9	523	2	AG1189	ABC transporter AT
717	38	33.9	314	2	I37383	FAS soluble protei	790	38	33.9	523	2	AH1547	ABC transporter AT
718	38	33.9	316	2	F85629	hypothetical prote	791	38	33.9	525	2	AF0349	GMP synthase (glut
719	38	33.9	317	2	S54548	hypothetical prote	792	38	33.9	532	2	S26877	globul protein - re
720	38	33.9	322	2	E71137	hypothetical prote	793	38	33.9	534	2	S74322	chaperonin groEL-2
721	38	33.9	323	2	H69346	tyrosyl-tRNA synth	794	38	33.9	555	2	AG1914	carbon dioxide con
722	38	33.9	323	2	D86216	protein T23G18.8 (	795	38	33.9	557	2	E95945	probable urocanate
723	38	33.9	323	2	E71134	hypothetical prote	796	38	33.9	559	2	B47175	reverse transcript
724	38	33.9	333	2	S42424	apoptosis-mediatin	797	38	33.9	560	1	DOCGA	NAD-diphthamide AD
725	38	33.9	335	2	A40036	interleukin-5 rece	798	38	33.9	560	2	T46189	calcium-dependent
726	38	33.9	336	2	A40267	hypothetical prote	799	38	33.9	560	2	F70719	hypothetical prote
727	38	33.9	336	2	AB2525	hypothetical prote	800	38	33.9	560	2	F70719	hypothetical prote
728	38	33.9	345	1	PPPA	papain (EC 3.4.22.	801	38	33.9	564	2	C84188	glutathione-disulf
729	38	33.9	347	2	D69166	NS,N10-methylene	802	38	33.9	565	2	T47625	hypothetical prote
730	38	33.9	350	2	E81856	probable RTX fam1	803	38	33.9	566	2	T34053	hypothetical prote
731	38	33.9	352	2	T21909	hypothetical prote	804	38	33.9	571	1	RNCW7H	transcription init
732	38	33.9	353	2	I40376	carbamoylphosphate	805	38	33.9	571	1	RNCW7H	transcription init
733	38	33.9	364	2	A84099	nifs family enzyme	806	38	33.9	571	2	I40872	transcription init
734	38	33.9	367	2	D72469	probable Sna5 prote	807	38	33.9	571	2	A81653	RNA polymerase sig
735	38	33.9	369	2	T25321	hypothetical prote	808	38	33.9	572	2	UC5317	dihydropyrimidinas
736	38	33.9	371	2	A10301	probable exported	809	38	33.9	575	2	S49985	dihydropyrimidinas
737	38	33.9	372	2	AF1220	NADPH-dependent bu	810	38	33.9	575	2	C85059	probable calcium d
738	38	33.9	372	2	A11573	NADPH-dependent bu	811	38	33.9	586	2	C83262	hypothetical prote
739	38	33.9	376	2	D97175	nifs family enzyme	812	38	33.9	587	2	E82431	methyl-accepting c
740	38	33.9	376	2	B96698	unknown protein p1	813	38	33.9	589	2	AB0613	conserved hypotet
741	38	33.9	377	2	S44844	KO6H7.4 protein -	814	38	33.9	591	2	P95152	v-type sodium ATP
742	38	33.9	379	2	F71533	hypothetical prote	815	38	33.9	592	2	F81417	MCP-domain signal
743	38	33.9	381	2	S61229	cycH protein - Rhl	816	38	33.9	596	2	T23685	hypothetical prote
744	38	33.9	382	2	S51962	FUM49 protein - Ye	817	38	33.9	600	2	C69371	conserved hypotet
745	38	33.9	382	2	F82428	iron-containing al	818	38	33.9	602	2	T13219	major capsid prote
746	38	33.9	388	1	S22387	cuticle-degrading	819	38	33.9	602	2	C75120	hypothetical prote
747	38	33.9	394	2	F82507	proteinase VCA0045	820	38	33.9	614	1	QRECBT	vitamin b12 recept
748	38	33.9	396	2	AE2151	glycerol dehydroge	821	38	33.9	614	2	A98241	hypothetical prote
749	38	33.9	397	2	S30023	antiviral protein	822	38	33.9	614	2	F86088	hypothetical prote
750	38	33.9	399	1	D64327	H+-transporting tw	823	38	33.9	622	2	A37442	murine ecotropic r
751	38	33.9	400	2	B81087	FtppC/C-related pro	824	38	33.9	624	2	A53035	ecotropic retrovir
752	38	33.9	407	2	G90875	hypothetical prote	825	38	33.9	627	2	B70122	glucose-inhibited
753	38	33.9	414	2	D86764	hypothetical prote	826	38	33.9	627	2	T02415	probable homeodoma
754	38	33.9	420	2	S73475	serine-tRNA ligase	827	38	33.9	627	2	D96956	ntic family transc
755	38	33.9	420	2	S21052	interleukin-5 rece	828	38	33.9	629	2	S29685	retroviral recepto
756	38	33.9	421	2	C70038	maltoase/maltodextr	829	38	33.9	629	2	T07426	probable polygalac
757	38	33.9	426	1	A48829	transcription fact	830	38	33.9	630	1	A37097	fibrin - chicken
758	38	33.9	429	1	B82181	GGDPF family prote	831	38	33.9	630	1	AC1681	probable ABC trans
759	38	33.9	431	2	A72549	probable pyruvate	832	38	33.9	634	2	E96840	hypothetical prote

833	38	33.9	640	2	T32885	hypothetical prote	906	37.5	33.5	113	1	RDOP1	acidic ribosomal p
834	38	33.9	650	2	T00094	endostyle-specific	907	37.5	33.5	114	2	E86533	protein P282.12 (l
835	38	33.9	650	2	AB1738	probable Na+/H+ an	908	37.5	33.5	150	2	T05295	hypothetical prote
836	38	33.9	650	2	AI1368	probable Na+/H+ an	909	37.5	33.5	157	2	P83464	flagellar motor sw
837	38	33.9	654	2	I56134	tumor necrosis fac	910	37.5	33.5	162	2	T52639	hypothetical prote
838	38	33.9	657	2	A46128	histidine ammonia-	911	37.5	33.5	171	2	S08245	hypothetical prote
839	38	33.9	657	2	AS4011	cationic amino aci	912	37.5	33.5	189	2	S39864	late competence op
840	38	33.9	663	2	AF1799	hypothetical prote	913	37.5	33.5	231	2	G70000	two-component resp
841	38	33.9	666	2	D63103	DNA helicase (EC 3	914	37.5	33.5	238	2	B69373	phosphoribosylform
842	38	33.9	666	2	D63366	conserved hypocher	915	37.5	33.5	240	2	D75203	hypothetical prote
843	38	33.9	682	1	HHBYK2	dnak-type molecula	916	37.5	33.5	271	2	G64959	hypothetical prote
844	38	33.9	687	2	T16352	hypothetical prote	917	37.5	33.5	271	2	E85813	hypothetical prote
845	38	33.9	687	2	D84126	penicillin-binding	918	37.5	33.5	271	2	E90965	hypothetical prote
846	38	33.9	719	1	JC4580	replication licens	919	37.5	33.5	276	2	AD1765	hypothetical cell
847	38	33.9	719	1	S70583	replication licens	920	37.5	33.5	279	2	A86312	Flu6.5 protein -
848	38	33.9	750	2	C87159	cation-transportin	921	37.5	33.5	282	2	S75960	nitrate transport
849	38	33.9	750	2	S77653	cation-transportin	922	37.5	33.5	291	2	AI3092	hypothetical prote
850	38	33.9	796	2	D97065	transketolase [imp	923	37.5	33.5	293	2	T46812	isopentenyl-diphos
851	38	33.9	802	1	A44223	DNA excision repai	924	37.5	33.5	293	2	T51248	isopentenyl-diphos
852	38	33.9	809	2	E71265	hypothetical prote	925	37.5	33.5	298	2	C86871	conserved hypocher
853	38	33.9	812	2	S74856	hypothetical prote	926	37.5	33.5	305	2	T52027	isopentenyl-diphos
854	38	33.9	819	1	B72128	hypothetical prote	927	37.5	33.5	323	2	UT0755	ethylene-forming e
855	38	33.9	819	1	E86494	endopeptidase Va (	928	37.5	33.5	323	2	AB6184	hypothetical prote
856	38	33.9	821	2	E87503	1,4-beta-D-glucan	929	37.5	33.5	337	2	P85098	hypothetical prote
857	38	33.9	826	1	A31822	villin - chicken	930	37.5	33.5	357	2	A96194	hypothetical prote
858	38	33.9	833	2	H90821	probable portal pr	931	37.5	33.5	393	2	T00647	glycosyl transfera
859	38	33.9	859	2	S51546	probable portal pr	932	37.5	33.5	398	2	C86749	hypothetical prote
860	38	33.9	861	2	B85844	probable portal pr	933	37.5	33.5	407	2	H85091	hypothetical prote
861	38	33.9	871	2	S62415	major facilitator	934	37.5	33.5	424	2	S12785	protein ch-42 prec
862	38	33.9	881	2	E82097	protein-P-II uridy	935	37.5	33.5	440	2	AF1953	two-component hybr
863	38	33.9	886	2	T47455	centromere protein	936	37.5	33.5	482	2	T33651	hypothetical prote
864	38	33.9	915	2	C71455	alanine-tRNA ligase	937	37.5	33.5	503	2	T52172	probable cytochrom
865	38	33.9	918	2	E90542	lipoprotein [impor	938	37.5	33.5	529	2	E97025	spovB related memb
866	38	33.9	933	2	S59317	DIP2 protein - yea	939	37.5	33.5	532	2	T33511	hypothetical prote
867	38	33.9	954	2	G71496	hypothetical prote	940	37.5	33.5	567	2	T33650	hypothetical prote
868	38	33.9	956	2	H81654	conserved hypocher	941	37.5	33.5	605	2	JC5239	insulin-like growt
869	38	33.9	979	2	D96574	hypothetical prote	942	37.5	33.5	605	2	A41915	insulin-like growt
870	38	33.9	985	2	D82776	pyruvate dehydrog	943	37.5	33.5	642	2	G69786	ABC transporter (A
871	38	33.9	1003	1	GNMVLV	HIV-1 retropepsin	944	37.5	33.5	702	2	G83386	elongation factor
872	38	33.9	1005	2	F90099	hypothetical prote	945	37.5	33.5	837	2	B82932	preprotein translo
873	38	33.9	1012	1	GNMVL	HIV-1 retropepsin	946	37.5	33.5	912	2	T31223	creat protein homol
874	38	33.9	1015	1	GNMVL	HIV-1 retropepsin	947	37.5	33.5	957	2	AH2227	cation-transportin
875	38	33.9	1037	2	SS1900	hypothetical prote	948	37.5	33.5	1005	2	T18537	Ig heavy chain - c
876	38	33.9	1072	2	AD1280	SNF2-type helicase	949	37.5	33.5	1076	2	T39580	ncaa protein - Alc
877	38	33.9	1181	2	B64516	hypothetical prote	950	37.5	33.5	1113	2	H84105	hypothetical prote
878	38	33.9	1187	2	T46637	transcription fact	951	37.5	33.5	1114	2	S51470	hypothetical prote
879	38	33.9	1188	2	T46608	zinc finger protei	952	37.5	33.5	1224	1	S58884	Ran-binding protei
880	38	33.9	1190	2	A82615	cobalamine-depende	953	37.5	33.0	72	2	A35731	Ca2+-transporting
881	38	33.9	1212	2	A96971	P-glycoprotein-lik	954	37.5	33.0	75	2	AC1755	hypothetical prote
882	38	33.9	1229	2	D85023	P-glycoprotein-lik	955	37.5	33.0	87	2	H64540	hypothetical prote
883	38	33.9	1230	2	TS2319	probable P-glycopr	956	37.5	33.0	87	2	C71966	hypothetical prote
884	38	33.9	1230	2	E85023	probable P-glycopr	957	37.5	33.0	88	2	E75144	hypothetical prote
885	38	33.9	1278	2	E86155	period protein hom	958	37.5	33.0	93	2	H69289	conserved hypocher
886	38	33.9	1290	2	T00018	period protein hom	959	37.5	33.0	104	2	H90489	partial transposas
887	38	33.9	1291	2	T00019	period protein hom	960	37.5	33.0	116	2	F82110	arsenate reductase
888	38	33.9	1305	2	T00670	probable inositol	961	37.5	33.0	116	2	C65214	hypothetical 13.0
889	38	33.9	1350	2	T31353	polyprotein - Arab	962	37.5	33.0	116	2	P86099	hypothetical prote
890	38	33.9	1471	2	T19506	hypothetical prote	963	37.5	33.0	116	2	B91259	hypothetical prote
891	38	33.9	1489	2	G83771	glucosyltransferas	964	37.5	33.0	124	2	G84294	hypothetical prote
892	38	33.9	1539	2	S22737	hypothetical prote	965	37.5	33.0	127	2	D75264	transcription regu
893	38	33.9	1614	2	T29861	hypothetical prote	966	37.5	33.0	130	2	S55385	PEA-15 protein - m
894	38	33.9	1635	2	AI0452	hemolysin (importe	967	37.5	33.0	135	2	D71659	hypothetical prote
895	38	33.9	1778	2	T50074	probable nucleopor	968	37.5	33.0	135	2	S22510	H+-transporting tw
896	38	33.9	1849	2	T00415	hypothetical prote	969	37.5	33.0	142	2	T24862	hypothetical prote
897	38	33.9	1935	1	S06006	myosin beta heavy	970	37.5	33.0	142	2	S75218	hypothetical prote
898	38	33.9	1935	1	A59286	myosin heavy chain	971	37.5	33.0	142	2	D86348	F24U8.15 protein (
899	38	33.9	2020	2	C48399	ABC-type transport	972	37.5	33.0	143	2	JC5246	allograft inflama
900	38	33.9	2025	2	T03884	hypothetical prote	973	37.5	33.0	146	2	JC4902	ionized calcium bi
901	38	33.9	2241	2	S09811	hypothetical prote	974	37.5	33.0	147	2	C95869	probable transcrip
902	38	33.9	2829	2	A42771	reticulocyte-bind	975	37.5	33.0	147	2	I55617	allograft inflama
903	38	33.9	4684	2	A59404	plectin (imported)	976	37.5	33.0	151	2	D86891	hypothetical prote
904	38	33.9	4687	1	A39638	plectin - rat	977	37.5	33.0	151	2	D86891	hypothetical prote
905	38	33.9	92	2	H82371	conserved hypocher	978	37.5	33.0	154	2	AB1270	hypothetical prote

```
979 37 33.0 154 2 AD1632 hypothetical prote
980 37 33.0 156 2 E90510 conserved hypothet
981 37 33.0 157 2 AD2320 hypothetical prote
982 37 33.0 159 2 P84091 hypothetical prote
983 37 33.0 163 2 H64320 molybdenum cofact
984 37 33.0 168 2 S62881 calcium binding pr
985 37 33.0 169 2 S77820 hypothetical excinucle
986 37 33.0 171 2 C64122 hypothetical prote
987 37 33.0 184 2 S56441 18.2K protein prec
988 37 33.0 184 2 B91278 hypothetical prote
989 37 33.0 184 2 B86119 hypothetical prote
990 37 33.0 185 2 AE1320 hypothetical prote
991 37 33.0 185 2 S50537 hypothetical prote
992 37 33.0 186 2 AB0062 conserved hypothet
993 37 33.0 187 2 H81033 oligoribonuclease
994 37 33.0 187 2 F81978 probable oligoribo
995 37 33.0 187 2 AG2721 conserved hypothet
996 37 33.0 189 2 T46076 conserved hypothet
997 37 33.0 190 2 T08258 conserved hypothet
998 37 33.0 192 2 D97503 hypothetical prote
999 37 33.0 195 2 F81255 amidotransferase H
1000 37 33.0 195 2 A96731 unknown protein F5
```

## ALIGNMENTS

## RESULT 1

homocitrate synthase (EC 4.1.3.21) [validated] - Thermus aquaticus

C/Species: Thermus aquaticus

C/Date: 28-Jul-2000 #sequence\_revision 28-Jul-2000 #text\_change 09-Jul-2004

C/Accession: T51170

R/Kosuge, T.; Hoshino, T.

submitted to the EMBL Data Library, October 1998

A/Description: lysine is synthesized through the alpha-aminoadipate pathway in Thermus

A/Reference number: Z25321

A/Accession: T51170

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-376 <KOS>

A/Cross-references: UNIPROT:O87198; EMBL:AB018379; PIDD:BAJ3785.1

A/Experimental source: strain HB27

C/Genetics:

A/Function:

A/Description: EC 4.1.3.21 [validated; PMID:99085673]

A/Superfamily: hydroxymethylglutaryl-CoA lyase

C/Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase

Query Match 51.8%; Score 58; DB 2; Length 376;

Best Local Similarity 47.4%; Pred. No. 2.9;

Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLLEQW 19

DB 355 LADRGQTLLELDRLRLREW 373

## RESULT 2

TVHUA

transforming protein ralA - human

N/Alternate names: GTP-binding protein ral

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004

C/Accession: S04596; A34387

R/Chardin, P.; Tavlitian, A.

Nucleic Acids Res. 17, 4380, 1989

A/Title: Coding sequences of human ralA and ralB cDNAs.

A/Reference number: S04596; PMID:89296492; PMID:2662142

A/Accession: S04596

A/Molecule type: mRNA

A/Residues: 1-206 <CHA>

A/Cross-references: UNIPROT:P11233; GB:X15014; NID:g35845; PIDD:CAA33118.1; PID:g35846

J/Polakis, P.G.; Weber, R.F.; Nevins, B.; Didsbury, J.R.; Evans, T.; Snyderman, R.

R. Biol. Chem. 264, 16383-16389, 1989

A/Title: Identification of the ral and rac1 gene products, low molecular mass GTP-binding

A/Reference number: A34387; PMID:89380251; PMID:2550440

A/Accession: A34387

A/Molecule type: mRNA

A/Residues: 1,'VDYL',3-206 <POL>

A/Cross-references: GB:M29893; NID:g190849; PIDD:AAA6542.1; PID:g190850

A/Note: parts of this sequence were confirmed by peptide sequencing

C/Genetics:

A/Gene: GDB:RALA

A/Cross-references: GDB:120723; OMIM:179550

A/Map position: 7pter-7cen

C/Superfamily: ras transforming protein; translation elongation factor Tu homology

C/Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleoti

F:15-130/Domain: translation elongation factor Tu homology <ETU>

F:21-28/Region: nucleotide-binding motif A (P-loop)

F:127-130/Region: GTP-binding NKXD motif

F:157-159/Region: GTP-binding SAK/L motif

F:27,28,46,127,128,130,157/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #stat

F:203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

F:203/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match 45.5%; Score 51; DB 1; Length 206;

Best Local Similarity 42.9%; Pred. No. 13;

Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLLEQWNL 21

DB 131 LBDKQVSEAKNRABQNNV 151

## RESULT 3

hypothetical protein BH1956 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C/Accession: D83894

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; PMID:120512582; PMID:11058132

A/Accession: D83894

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-344 <STO>

A/Cross-references: UNIPROT:Q9KHI1; GB:AP001513; GB:BA000004; NID:g10174345; PIDD:BA056;

A/Experimental source: strain C-125

C/Genetics:

A/Gene: BH1956

Query Match 45.5%; Score 51; DB 2; Length 344;

Best Local Similarity 41.4%; Pred. No. 23;

Matches 12; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

QY 1 MADNGTIVBELKQLLEQWNL 21

DB 273 MGDNGQATVGENKQALVDLRRLLEPWKI 301

## RESULT 4

E97225

carbamoylphosphate synthase small chain [imported] - Clostridium acetobutylicum

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C/Accession: E97225

R/Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A/Reference number: A96900; PMID:12159325; PMID:21359325

A/Accession: E97225

```

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <KIR>
A:Cross-references: UNIPROT:Q9JFT2; GB:AE001437; P1DN:AAK80592.1; P1D:G15025673; GSPDB:G:
C:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2645
C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbam
OY
Query Match 45.5%; Score 51; DB 2; Length 351;
Best Local Similarity 42.1%; Pred. No. 24;
Matches 8; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
4 NGTTVEELKQLEQWLV 22
||::|||::|:|
Db 132 NGELISIELKQMDASNI 150

RESULT 5
C64087
exopolysphatase ppx homolog - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: C64087
R:Reichmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;
J. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J.;
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A.:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64087
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-323 <TIGR>
A:Cross-references: UNIPROT:P44828; GB:U32752; GB:L42023; NID:G1573692; P1DN:AAK22355.1
OY
Query Match 44.6%; Score 50; DB 2; Length 323;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
4 NGTTVEELKQLEQ 18
|||::|:|
Db 238 NGTTAERLALAIQ 252

RESULT 6
F82930
DNA ligase U0121 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
C:Accession: F82930
R:Glase, J.I.; Lebkowitz, E.J.; Glase, J.S.; Heiner, C.R.; Chen, E.Y.; Caswell, G.H.
Submitted to Genbank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
A:Reference number: A82870
A:Accession: F82930
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-673 <GLA>
A:Cross-references: GB:AE002113; GB:AF222894; NID:G6899078; P1DN:AAF30527.1; GSPDB:GN001
C:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: lig; U0121
A:Genetic code: SGC3
C:Superfamily: NAD+-dependent DNA ligase, ligA type
OY
Query Match 44.6%; Score 50; DB 2; Length 673;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
9 VEEIKQLLEQWV 20
::|||::|:|

```

```

Db          8 IDELKQKLDQNN 19

RESULT 7
S41034
hypothetical protein R10B12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41034
R:Smith, A.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41034
A:Accession: S41034
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-882 <SM1>
A:Cross-references: UNIPROT:O81115; EMBL:Z29561; NID:G450897; PID:G450898
C:Genetics:
A:Introns: 72/2; 324/3; 359/1; 400/2; 722/1; 743/1; 782/1; 818/1

Query Match          44.6%; Score 50; DB 2; Length 882;
Best Local Similarity 47.6%; Pred. No. 84;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY          2 ADNGITVEELKQLLEQNNLV 22
| | | | | | | | | |
Db          548 ATGTDIVRLQLQFMSQNNV 568

RESULT 8
S50566
hypothetical protein YER063w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50566
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612.
A:Description number: S50427
A:Accession: S50566
A:Molecule type: DNA
A:Residues: 1-218 <DIE>
A:Cross-references: UNIPROT:P40040; EMBL:U18813; NID:G1381127; PID:G603299; GSPDB:GN000001
C:Genetics:
A:Gene: SGD:THO1; MIPS:YER063w
A:Cross-references: SGD:S0000865
A:Map position: 5R

Query Match          43.8%; Score 49; DB 2; Length 218;
Best Local Similarity 52.4%; Pred. No. 27;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY          1 MADNGITVEELKQLLEQNNLV 21
| | | | | | | | | |
Db          1 MADYSLTVVQLKDLTKNNL 21

RESULT 9
B32840
anthranilate synthase (EC 4.1.3.27) component I - Leptospira biflexa
C:Species: Leptospira biflexa
C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 09-Jul-2004
C:Accession: B32840
R:Yelton, D.B.; Peng, S.L.
J: Bacteriol. 171, 2083-2089, 1989
A:Title: Identification and nucleotide sequence of the Leptospira biflexa serovar patoc
A:Reference number: A32840; MUID:89197778; PMID:2703466
A:Accession: B32840
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <YEL>
A:Cross-references: UNIPROT:P20463; GB:M22468; NID:G149627; PID:AA888216.1; PID:G149628
C:Superfamily: anthranilate synthase component I

```



```

560545
envelope polypotein gp41 - human immunodeficiency virus type 1 (isolate CI-45-1) (Fragm
C:Species: human immunodeficiency virus type 1, HIV-1
A:Varety: isolate CI-45-1
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60545
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700; PMID:8011235
A:Accession: S60545
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-294 <JAN>
A:Cross-references: UNIPROT:Q76190; EMBL:X72047; NID:g468669; PIDN:CAA50930.1; PID:g4686
A:Experimental source: isolate CI-45-1
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Genetics:
C:Superfamily: type B retrovirus env polypotein
C:Keywords: AIDS; glycoprotein; immunodeficiency; polypotein

Query Match 42.4%; Score 47.5; DB 2; Length 294;
Best Local Similarity 45.0%; Pred. No. 58;
Matches 9; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

OY 4 NGTTTVE-ELKQLEQNLV 22
|||||: :|||: |
Db 136 NGTTTLOCKIKQIVNMOKV 155

RESULT 15
560524
envelope polypotein gp41 - human immunodeficiency virus type 1 (isolate CI-45-3) (Fragm
C:Species: human immunodeficiency virus type 1, HIV-1
A:Varety: isolate CI-45-3
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60524
R:Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A:Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700; PMID:8011235
A:Accession: S60524
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-294 <JAN>
A:Cross-references: UNIPROT:Q76168; EMBL:X72027; NID:g468780; PIDN:CAA50910.1; PID:g4687
A:Experimental source: isolate CI-45-3
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Genetics:
C:Superfamily: type B retrovirus env polypotein
C:Keywords: AIDS; glycoprotein; immunodeficiency; polypotein

Query Match 42.4%; Score 47.5; DB 2; Length 294;
Best Local Similarity 45.0%; Pred. No. 58;
Matches 9; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

OY 4 NGTTTVE-ELKQLEQNLV 22
|||||: :|||: |
Db 136 NGTTTLOCKIKQIVNMOKV 155

RESULT 16
566237
glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) [validated] - yeast (Saccharomyces
N:Alternate names: phosphoglucosamine acetylase; phosphoglucosamine transferase; probosc
C:Species: saccharomyces cerevisiae
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C:Accession: S56237; S48321; S62296
R:Murakami, Y.; Naito, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasamura, S.I.; Sasamura
submitted to the EMBL Data Library, May 1995
Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cere

```

```

A:Reference number: S56166
A:Accession: S56237
A:Molecule type: DNA
A:Residues: 1-159 <MOD>
A:Cross-references: UNIPROT:P43577; EMBL:D50617; NID:g836685; PIDN:BAA09221.1; PID:g83673; R.Churcher, C.
submitted to the EMBL Data Library, September 1994
A:Reference number: S48310
A:Accession: S48321
A:Molecule type: DNA
A:Residues: 1-111, 'ASS' <CHU>
A:Cross-references: EMBL:D46255; NID:g559925; PIDN:CAA6352.1; PID:g559937; GSPDB:GNO0006
R.Murakami, Y.
submitted to the EMBL Data Library, December 1994
A:Reference number: S62230
A:Accession: S62296
A:Molecule type: DNA
A:Residues: 1-159 <MOD>
A:Cross-references: EMBL:D44596; NID:g1100783; PIDN:BAA08000.1; PID:g1100787
C:Genetics:
A:Gene: SGD:GNA1; GNA1; MIPS:YPL017c
A:Cross-references: MIPS:YPL017c; SGD:S0001877
A:Map position: 6L
C:Function:
A:Description: EC 2.3.1.4 [validated, MUID:99085039]; glucosamine-phosphate N-acetyltran:
A:Note: phosphoglucosamine acetyltransferase activity has been shown in vitro, by incubat
A:acetylglucosamine is produced from glucosamine 6-phosphate, indicating that 142-Phe and
C:Superfamily: Saccharomyces glucosamine-phosphate N-acetyltransferase
C:Keywords: acyltransferase; coenzyme A

Query Match 42.0%; Score 47; DB 1; Length 159;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTTVEELKOLLEOWN 20
DB 31 GTTPESFSKLIKTYN 46

RESULT 17
AC0897
TDC operon transcription activator STY3428 [imported] - Salmonella enterica subsp. enteri
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0897
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moll, S.; O.Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0897
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07769.1; PID:g16504318; GSPDB:GNO0176
C:Genetics:
A:Gene: STY3428
C:Superfamily: regulatory protein 1lvv

Query Match 42.0%; Score 47; DB 2; Length 312;
Best Local Similarity 64.7%; Pred. No. 72;
Matches 11; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 5 GTTVEELKOLLEOWN 21
DB 185 GTTLESIKD--EOWAL 199

RESULT 18
AG2311

```





Db 49 DRGTTTEBATECRCKRDPHNAKYIREVNETWN 81

RESULT 23

G82238

adenovylmethionine-8-amino-7-oxononanoate aminotransferase VC1111 [imported] - *Vibrio cholerae*

C:Species: *Vibrio cholerae*

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C:Accession: G82238

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardon, D.; Ermolenko, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers, F.1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the *cholera* pathogen *Vibrio cholerae*.

A:Reference number: A82035; PMID:20406833; PMID:10952301

A:Accession: G82238

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-428 <HEI>

A:Cross-references: UNIPROT:Q9K525; GB:AE004192; GB:AE003852; NID:9655581; PIDN:AAF9427

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1111

A:Map position: 1

C:Superfamily: ornithine-oxo-acid aminotransferase

Query Match 41.5%; Score 46.5; DB 2; Length 428;

Best Local Similarity 42.9%; Pred. No. 1.2e+02;

Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 MADNGTITVE-ELKQLEQWN 20

Db 107 LADSGSVAVEVSLKMLQVWH 127

RESULT 24

E80178

hypothetical protein pdcfs [imported] - *Sulfolobus solfataricus*

C:Species: *Sulfolobus solfataricus*

C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C:Accession: E80178

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F. et al.; Ragun, M.A.; Sengen, C.W.; Van der Oost, J.

submitted to GenBank April 2001

A:Description: *Sulfolobus solfataricus* complete genome.

A:Reference number: A99139

A:Accession: E90178

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-118 <KUR>

A:Cross-references: UNIPROT:Q980F8; GB:AE006641; NID:913613498; PIDN:AAK40684.1; GSPDB:C

C:Genetics:

A:Gene: pdcfs

C:Superfamily: DNA-binding protein, TPA19 type

Query Match 41.1%; Score 46; DB 2; Length 118;

Best Local Similarity 83.3%; Pred. No. 36;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ITVEELKQLEQ 18

Db 88 ITDEELKQLEQ 99

RESULT 25

E69527

hypothetical protein AF2221 - *Archaeoglobus fulgidus*

C:Species: *Archaeoglobus fulgidus*

C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C:Accession: E69527

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Moese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon

A:Reference number: A69250; PMID:98049343; PMID:9989475

A:Accession: E69527

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-340 <LE>

A:Cross-references: UNIPROT:Q28062; GB:AE000952; GB:AE000782; NID:92689275; PIDN:AA89043

C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF2221

Query Match 41.1%; Score 46; DB 2; Length 340;

Best Local Similarity 53.3%; Pred. No. 1.1e+02;

Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 7 ITVEELKQLEQWN 21

Db 208 LDVQELKLEKXNI 222

RESULT 26

C71407

hypothetical protein - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

A:Variety: Columbia

C>Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004

C:Accession: C71407

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dike P.; Wedler, H.; Wedler, E.; Wambutt, R.; Welzenegger, T.; Pohl, T.M.; Terry, N.; Glele avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, ernof, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansc C.; Chalwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thal*

A:Reference number: A71400; PMID:98121113; PMID:9461215

A:Accession: C71407

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-420 <BEV>

A:Cross-references: UNIPROT:Q23306; GB:Z97336; NID:92244788; PID:92244806

C:Genetics:

A:Map position: 4COP9-4G3845

C:Superfamily: Arabidopsis thaliana hypothetical protein PL07554.0

Query Match 41.1%; Score 46; DB 2; Length 420;

Best Local Similarity 44.4%; Pred. No. 1.3e+02;

Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 2 ADNGTITVE-VEELKQLEQWN 20

Db 127 SDNGTITVEDIVNDLEHLQLEVEN 153

RESULT 27

H90563

hypothetical protein MYPU 4160 [imported] - *Mycoplasma pulmonis* (strain UAB CTIP)

C:Species: *Mycoplasma pulmonis*

C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C:Accession: H90563

R:Chandaud, I.; Heilig, R.; Perris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*

A:Reference number: A99512; PMID:21267165; PMID:11353084

A:Accession: H90563

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-472 <KUR>

A:Cross-references: UNIPROT:Q98QF0; GB:AL445566; PID:G14089830; PIDN:CAC13589.1; GSPDB:G

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPN\_4160  
A:Genetic code: SGC3

Query Match 41.1%; Score 46; DB 2; Length 472;  
Best Local Similarity 47.1%; Pred. No. 1.5e+02;  
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTITVEELKOLLEQNN 20  
|||::|::|::|::|  
DB 105 NGSISISEIKQIEQNN 121

## RESULT 28

H72403 glycine dehydrogenase (decarboxylating) subunit 2 - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: H72403  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
C.M.

Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: H72403  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-474 <ARN>  
A:Cross-references: UNIPROT:Q9WY57; GB:AE001706; GB:AE000512; NID:g4980707; PIDN:AAD3530  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TW0214

C:Superfamily: glycine dehydrogenase (decarboxylating)

Query Match 41.1%; Score 46; DB 2; Length 474;  
Best Local Similarity 53.3%; Pred. No. 1.5e+02;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 NGTITVEELKOLLEQ 18  
|||::|::|::|::|  
DB 184 NGKWDVEDLKKLDE 198

## RESULT 29

AC0845 probable sigma-54-dependent transcriptional regulator STY2961 [imported] - Salmonella ent

C:Species: Salmonella enterica subsp. enterica serovar typh

A:Note: this species has also been called Salmonella typh

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 28-Apr-2003

C:Accession: AC0845  
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moutle, S.; O'Gaora, P.

Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AC0845  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-506 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD05946.1; PID:g16503917; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY2961

C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), PhlA ty

Query Match 41.1%; Score 46; DB 2; Length 506;  
Best Local Similarity 53.3%; Pred. No. 1.6e+02;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKOL 15  
|||||::|::|::|  
DB 277 MADNGTITVEELKOL 291

## RESULT 30

A65051 ygaA protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C:Accession: A65051

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coi

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A65051

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-529 <BLAT>

A:Cross-references: UNIPROT:P37013; GB:AE000354; GB:U00096; NID:g2367149; PIDN:AACT5751.1

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: ygaA

C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), PhlA ty

F;212-434/Domain: RNA polymerase sigma factor interaction domain homology <SFI>  
Query Match 41.1%; Score 46; DB 2; Length 529;  
Best Local Similarity 53.3%; Pred. No. 1.7e+02;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

## RESULT 31

E91074 probable 2-component transcription regulator [imported] - Escherichia coli (strain O157:H

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C:Accession: E91074

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

gatawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: E91074

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-529 <HAY>

A:Cross-references: UNIPROT:Q8X854; GB:BA000007; PIDN:BA836988.1; PID:g13363036; GSPDB:GT

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECG365

C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), PhlA ty

Query Match 41.1%; Score 46; DB 2; Length 529;  
Best Local Similarity 53.3%; Pred. No. 1.7e+02;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKOL 15  
|||||::|::|::|  
DB 302 MADNGTITVEELKOL 316

## RESULT 32

D85919 probable 2-component transcription regulator ygaA [imported] - Escherichia coli (strain C

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C:Accession: D85919

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.U.; Mayhew,  
Hiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouets, K.; Apodaca,  
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: AB5480; MWID:21074935; PMID:11206551  
A:Accession: D85919  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-529 <STO>  
A:Cross-references: UNIPROT:Q8X854; GB:AB005174; NID:912517154; PIDN:AAG57816.1; GSPDB:G  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: ypaA  
C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), FliA ty

Query Match 41.1%; Score 46; DB 2; Length 529;  
Best Local Similarity 53.3%; Pred. No. 1.7e+02;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQL 15  
DB 302 MADNGTIVBELKQL 316

RESULT 33  
JC6129  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63k SF  
N:Alternate names: 63k calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1  
C:Species: Homo sapiens (man)  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: JC6129; G02260  
R:Jiang, X.; Li, J.; Parkind, M.; Epstein, P.M.  
Proc. Natl. Acad. Sci. U.S.A. 93, 11236-11241, 1996  
A:Title: Inhibition of calmodulin-dependent phosphodiesterase induces apoptosis in human  
A:Reference number: JC6129; MWID:97008163; PMID:8855339  
A:Accession: JC6129  
A:Molecule type: mRNA  
A:Residues: 1-536 <JIA>  
A:Cross-references: UNIPROT:Q01064; GB:U56976; NID:91621591; PIDN:AAC50769.1; PID:916215  
A:Experimental source: lymphoblastoid B-cell  
R:Houston, M.D.; Erdogan, S.; Rena, G.; Sullivan, M.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: H00937  
A:Accession: G02260  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 201-203, 'W', 205-358, 'S', 360-384 <HOU>  
A:Cross-references: EMBL:U40584; NID:91110534; PID:91110535  
C:Comment: This enzyme is a useful target for inducing the death of leukemic cells, and  
C:Genetics:  
A:Gene: GDB:PDE1B; PDE1B  
A:Cross-references: GDB:120264; OMIM:171891  
A:Map position: 16p13.11  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent, 3',5'  
C:Keyword: alternative splicing; calmodulin binding; cAMP binding; phosphoric diester h  
F:222-439/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 41.1%; Score 46; DB 1; Length 536;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVBELKQLE 17  
DB 47 DNGTIVBELKQLE 61

RESULT 34  
G81328  
60 kD chaperonin (cpn60) Cj1221 [imported] - Campylobacter jejuni (strain NCTC 11168)  
C:Species: Campylobacter jejuni  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: G81328  
R:Parhill, J.; Wren, B.W.; Mungall, K.; Kelley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrer  
Nature 403, 665-668, 2000  
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h  
A:Reference number: AB1250; MWID:20150912; PMID:10688204

A:Accession: G81328  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-545 <PAR>  
A:Cross-references: UNIPROT:O69289; GB:AL139077; GB:AL111168; NID:96968444; PIDN:CA87347;  
A:Experimental source: serotype O2, strain NCTC 11168  
C:Genetics:  
A:Gene: groEL; Cj1221  
C:Superfamily: chaperonin groEL

Query Match 41.1%; Score 46; DB 2; Length 545;  
Best Local Similarity 47.4%; Pred. No. 1.8e+02;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 NGTIVBELKQLEONLV 22  
DB 171 NGTIVBELKQLEONLV 189

RESULT 35  
AB2913  
hypothetical protein UN263 [imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: AB2913  
R:Glaes, J.I.; Lefkowitz, B.J.; Glaes, J.S.; Heiner, C.R.; Chen, E.Y.; Caswell, G.H.  
submitted to Genbank, February 2000  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini  
A:Reference number: AB2870  
A:Accession: AB2913  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-594 <GIA>  
A:Cross-references: GB:AE002123; GB:AF222894; NID:96899229; PIDN:AAF30672.1; GSPDB:GN001;  
A:Experimental source: serovar 3; biovar 1  
C:Genetics:  
A:Gene: UN263  
A:Genetic code: SGC3

Query Match 41.1%; Score 46; DB 2; Length 594;  
Best Local Similarity 72.7%; Pred. No. 1.9e+02;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 ELKQLEONLV 21  
DB 347 ELKQLEONLV 357

RESULT 36  
AB2591  
conserved hypothetical protein Atu0119 [imported] - Agrobacterium tumefaciens (strain C58  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AB2591  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gallet, W.; Grant, C.; Guenther, D.; Kutyavina, T.; Levy, R.; Li, M.; McClellan  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E  
ster, B.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MWID:21608550; PMID:11743193  
A:Accession: AB2591  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <KUR>  
A:Cross-references: UNIPROT:Q8UJ19; GB:AB008688; PIDN:PAL41144.1; PID:917738440; GSPDB:G  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu0119  
A:Map position: circular chromosome

Query Match 40.6%; Score 45.5; DB 2; Length 88;



Qy 4 NGTITVEELKQLLEQWN 20  
 ||:|:|:|:|:|:|  
 Db 3 NGSIPVDEVIEHLRNMN 19

## RESULT 42

D49591

Membrane protein M - porcine epidemic diarrhoea virus

C/Species: porcine epidemic diarrhoea virus

C/Date: 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change 09-Jul-2004

C/Accession: D49591

R/Duarte, M.; Tobler, K.; Bridgen, A.; Kassehaert, D.; Ackermann, M.; Laude, H.

Virology 198, 466-476, 1994

A/Title: Sequence analysis of the porcine epidemic diarrhoea virus genome between the nuc

A/Reference number: A49591; MUID:94120721; PMID:8291220

A/Accession: D49591

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-226 &lt;DNA&gt;

A/Cross-references: UNIPROT:Q91A09; GB:Z24733

C/Superfamily: coronavirus E1 membrane glycoprotein

Query Match 40.2%; Score 45; DB 2; Length 226;  
 Best Local Similarity 47.1%; Pred. No. 96;

Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 NGTITVEELKQLLEQWN 20  
 ||:|:|:|:|:|:|  
 Db 3 NGSIPVDEVIEHLRNMN 19

## RESULT 43

T38795

Conserved uncharacterized protein domain-containing protein - fission yeast (Schizosacch

C/Species: Schizosaccharomyces pombe

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: T38795

R/Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

Submitted to the EMBL Data Library, August 1996

A/Reference number: Z21812

A/Accession: T38795

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-264 &lt;GEN&gt;

A/Cross-references: UNIPROT:O14171; EMBL:Z98602; PDB:1CAB11276.1; GSPDB:GN00066; SPDB:SF

C/Genetics:

A/Genes: SPDB:SPAC4D7.046

A/Intons: 69/3; 156/2; 228/3

C/Superfamily: conserved hypothetical protein YBR002c

Query Match 40.2%; Score 45; DB 2; Length 264;  
 Best Local Similarity 40.9%; Pred. No. 1.1e+02;

Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLLEQWN 22  
 ||:|:|:|:|:|:|  
 Db 181 MADGTTTPEIDIDEDIFEXKLL 202

Qy 1 MADNGTITVEELKQLLEQWN 22  
 ||:|:|:|:|:|:|  
 Db 181 MADGTTTPEIDIDEDIFEXKLL 202

## RESULT 44

T43492

Hypothetical protein DKFZp434A219.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 23-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C/Accession: T43492

R/Pousetka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Submitted to the Protein Sequence Database, December 1999

A/Reference number: Z22516

A/Accession: T43492

A/Status: preliminary

A/Molecule type: mRNA  
 A/Residues: 1-318 <AAA>  
 A/Cross-references: UNIPROT:O14703; EMBL:AL133583  
 A/Experimental source: adult testis; clone DKFZp434A219  
 C/Genetics:  
 A/Note: DKFZp434A219.1

Query Match 40.2%; Score 45; DB 2; Length 318;  
 Best Local Similarity 38.1%; Pred. No. 1.4e+02;

Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLLEQWN 21  
 ||:|:|:|:|:|:|  
 Db 13 MPDTGANIPALNELLSVNM 33

## RESULT 45

F72404

Flagellar motor switch protein FlgG - Thermotoga maritima (strain MSB8)

C/Species: Thermotoga maritima

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C/Accession: F72404

R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cocton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A/Reference number: A72200; MUID:99287316; PMID:10360571

A/Accession: F72404

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-335 &lt;ARN&gt;

A/Cross-references: UNIPROT:Q9WY63; GB:AE001706; GB:AE000512; NID:94980707; PDB:1ADJ351;

C/Genetics:

A/Experimental source: strain MSB8

C/Genetics:

A/Genes: TW0220

C/Superfamily: flagellar switch protein FlgG

Query Match 40.2%; Score 45; DB 2; Length 335;  
 Best Local Similarity 47.4%; Pred. No. 1.5e+02;

Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLLEQWN 19  
 ||:|:|:|:|:|:|  
 Db 43 IANIGRVTPKQVLEBF 61

## RESULT 46

F82012

Hypothetical protein NMA0184 [imported] - Neisseria meningitidis (strain Z2491 serogroup

C/Species: Neisseria meningitidis

C/Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004

C/Accession: F82012

R/Parikh, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel]

; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A/Reference number: A81775; MUID:20222356; PMID:10761919

A/Accession: F82012

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-468 &lt;PAR&gt;

A/Cross-references: UNIPROT:Q9JWY2; GB:AL162752; GB:AL157959; NID:97378778; PDB:1CAB8349;

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Genes: NMA0184

Query Match 40.2%; Score 45; DB 2; Length 468;  
 Best Local Similarity 56.2%; Pred. No. 2.1e+02;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 4 NGTITVEELKQLLEQWN 19  
 ||:|:|:|:|:|:|

Db 440 NGHTSABSLSLAEQW 455

RESULT 47  
T10938  
Calcium-dependent protein kinase (EC 2.7.1.-) - sweet potato  
C/Species: Ipomoea batatas (sweet potato)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T10938  
R/Kojima, H.; Sasaki, M.; Mano, S.; Nakamura, K.  
Submitted to the EMBL Data Library, September 1996  
A/Description: cDNA for a homologue of calcium-dependent protein kinase from petioles of  
A/Reference number: Z17218  
A/Accession: T10938  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-514 <KOJ>  
A/Cross-references: UNIPROT:Q96469; EMBL:D87707  
A/Experimental source: cv. Kokei No.14; petiole  
C/Genetics:  
A/Gene: CDPK  
C/Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
C/Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F/64-374/Domain: protein kinase repeat homology <KIN>  
F/403-435/Domain: calmodulin repeat homology <EFH>

Query Match 40.2%; Score 45; DB 1; Length 514;  
Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 DNGTIVBELKQLE 18  
:|||||:|  
Db 383 NSGTIVBELKQIAQ 398

RESULT 48  
A44162  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp  
N/Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: A44162; B40283  
R/Bentley, J.K.; Kadlec, A.; Sherbert, C.H.; Seger, D.; Sonnenburg, W.K.; Charbonneau,  
J. Biol. Chem. 267, 18676-18682, 1992  
A/Title: Molecular cloning of cDNA encoding a "63"-kDa calmodulin-stimulated phosphodies  
A/Reference number: A44162; MUID:92406781; PMID:1326531  
A/Accession: A44162  
A/Molecule type: mRNA  
A/Residues: 1-534 <BEN>  
A/Cross-references: UNIPROT:Q01061; GB:M94867; NID:g162782; PIDN:AAA74558.1; PID:g162783  
A/Experimental source: brain  
A/Note: sequence extracted from NCBI backbone (NCBI:P113352)  
R/Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.  
Biochemistry 30, 7940-7947, 1991  
A/Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nuc  
A/Reference number: A40283; MUID:91329366; PMID:165112  
A/Accession: B40283  
A/Molecule type: protein  
A/Residues: 29-55, 'P', 48, 'R', 50-52, 'IS', 55-85, 196-215, 277, 'D', 279, 'T', 281-287, 'T', 289-2  
A/Experimental source: brain  
C/Comment: This enzyme is a useful target for inducing the death of leukemic cells, and  
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h  
F/220-437/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNDP>

Query Match 40.2%; Score 45; DB 1; Length 534;  
Best Local Similarity 53.3%; Pred. No. 2.4e+02;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 DNGTIVBELKQLE 17  
:|||||:|  
Db 46 ENGAVIIBELKQLE 60

RESULT 49  
A44161  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp  
N/Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: A44161  
R/Repaske, D.R.; Swinnen, J.V.; Jin, S.L.; Van Wyk, J.J.; Conti, M.  
J. Biol. Chem. 267, 18683-18688, 1992  
A/Title: A polymerase chain reaction strategy to identify and clone cyclic nucleotide ph  
A/Reference number: A44161; MUID:92406782; PMID:1326532  
A/Accession: A44161  
A/Molecule type: mRNA  
A/Residues: 1-535 <REP>  
A/Cross-references: UNIPROT:Q01066; GB:M94537; NID:g203268; PIDN:AAA16530.1; PID:g203269  
A/Experimental source: brain  
A/Note: sequence extracted from NCBI backbone (NCBI:P113357)  
C/Comment: This enzyme is a useful target for inducing the death of leukemic cells, and t  
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h  
F/221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNDP>

Query Match 40.2%; Score 45; DB 1; Length 535;  
Best Local Similarity 53.3%; Pred. No. 2.4e+02;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 DNGTIVBELKQLE 17  
:|||||:|  
Db 46 ENGAVIIBELKQLE 60

RESULT 50  
A46378  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp  
N/Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: A46378; B44161  
R/Poll, J.W.; Kincaid, R.L.  
Proc. Natl. Acad. Sci. U.S.A. 89, 11079-11083, 1992  
A/Title: Molecular cloning of DNA encoding a calmodulin-dependent phosphodiesterase enric  
A/Reference number: A46378; MUID:9306388; PMID:1332068  
A/Accession: A46378  
A/Molecule type: mRNA; protein  
A/Residues: 1-535 <POL>  
A/Cross-references: UNIPROT:Q01065; GB:L01695; NID:g200269; PIDN:AAA39902.1; PID:g200270  
A/Experimental source: brain  
A/Note: sequence extracted from NCBI backbone (NCBI:P118901; NCBI:P118903)  
R/Repaske, D.R.; Swinnen, J.V.; Jin, S.L.; Van Wyk, J.J.; Conti, M.  
J. Biol. Chem. 267, 18683-18688, 1992  
A/Title: A polymerase chain reaction strategy to identify and clone cyclic nucleotide ph  
A/Reference number: A44161; MUID:92406782; PMID:1326532  
A/Accession: B44161  
A/Molecule type: mRNA  
A/Residues: 221-223, 'R', 225-336 <REP>  
A/Cross-references: GB:M94538; NID:g192368; PIDN:AAA37367.1; PID:g192369  
A/Note: sequence extracted from NCBI backbone (NCBI:P113365)  
C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h  
F/221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNDP>

Query Match 40.2%; Score 45; DB 1; Length 535;  
Best Local Similarity 53.3%; Pred. No. 2.4e+02;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 DNGTIVBELKQLE 17  
:|||||:|  
Db 46 ENGAVIIBELKQLE 60

Thu May 12 09:59:46 2005

us-10-712-812-5.rpr

Page 19

Search completed: May 11, 2005, 21:23:10  
Job time : 48 secs

---

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: May 11, 2005, 21:15:49 ; Search time 106.255 Seconds  
(without alignments)  
106.025 Million cell updates/sec

Title: US-10-712-812-5  
Perfect score: 112  
Sequence: 1 MADNGTIVEELKQLEQNNLV 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	143	2	Q6SR10
2	112	100.0	143	2	Q6SR14
3	112	100.0	143	2	Q6SR18
4	112	100.0	143	2	Q6SRJ2
5	112	100.0	143	2	Q6SRJ6
6	112	100.0	143	2	Q6SRK4
7	112	100.0	143	2	Q6SRK8
8	112	100.0	143	2	Q6SRL2
9	112	100.0	143	2	Q6SRL6
10	112	100.0	143	2	Q6SRM0
11	112	100.0	143	2	Q6SRM4
12	112	100.0	143	2	Q6SRM8
13	112	100.0	143	2	Q6SRN2
14	112	100.0	143	2	Q6SRN6
15	112	100.0	143	2	Q6SRP0
16	112	100.0	143	2	Q6SRP4
17	112	100.0	143	2	Q6SRP8
18	112	100.0	221	1	Q6SRP8
19	112	100.0	221	1	Q6SRP8
20	112	100.0	221	2	Q6SRP8
21	112	100.0	221	2	Q6SRP8
22	112	100.0	221	2	Q6SRP8
23	112	100.0	221	2	Q6SRP8
24	112	100.0	221	2	Q6SRP8
25	112	100.0	221	2	Q6SRP8
26	112	100.0	221	2	Q6SRP8
27	112	100.0	221	2	Q6SRP8
28	112	100.0	221	2	Q6SRP8
29	112	100.0	221	2	Q6SRP8
30	112	100.0	221	2	Q6SRP8
31	112	100.0	221	2	Q6SRP8

32	112	100.0	221	2	Q6RD49	Q6RD49	sars corona
33	112	100.0	221	2	Q6RD60	Q6RD60	sars corona
34	112	100.0	221	2	Q6RD63	Q6RD63	sars corona
35	112	100.0	221	2	Q6RD68	Q6RD68	sars corona
36	112	100.0	221	2	Q6RD69	Q6RD69	sars corona
37	112	100.0	221	2	Q6RD70	Q6RD70	sars corona
38	112	100.0	221	2	Q6RD71	Q6RD71	sars corona
39	112	100.0	221	2	Q6RD72	Q6RD72	sars corona
40	112	100.0	221	2	Q6RD73	Q6RD73	sars corona
41	112	100.0	221	2	Q6RD74	Q6RD74	sars corona
42	112	100.0	221	2	Q6RD75	Q6RD75	sars corona
43	108	96.4	221	2	Q6RD76	Q6RD76	sars corona
44	108	96.4	221	2	Q6RD77	Q6RD77	sars corona
45	106	94.6	143	3	Q6SRK0	Q6SRK0	sars corona
46	58	51.8	376	1	HOSC_THET2	HOSC_THET2	thetanus the
47	55.5	49.6	409	2	Q6RD78	Q6RD78	sars corona
48	55	49.1	229	2	Q6RD79	Q6RD79	sars corona
49	53.5	47.8	512	2	Q6RD80	Q6RD80	sars corona
50	53	47.3	279	2	Q6RD81	Q6RD81	sars corona
51	52.5	46.9	213	2	Q6RD82	Q6RD82	sars corona
52	52.5	46.9	213	2	Q6RD83	Q6RD83	sars corona
53	52	46.4	16367	2	Q6RD84	Q6RD84	sars corona
54	51.5	46.0	352	2	Q6RD85	Q6RD85	sars corona
55	51	45.5	184	2	Q6RD86	Q6RD86	sars corona
56	51	45.5	206	1	Q6RD87	Q6RD87	sars corona
57	51	45.5	326	2	Q6RD88	Q6RD88	sars corona
58	51	45.5	344	2	Q6RD89	Q6RD89	sars corona
59	51	45.5	351	1	Q6RD90	Q6RD90	sars corona
60	51	45.5	564	1	Q6RD91	Q6RD91	sars corona
61	51	45.5	572	1	Q6RD92	Q6RD92	sars corona
62	51	45.5	689	2	Q6RD93	Q6RD93	sars corona
63	50.5	45.1	193	2	Q6RD94	Q6RD94	sars corona
64	50.5	45.1	203	2	Q6RD95	Q6RD95	sars corona
65	50.5	45.1	203	2	Q6RD96	Q6RD96	sars corona
66	50.5	45.1	204	2	Q6RD97	Q6RD97	sars corona
67	50.5	45.1	218	2	Q6RD98	Q6RD98	sars corona
68	50.5	45.1	342	2	Q6RD99	Q6RD99	sars corona
69	50.5	45.1	409	2	Q6RD00	Q6RD00	sars corona
70	50.5	45.1	450	2	Q6RD01	Q6RD01	sars corona
71	50.5	45.1	451	2	Q6RD02	Q6RD02	sars corona
72	50.5	45.1	852	2	Q6RD03	Q6RD03	sars corona
73	50.5	45.1	930	2	Q6RD04	Q6RD04	sars corona
74	50	44.6	149	2	Q6RD05	Q6RD05	sars corona
75	50	44.6	174	2	Q6RD06	Q6RD06	sars corona
76	50	44.6	323	1	Q6RD07	Q6RD07	sars corona
77	50	44.6	446	1	Q6RD08	Q6RD08	sars corona
78	50	44.6	673	2	Q6RD09	Q6RD09	sars corona
79	50	44.6	846	1	Q6RD10	Q6RD10	sars corona
80	50	44.6	861	1	Q6RD11	Q6RD11	sars corona
81	50	44.6	882	2	Q6RD12	Q6RD12	sars corona
82	50	44.6	13536	2	Q6RD13	Q6RD13	sars corona
83	49.5	44.2	177	2	Q6RD14	Q6RD14	sars corona
84	49.5	44.2	201	2	Q6RD15	Q6RD15	sars corona
85	49.5	44.2	208	2	Q6RD16	Q6RD16	sars corona
86	49.5	44.2	573	2	Q6RD17	Q6RD17	sars corona
87	49.5	44.2	855	2	Q6RD18	Q6RD18	sars corona
88	49	43.8	123	2	Q6RD19	Q6RD19	sars corona
89	49	43.8	183	2	Q6RD20	Q6RD20	sars corona
90	49	43.8	218	1	Q6RD21	Q6RD21	sars corona
91	49	43.8	462	1	Q6RD22	Q6RD22	sars corona
92	49	43.8	1744	2	Q6RD23	Q6RD23	sars corona
93	48.5	43.3	163	2	Q6RD24	Q6RD24	sars corona
94	48.5	43.3	174	2	Q6RD25	Q6RD25	sars corona
95	48.5	43.3	179	2	Q6RD26	Q6RD26	sars corona
96	48.5	43.3	185	2	Q6RD27	Q6RD27	sars corona
97	48.5	43.3	193	2	Q6RD28	Q6RD28	sars corona
98	48.5	43.3	196	2	Q6RD29	Q6RD29	sars corona
99	48.5	43.3	203	2	Q6RD30	Q6RD30	sars corona
100	48.5	43.3	211	2	Q6RD31	Q6RD31	sars corona
101	48.5	43.3	490	2	Q6RD32	Q6RD32	sars corona
102	48.5	43.3	842	2	Q6RD33	Q6RD33	sars corona
103	48.5	43.3	842	2	Q6RD34	Q6RD34	sars corona
104	48.5	43.3	855	2	Q6RD35	Q6RD35	sars corona

105	48.5	43.3	872	2	Q91U20	Q91u20 human immun	178	47	42.0	159	1	GNA1_YEAST	P43577	saccharomyc
106	48.5	43.3	872	2	Q91U21	Q91u21 human immun	179	47	42.0	184	2	Q8KX60	Q8Kx60 uncultured	
107	48	42.9	125	2	Q05614	Q05614 pseudomonas	180	47	42.0	184	2	Q68H75	Q68h75 clostridium	
108	48	42.9	143	2	Q67T02	Q67t02 symbiobacte	181	47	42.0	199	2	Q7WV58	Q7Wv58 porphyromon	
109	48	42.9	206	1	RALA_CALJA	Pe33320 callithrix	182	47	42.0	312	2	Q8ZK33	Q8Zk33 salmonella	
110	48	42.9	206	1	RALA_MOUSE	Pe33321 mus musculus	183	47	42.0	335	2	Q8YP24	Q8Yp24 anabaena sp	
111	48	42.9	206	1	RALA_RAT	Pe33322 rattus norv	184	47	42.0	493	2	Q8A2F4	Q8A2f4 bacteroides	
112	48	42.9	206	2	Q9CXI0	Q9cxi0 mus musculus	185	47	42.0	508	2	Q6HU05	Q6hu05 bacillus an	
113	48	42.9	206	2	Q918H8	Q918h8 xenopus lae	186	47	42.0	510	2	Q636N5	Q636n5 bacillus ce	
114	48	42.9	213	2	Q74076	Q74076 human immun	187	47	42.0	510	2	Q732T5	Q732t5 bacillus ce	
115	48	42.9	226	2	Q37049	Q37049 porcine epi	188	47	42.0	510	2	Q81WP5	Q81wp5 bacillus th	
116	48	42.9	226	2	Q37351	Q37351 porcine epi	189	47	42.0	510	2	Q6HP24	Q6hp24 bacillus th	
117	48	42.9	226	2	Q72839	Q72839 porcine epi	190	47	42.0	547	1	CH60_WOLRE	Q93gw2 wolinnella r	
118	48	42.9	226	2	Q67058	Q67058 porcine epi	191	47	42.0	677	2	Q9ST62	Q9st62 solanum tub	
119	48	42.9	235	2	Q8TS68	Q8ts68 methanosaarc	192	47	42.0	627	2	Q9KEY2	Q9key2 bacillus ha	
120	48	42.9	254	1	YMI2_CAREL	Q22306 caenorhabdi	193	47	42.0	657	2	Q8AFL5	Q8af5 chimpanzee	
121	48	42.9	294	2	Q6BET9	Q6beu9 caenorhabdi	194	47	42.0	659	1	SPA2_SYNY3	P72587 synchocyst	
122	48	42.9	299	2	Q84S01	Q84sq1 oryza sativ	195	47	42.0	759	1	PURL_THEAC	Q91h34 thecoplastm	
123	48	42.9	309	2	Q17902	Q17902 caenorhabdi	196	47	42.0	863	2	Q76148	Q76148 anopheles s	
124	48	42.9	462	1	YUAI_YEAST	Q12059 saccharomyc	197	47	42.0	867	2	Q7QEB3	Q7qeJ3 anopheles g	
125	48	42.9	517	2	Q630H3	Q630h3 bacillus ce	198	47	42.0	961	1	GCSF_STRAW	Q827d7 streptomyce	
126	48	42.9	517	2	Q81JMS	Q81jm5 bacillus an	199	47	42.0	1027	2	Q9WPF5	Q9wfp5 chimpanzee	
127	48	42.9	517	2	Q6HAK8	Q6hak8 bacillus th	200	47	42.0	1067	2	Q9S257	Q9s257 arabidopsis	
128	48	42.9	530	2	Q72X14	Q72x14 bacillus ce	201	47	42.0	2156	2	Q81DB7	Q81db7 bacillus fe	
129	48	42.9	536	2	Q814J7	Q814j7 bacillus ce	202	47	42.0	2816	2	Q85983	Q85983 oscillatoria	
130	48	42.9	553	2	Q9W632	Q9w632 hyphantaria	203	47	42.0	4091	2	Q7Q4A8	Q7q4a8 anopheles g	
131	48	42.9	647	2	Q8CA10	Q8ca10 mus musculu	204	46.5	41.5	104	2	Q78877	Q78877 human immun	
132	48	42.9	654	2	Q97553	Q97553 sulfolobus	205	46.5	41.5	104	2	Q78881	Q78881 human immun	
133	48	42.9	856	2	Q6APR6	Q6apr6 desulfotale	206	46.5	41.5	159	2	Q9JES7	Q9jes7 human immun	
134	48	42.9	1762	2	Q6A070	Q6a070 mus musculu	207	46.5	41.5	161	2	Q70R49	Q70r49 human immun	
135	48	42.9	4437	2	Q8GGP3	Q8ggp3 streptomyce	208	46.5	41.5	162	2	Q70QK1	Q70qk1 human immun	
136	47.5	42.4	155	2	Q73383	Q73383 human immun	209	46.5	41.5	169	2	Q70QZ6	Q70qz6 human immun	
137	47.5	42.4	168	2	Q8Q2G9	Q8q2g9 human immun	210	46.5	41.5	169	2	Q70R29	Q70r29 human immun	
138	47.5	42.4	171	2	Q70R72	Q70r72 human immun	211	46.5	41.5	176	2	Q70R40	Q70r40 human immun	
139	47.5	42.4	178	2	Q99F39	Q99f39 human immun	212	46.5	41.5	183	2	Q9DVA1	Q9dva1 human immun	
140	47.5	42.4	184	2	Q90CQ8	Q90cq8 human immun	213	46.5	41.5	184	2	Q8Q1U2	Q8q1u2 human immun	
141	47.5	42.4	186	2	Q7SKV1	Q7skv1 human immun	214	46.5	41.5	184	2	Q8Q1U3	Q8q1u3 human immun	
142	47.5	42.4	195	2	Q70Q73	Q70q73 human immun	215	46.5	41.5	184	2	Q8Q1U4	Q8q1u4 human immun	
143	47.5	42.4	195	2	Q70R05	Q70rc5 human immun	216	46.5	41.5	184	2	Q8Q1U5	Q8q1u5 human immun	
144	47.5	42.4	197	2	Q6SUT1	Q6sut1 human immun	217	46.5	41.5	184	2	Q8Q1U6	Q8q1u6 human immun	
145	47.5	42.4	199	2	Q7SKT3	Q7skt3 human immun	218	46.5	41.5	184	2	Q8Q1U7	Q8q1u7 human immun	
146	47.5	42.4	199	2	Q7ZNU0	Q7znj0 human immun	219	46.5	41.5	184	2	Q8Q1U8	Q8q1u8 human immun	
147	47.5	42.4	202	2	Q8U8I0	Q8j8i0 human immun	220	46.5	41.5	184	2	Q8Q1U9	Q8q1u9 human immun	
148	47.5	42.4	202	2	Q90NU1	Q90nu1 human immun	221	46.5	41.5	184	2	Q8Q1V0	Q8q1v0 human immun	
149	47.5	42.4	202	2	Q8AL44	Q8al44 human immun	222	46.5	41.5	184	2	Q8Q1V1	Q8q1v1 human immun	
150	47.5	42.4	203	2	Q8J6H4	Q8j6h4 human immun	223	46.5	41.5	190	2	Q8US55	Q8us55 human immun	
151	47.5	42.4	204	2	Q6RUL9	Q6rhl9 human immun	224	46.5	41.5	191	2	Q70R37	Q70r37 human immun	
152	47.5	42.4	205	2	Q8U8I6	Q8j8i6 human immun	225	46.5	41.5	194	2	Q91VY5	Q91v5 human immun	
153	47.5	42.4	208	2	Q9QC11	Q9qql1 human immun	226	46.5	41.5	195	2	Q9QNX2	Q9qnx2 human immun	
154	47.5	42.4	209	2	Q8US45	Q8us45 human immun	227	46.5	41.5	196	2	Q70R78	Q70r78 human immun	
155	47.5	42.4	210	2	Q70QW2	Q70qw2 human immun	228	46.5	41.5	197	2	Q6SUT1	Q6sut1 human immun	
156	47.5	42.4	211	2	Q70QW4	Q70qw4 human immun	229	46.5	41.5	197	2	Q6SUT3	Q6sut3 human immun	
157	47.5	42.4	211	2	Q8AD04	Q8ad04 human immun	230	46.5	41.5	197	2	Q6SUT8	Q6sut8 human immun	
158	47.5	42.4	216	2	Q70Q01	Q70qql human immun	231	46.5	41.5	197	2	Q6SUT9	Q6sut9 human immun	
159	47.5	42.4	217	2	Q70Q51	Q70qql human immun	232	46.5	41.5	197	2	Q6SUT0	Q6sut0 human immun	
160	47.5	42.4	219	2	Q7ZBA3	Q7zba3 human immun	233	46.5	41.5	197	2	Q6SUT2	Q6sut2 human immun	
161	47.5	42.4	221	2	Q7ZP24	Q7zpd4 human immun	234	46.5	41.5	197	2	Q6SUT3	Q6sut3 human immun	
162	47.5	42.4	224	2	Q7ZME5	Q7zme5 human immun	235	46.5	41.5	197	2	Q9DVI5	Q9dvi5 human immun	
163	47.5	42.4	234	2	Q76168	Q76168 human immun	236	46.5	41.5	198	2	Q7SKS3	Q7skS3 human immun	
164	47.5	42.4	234	2	Q76190	Q76190 human immun	237	46.5	41.5	199	2	Q7SU41	Q7su41 human immun	
165	47.5	42.4	342	2	Q91083	Q91i83 human immun	238	46.5	41.5	201	2	Q97D99	Q97d99 clostridium	
166	47.5	42.4	405	2	Q66LA6	Q66la6 human immun	239	46.5	41.5	201	2	Q6J9D6	Q6j9d6 human immun	
167	47.5	42.4	486	2	Q7ZMJ2	Q7zml2 human immun	240	46.5	41.5	201	2	Q7SU31	Q7su31 human immun	
168	47.5	42.4	495	2	Q74826	Q74826 human immun	241	46.5	41.5	201	2	Q7SU42	Q7su42 human immun	
169	47.5	42.4	583	2	Q8EP19	Q8ep19 oceanobacil	242	46.5	41.5	201	2	Q7SU43	Q7su43 human immun	
170	47.5	42.4	846	2	Q6BBR0	Q6bbr0 human immun	243	46.5	41.5	202	2	Q7ZP14	Q7zP14 human immun	
171	47.5	42.4	849	2	Q8J9B8	Q8j9b8 human immun	244	46.5	41.5	202	2	Q8AL57	Q8al57 human immun	
172	47.5	42.4	861	2	Q6XJ64	Q6xj64 human immun	245	46.5	41.5	203	2	Q7SUG2	Q7sug2 human immun	
173	47.5	42.4	863	2	Q8UFP6	Q8ufp6 human immun	246	46.5	41.5	203	2	Q7SUG4	Q7sug4 human immun	
174	47.5	42.4	869	2	Q8UI69	Q8ui69 human immun	247	46.5	41.5	203	2	Q7SUI9	Q7sui9 human immun	
175	47.5	42.4	874	2	Q8UI66	Q8ui66 human immun	248	46.5	41.5	203	2	Q8AL98	Q8al98 human immun	
176	47.5	42.4	874	2	Q8UI68	Q8ui68 human immun	249	46.5	41.5	205	2	Q7SKV0	Q7skv0 human immun	
177	47.5	42.4	1119	2	Q6TUP9	Q6tuf9 rattus norv	250	46.5	41.5	206	2	Q7SUS3	Q7sus3 human immun	

251	46.5	41.5	206	2	Q7SU37	Q7bu37 human immun	324	46	41.1	512	2	Q6DBR9	Q6db9 erwinia car
252	46.5	41.5	206	2	Q7SU58	Q7bu58 human immun	325	46	41.1	513	2	Q6YIH2	Q6yih2 oryza sativ
253	46.5	41.5	206	2	Q7SUH8	Q7buH8 human immun	326	46	41.1	516	2	Q6GKP3	Q6gkp3 homo sapien
254	46.5	41.5	206	2	Q7SUI2	Q7buI2 human immun	327	46	41.1	534	2	Q6KCS3	Q6kcs3 nicotiana p
255	46.5	41.5	206	2	Q7SUI3	Q7buI3 human immun	328	46	41.1	536	1	CNIB_HUMAN	001064 human
256	46.5	41.5	207	2	Q6SUS8	Q6buS8 human immun	329	46	41.1	542	2	Q7VC71	Q7vc71 prochloroco
257	46.5	41.5	209	2	Q7SUI6	Q7bu68 human immun	330	46	41.1	545	1	CH60_CAMJ6	Q6z289 campylobact
258	46.5	41.5	214	2	Q7SUI34	Q7bu34 human immun	331	46	41.1	558	1	Q8DK21	Q8dk21 synchococc
259	46.5	41.5	215	2	Q8J9D8	Q8j9d8 human immun	332	46	41.1	572	1	DPY4_HUMAN	014511 homo sapien
260	46.5	41.5	218	2	Q7SUM0	Q7sum0 human immun	333	46	41.1	594	2	Q9PCM8	Q9pcm8 ureaplasma
261	46.5	41.5	218	2	Q7SUM1	Q7sum1 human immun	334	46	41.1	644	2	Q9PM17	Q9pm17 arabidopsis
262	46.5	41.5	218	2	Q9WLK7	Q9wlk7 human immun	335	46	41.1	797	2	Q8AB88	Q8ab88 bacteroides
263	46.5	41.5	220	2	Q7SU44	Q7bu44 human immun	336	46	41.1	999	2	Q6GIM3	Q6gim3 rattus norv
264	46.5	41.5	220	2	Q7ZMF5	Q7zmf5 human immun	337	46	41.1	1052	1	MS1P_RAT	Q9wz3 ratuans norv
265	46.5	41.5	223	2	Q7SUJ9	Q7buJ9 human immun	338	46	41.1	1284	2	Q7WRJ5	Q7wrj5 anabaena c1
266	46.5	41.5	265	2	Q9WTT3	Q9wt3 human immun	339	46	41.1	2785	2	Q9SIA9	Q9sia9 microcyctis
267	46.5	41.5	276	2	Q9WE10	Q9we10 human immun	340	46	41.1	2795	2	Q8RTG5	Q8rtg5 microcyctis
268	46.5	41.5	277	2	Q8DBM8	Q8dbm8 vibrio vuln	341	46	41.1	2795	2	Q9RNB1	Q9rnb1 microcyctis
269	46.5	41.5	278	2	Q76212	Q76212 human immun	342	46	41.1	4416	2	Q9J3F3	Q9j3f3 murine hepa
270	46.5	41.5	288	2	Q73316	Q73316 human immun	343	46	41.1	4416	2	Q9J3F8	Q9j3f8 murine hepa
271	46.5	41.5	301	2	Q70212	Q70212 human immun	344	46	41.1	7124	1	RIAB_MOUSE	Q9pyz3 m repilicase
272	46.5	41.5	328	2	Q9TUB4	Q9tub4 human immun	345	46	41.1	7389	1	BPA1_MOUSE	Q91z6 mus musculi
273	46.5	41.5	327	2	Q7ZP53	Q7zpj3 human immun	346	45.5	40.6	70	1	SLYX_AGRIS	Q8uj19 agrobacteri
274	46.5	41.5	359	2	P87967	P87967 human immun	347	45.5	40.6	70	1	SLYX_RHIME	Q92kt8 rhizobium m
275	46.5	41.5	386	2	Q8Q843	Q8q843 human immun	348	45.5	40.6	177	2	Q8JFI9	Q8jfi9 human immun
276	46.5	41.5	386	2	Q8Q846	Q8q846 human immun	349	45.5	40.6	177	2	Q8JF20	Q8jfe20 human immun
277	46.5	41.5	409	2	Q41635	Q41635 human immun	350	45.5	40.6	179	2	Q7ZPM0	Q7zpm0 human immun
278	46.5	41.5	426	2	Q87ON7	Q87on7 vibrio para	351	45.5	40.6	183	2	Q7ZNA1	Q7zna1 human immun
279	46.5	41.5	428	2	Q6LPR1	Q6lpr1 photobacter	352	45.5	40.6	183	2	Q9DV55	Q9dvs5 human immun
280	46.5	41.5	428	2	Q9KS25	Q9kx25 vibrio chol	353	45.5	40.6	187	2	Q6UDP2	Q6udp2 human immun
281	46.5	41.5	429	2	Q82V01	Q82v01 nitrosomon	354	45.5	40.6	194	2	Q6VGY9	Q6vgy9 human immun
282	46.5	41.5	462	2	Q82V00	Q82v00 nitrosomon	355	45.5	40.6	195	2	Q7ZND6	Q7znd6 human immun
283	46.5	41.5	801	2	Q9WMU9	Q9wm9 human immun	356	45.5	40.6	195	2	Q7ZNG0	Q7zng0 human immun
284	46.5	41.5	847	2	Q9WIS1	Q9wis1 human immun	357	45.5	40.6	196	2	Q68ID5	Q68id5 human immun
285	46.5	41.5	849	2	Q9YKT4	Q9ykc4 human immun	358	45.5	40.6	196	2	Q9JBI0	Q9jbi0 human immun
286	46.5	41.5	850	2	Q9YKT7	Q9ykc7 human immun	359	45.5	40.6	196	2	Q9JBI1	Q9jbi1 human immun
287	46.5	41.5	850	2	Q9QBY2	Q9qby2 human immun	360	45.5	40.6	196	2	Q9JBI2	Q9jbi2 human immun
288	46.5	41.5	858	2	Q6UF93	Q6uf93 human immun	361	45.5	40.6	196	2	Q9JBJ0	Q9jbj0 human immun
289	46.5	41.5	858	2	Q73293	Q73293 human immun	362	45.5	40.6	196	2	Q9JBJ5	Q9jbj5 human immun
290	46.5	41.5	1373	1	RPC2_CHAGL	Q8ma10 chaetocphae	363	45.5	40.6	196	2	Q9JBK0	Q9jbk0 human immun
291	46	41.1	114	2	Q8BSL3	Q8bsl3 populus tre	364	45.5	40.6	197	2	Q6SUT5	Q6sut5 human immun
292	46	41.1	118	1	Y352_SULSO	Q980f8 sulfolobus	365	45.5	40.6	197	2	Q6SUT4	Q6sut4 human immun
293	46	41.1	119	2	Q6PRV2	Q6prv2 coturnix co	366	45.5	40.6	197	2	Q6SUT6	Q6sut6 human immun
294	46	41.1	124	2	Q6RJZ7	Q6rjz7 capsicum an	367	45.5	40.6	197	2	Q6SUT5	Q6sut5 human immun
295	46	41.1	124	2	Q6M9L5	Q6m9l5 paracichlamyd	368	45.5	40.6	197	2	Q9JBT1	Q9jbt1 human immun
296	46	41.1	126	2	P84137	P84137 bacillus bc	369	45.5	40.6	198	2	Q9JBC6	Q9jbc6 human immun
297	46	41.1	149	2	Q9VDI3	Q9vdi3 drosophila	370	45.5	40.6	199	2	Q70543	Q70543 human immun
298	46	41.1	185	2	Q938Z8	Q938z8 campylobact	371	45.5	40.6	199	2	Q7ZNI1	Q7zni1 human immun
299	46	41.1	185	2	Q938Z9	Q938z9 campylobact	372	45.5	40.6	199	2	Q9JBD1	Q9jbd1 human immun
300	46	41.1	185	2	Q939A0	Q939a0 campylobact	373	45.5	40.6	200	2	Q72062	Q72062 human immun
301	46	41.1	217	2	Q8CTQ3	Q8ctq3 staphylococ	374	45.5	40.6	201	2	Q6J9C1	Q6j9c1 human immun
302	46	41.1	217	2	Q7P7B3	Q7p7b3 fusobacteri	375	45.5	40.6	201	2	Q9JBD8	Q9jbd8 human immun
303	46	41.1	229	2	Q8ECT2	Q8ect2 shewanella	376	45.5	40.6	202	2	Q9JBI8	Q9jbi8 human immun
304	46	41.1	300	2	Q7WVC9	Q7wvc9 acinetobact	377	45.5	40.6	202	2	Q9JBI9	Q9jbi9 human immun
305	46	41.1	300	2	Q9F7D7	Q9f7d7 acinetobact	378	45.5	40.6	202	2	Q9JBJ2	Q9jbj2 human immun
306	46	41.1	306	2	Q8XLD5	Q8xld5 clostridium	379	45.5	40.6	202	2	Q9JBJ2	Q9jbj2 human immun
307	46	41.1	312	2	Q8ZLW0	Q8zlw0 salmonella	380	45.5	40.6	203	2	Q6SUN1	Q6sun1 human immun
308	46	41.1	340	1	YM21_ARCFU	Q82062 archaeoglob	381	45.5	40.6	203	2	Q70521	Q70521 human immun
309	46	41.1	401	2	Q8VQZ7	Q8vqz7 campylobact	382	45.5	40.6	203	2	Q70528	Q70528 human immun
310	46	41.1	401	2	Q90HM7	Q90hm7 human immun	383	45.5	40.6	203	2	Q9JBB6	Q9jbb6 human immun
311	46	41.1	410	2	Q8VQZ8	Q8vqz8 campylobact	384	45.5	40.6	203	2	Q9JBB8	Q9jbb8 human immun
312	46	41.1	420	2	Q23306	Q23306 arabidopsis	385	45.5	40.6	203	2	Q9JBB9	Q9jbb9 human immun
313	46	41.1	433	2	Q944M2	Q944m2 arabidopsis	386	45.5	40.6	203	2	Q9JBC5	Q9jbc5 human immun
314	46	41.1	457	2	Q741W2	Q741w2 lactobacill	387	45.5	40.6	203	2	Q9JBC9	Q9jbc9 human immun
315	46	41.1	458	2	Q741W2	Q741w2 lactobacill	388	45.5	40.6	203	2	Q9JBC9	Q9jbc9 human immun
316	46	41.1	472	2	Q98QF0	Q98qf0 giardia lam	389	45.5	40.6	203	2	Q9JBD2	Q9jbd2 human immun
317	46	41.1	474	1	Q98QF0	Q98qf0 mycoplasma	390	45.5	40.6	203	2	Q9JBF3	Q9jbf3 human immun
318	46	41.1	474	1	GC5B_THBMA	Q9w57 thermocoga	391	45.5	40.6	204	2	Q6RHM5	Q6rhm5 human immun
319	46	41.1	504	1	NORR_ECOL5	Q8x64 escherichia	392	45.5	40.6	204	2	Q9JBD7	Q9jbd7 human immun
320	46	41.1	504	1	NORR_ECOL1	Q8x66 escherichia	393	45.5	40.6	205	2	Q9JBP5	Q9jbp5 human immun
321	46	41.1	504	1	NORR_SHIFL	P37013 escherichia	394	45.5	40.6	205	2	Q6RHM3	Q6rhm3 human immun
322	46	41.1	506	1	NORR_SALTI	P59402 shigella fl	395	45.5	40.6	205	2	Q6RHM4	Q6rhm4 human immun
323	46	41.1	506	1	NORR_SALTY	Q8z466 salmonella	396	45.5	40.6	205	2	Q8AL66	Q8al66 human immun
						Q8znm8 salmonella						Q6SUP2	Q6sup2 human immun

397	45.5	40.6	207	2	Q6SUR4	Q6sur4 human immun	470	45	40.2	382	2	Q69BD1	Q69bd1 campylobact
398	45.5	40.6	215	2	Q9YXG5	Q9yxg5 human immun	471	45	40.2	382	2	Q69B11	Q69b11 campylobact
399	45.5	40.6	216	2	Q90XR12	Q90xr12 human immun	472	45	40.2	399	2	Q8LG40	Q8lg40 arabisdopsis
400	45.5	40.6	218	2	Q7SUL9	Q7sul9 human immun	473	45	40.2	399	2	Q67XY1	Q67xy1 arabisdopsis
401	45.5	40.6	219	2	Q7ZMC1	Q7zmc1 human immun	474	45	40.2	402	2	Q90IM7	Q90im7 human immun
402	45.5	40.6	219	2	Q9WLS0	Q9wls0 human immun	475	45	40.2	423	2	Q6XS08	Q6xs08 human immun
403	45.5	40.6	221	2	Q90QY4	Q90qy4 human immun	476	45	40.2	444	2	Q7JFT9	Q7jft9 wolbachia p
404	45.5	40.6	221	2	Q7ZMB5	Q7zmb5 human immun	477	45	40.2	458	2	Q6PDS5	Q6pds5 mus musculu
405	45.5	40.6	244	2	Q6IXG6	Q6ixg6 human immun	478	45	40.2	460	2	Q76HZ2	Q76hz2 bartonella
406	45.5	40.6	244	2	Q6IXH1	Q6ixh1 human immun	479	45	40.2	468	2	Q9JWX2	Q9jwx2 neisseria m
407	45.5	40.6	248	2	Q9WTT6	Q9wt6 human immun	480	45	40.2	483	2	Q94XU1	Q94xu1 spinacia ol
408	45.5	40.6	258	2	Q8ACR6	Q8acr6 human immun	481	45	40.2	495	2	Q9DBS6	Q9db6 mus musculu
409	45.5	40.6	258	2	Q9WDN2	Q9wdn2 human immun	482	45	40.2	514	2	Q96469	Q96469 ipomoea bat
410	45.5	40.6	289	2	Q83CA6	Q83cac coxiella bu	483	45	40.2	516	2	Q8C1D5	Q8c1d5 pasteurella
411	45.5	40.6	293	2	Q9J4P0	Q9j4p0 human immun	484	45	40.2	516	2	Q9CK28	Q9ck28 pasteurella
412	45.5	40.6	303	2	Q9J4N0	Q9j4n0 human immun	485	45	40.2	528	2	Q6F3J9	Q6f3j9 oryza sativ
413	45.5	40.6	343	2	Q91U97	Q91u97 human immun	486	45	40.2	531	2	Q989T4	Q989t4 rhizobium l
414	45.5	40.6	347	2	Q6CKS6	Q6cks6 kluyveromyc	487	45	40.2	534	1	CN1B_BOVIN	CN1b_bovin
415	45.5	40.6	347	2	Q91UB8	Q91ub8 human immun	488	45	40.2	535	1	CN1B_MOUSE	CN1b_mouse
416	45.5	40.6	359	2	P87965	P87965 human immun	489	45	40.2	535	1	CN1B_RAT	CN1b_rat
417	45.5	40.6	392	2	Q9APR4	Q9apr4 uncultured	490	45	40.2	536	2	Q9BE16	Q9be16 macaca faec
418	45.5	40.6	397	2	Q11547	Q11547 human immun	491	45	40.2	548	2	Q9YVD1	Q9yvd1 drosophila
419	45.5	40.6	402	2	Q6ELI3	Q6eli3 human immun	492	45	40.2	582	2	Q8BHS9	Q8bhs9 mus musculu
420	45.5	40.6	405	2	Q6ELI5	Q6eli5 human immun	493	45	40.2	595	2	Q89BH2	Q89bh2 bradyrhizob
421	45.5	40.6	410	2	Q8Q2F9	Q8q2f9 human immun	494	45	40.2	626	1	PR1M_LISIN	PR1m_lisin
422	45.5	40.6	422	2	Q8ZGX3	Q8zgx3 yerislinia pe	495	45	40.2	626	1	PR1M_LISMO	P47762 listeria in
423	45.5	40.6	425	1	B10A_SERMA	P36568 serralia ma	496	45	40.2	626	1	Q71ZL5	Q71z5 listeria mo
424	45.5	40.6	426	2	Q6D6F8	Q6d6f8 yerislinia pe	497	45	40.2	630	2	Q97J38	Q97j38 sulfolobus
425	45.5	40.6	426	2	Q8D003	Q8d003 yerislinia pe	498	45	40.2	643	1	SYT_HAEIN	SYT_haein
426	45.5	40.6	430	2	Q6W3J2	Q6w3j2 human immun	499	45	40.2	644	2	Q808I4	Q808i4 arabisdopsis
427	45.5	40.6	438	2	Q90C05	Q90c05 human immun	500	45	40.2	649	2	Q7RT54	Q7rt54 plasmodium
428	45.5	40.6	454	2	Q7ZBH6	Q7zbh6 simian-huma	501	45	40.2	673	2	Q8BVD6	Q8bvd6 mus musculu
429	45.5	40.6	455	2	Q7ZB10	Q7zb10 simian-huma	502	45	40.2	674	2	Q91Y31	Q91y31 mus musculu
430	45.5	40.6	456	2	Q7ZB12	Q7zb12 simian-huma	503	45	40.2	755	2	Q9M1Z2	Q9m1z2 arabisdopsis
431	45.5	40.6	501	2	Q6U9B2	Q6u9b2 bacterioph	504	45	40.2	808	2	Q8N270	Q8n270 homo sapien
432	45.5	40.6	582	1	MSBA_VIBPA	Q8716 vibrio para	505	45	40.2	877	1	SYA_WOLPM	SYA_wolpm
433	45.5	40.6	795	2	Q99BX6	Q99bx6 human immun	506	45	40.2	895	2	Q8C117	Q8c117 mus musculu
434	45.5	40.6	799	2	Q7ZGR4	Q7zgr4 human immun	507	45	40.2	897	2	Q8YMP3	Q8ymp3 anabaena sp
435	45.5	40.6	833	2	Q9QKH9	Q9qkh9 human immun	508	45	40.2	902	2	Q7PXP7	Q7pxp7 anophelis g
436	45.5	40.6	833	2	Q9OKI3	Q9ok13 human immun	509	45	40.2	974	2	Q6PG27	Q6pg27 homo sapien
437	45.5	40.6	841	2	Q8DYI7	Q8dy17 human immun	510	45	40.2	1052	1	MS1P_CRIGR	MS1p_crigr
438	45.5	40.6	849	2	Q6H1S7	Q6h1s7 human immun	511	45	40.2	1052	1	MS1P_HUMAN	MS1p_human
439	45.5	40.6	854	2	Q9WSE4	Q9wse4 human immun	512	45	40.2	1052	1	MS1P_MOUSE	MS1p_mouse
440	45.5	40.6	855	2	Q8UL67	Q8ul67 human immun	513	45	40.2	1052	1	Q6PG67	Q6pg67 mus musculu
441	45.5	40.6	858	2	Q90ZS4	Q90z24 human immun	514	45	40.2	1055	2	Q8OU80	Q8ou80 mus musculu
442	45.5	40.6	859	2	Q6JNM4	Q6jnm4 human immun	515	45	40.2	1366	2	Q8K7N9	Q8k7n9 streptococc
443	45.5	40.6	861	2	Q6JNP2	Q6jnp2 human immun	516	45	40.2	1366	2	Q8B2F2	Q8b2f2 streptococc
444	45.5	40.6	861	2	Q80367	Q80367 human immun	517	45	40.2	1372	2	Q878N3	Q878n3 streptococc
445	45.5	40.6	863	2	Q6BC68	Q6bc68 human immun	518	45	40.2	1504	2	Q6BD66	Q6bd66 homo sapien
446	45.5	40.6	867	2	Q8UB10	Q8ub10 oceanobacti	519	45	40.2	1723	2	Q9Y4F4	Q9y4f4 homo sapien
447	45	40.2	66	2	Q8ER91	Q8er91 oceanobacti	520	45	40.2	2443	2	Q96UJ7	Q96uj7
448	45	40.2	82	2	Q6MC16	Q6mc16 parachlamyd	521	45	40.2	2471	2	Q6COJ8	Q6coj8
449	45	40.2	104	2	Q980B8	Q980b8 sulfolobus	522	45	40.2	2811	2	Q7O9V2	Q7o9v2
450	45	40.2	118	2	Q99MNS	Q99mns rattus norv	523	45	40.2	7756	2	Q7O1MS	Q7o1ms
451	45	40.2	128	2	Q26723	Q26723 methanobact	524	45	39.7	84	2	Q4O374	Q4o374 human immun
452	45	40.2	154	2	Q8GXV2	Q8gxv2 arabisdopsis	525	45	39.7	84	2	Q4O376	Q4o376 human immun
453	45	40.2	184	2	Q8KP48	Q8kp48 peptostrept	526	45	39.7	84	2	Q4O380	Q4o380 human immun
454	45	40.2	204	1	HAM1_CLOPE	Q8x168 clostridium	527	45	39.7	84	2	Q4O382	Q4o382 human immun
455	45	40.2	226	1	VME1_PEDV7	P59771 porcine epi	528	45	39.7	84	2	Q4O384	Q4o384 human immun
456	45	40.2	226	1	VME1_PEDVB	P59770 porcine epi	529	45	39.7	84	2	Q4O386	Q4o386 human immun
457	45	40.2	226	2	Q91AU9	Q91au9 porcine epi	530	45	39.7	84	2	Q4O389	Q4o389 human immun
458	45	40.2	226	2	Q69ZM0	Q69zmo porcine epi	531	45	39.7	84	2	Q4O391	Q4o391 human immun
459	45	40.2	230	2	Q98FUS	Q98fus rhizobium l	532	45	39.7	84	2	Q4O393	Q4o393 human immun
460	45	40.2	262	2	Q8BMM1	Q8bmm1 mus musculu	533	45	39.7	84	2	Q4O395	Q4o395 human immun
461	45	40.2	264	1	YES4_SCHPO	Q1471 echizosacch	534	45	39.7	84	2	Q4O401	Q4o401 human immun
462	45	40.2	274	2	Q8RI36	Q8ri36 fusobacteri	535	45	39.7	84	2	Q4O402	Q4o402 human immun
463	45	40.2	296	2	Q7J3U0	Q7j3u0 treponema d	536	45	39.7	84	2	Q4O414	Q4o414 human immun
464	45	40.2	321	2	Q8UB39	Q8ub39 human immun	537	45	39.7	84	2	Q4O423	Q4o423 human immun
465	45	40.2	327	1	FLIG_THEMEA	Q871as vibrio para	538	45	39.7	84	2	Q4O424	Q4o424 human immun
466	45	40.2	335	1	FLIG_THEMEA	Q9w63 thermocoga	539	45	39.7	84	2	Q4O425	Q4o425 human immun
467	45	40.2	338	2	Q7WZ12	Q7wz12 haemophilus	540	45	39.7	84	2	Q4O428	Q4o428 human immun
468	45	40.2	368	2	Q754L5	Q754l5 ashuya goss	541	45	39.7	84	2	Q4O430	Q4o430 human immun
469	45	40.2	377	2	Q9FNC6	Q9fnc6 arabisdopsis	542	45	39.7	84	2	Q4O433	Q4o433 human immun

543	44.5	39.7	84	2	040435	040435 human immu	616	44.5	39.7	202	2	09JBC1	09jbc1 human immu
544	44.5	39.7	84	2	040441	040441 human immu	617	44.5	39.7	202	2	09JBC7	09jbc7 human immu
545	44.5	39.7	84	2	040442	040442 human immu	618	44.5	39.7	202	2	09JBC8	09jbc8 human immu
546	44.5	39.7	93	2	091293	091293 human immu	619	44.5	39.7	203	2	06SY32	06sy32 human immu
547	44.5	39.7	146	2	09UWV7	09UWV7 sulfolobus	620	44.5	39.7	203	2	06SY33	06sy33 human immu
548	44.5	39.7	156	2	09UWV8	09UWV8 human immu	621	44.5	39.7	203	2	06SY34	06sy34 human immu
549	44.5	39.7	157	2	070R53	070R53 human immu	622	44.5	39.7	203	2	06SY35	06sy35 human immu
550	44.5	39.7	158	2	09MWV3	09MWV3 human immu	623	44.5	39.7	203	2	06SY36	06sy36 human immu
551	44.5	39.7	159	2	09JER4	09JER4 human immu	624	44.5	39.7	203	2	06SY37	06sy37 human immu
552	44.5	39.7	159	2	09JER4	09JER4 human immu	625	44.5	39.7	203	2	07ZNH4	07znh4 human immu
553	44.5	39.7	168	2	06J4B0	06J4B0 human immu	626	44.5	39.7	203	2	09JB95	09jb95 human immu
554	44.5	39.7	168	2	070R09	070R09 human immu	627	44.5	39.7	203	2	09JB96	09jb96 human immu
555	44.5	39.7	169	2	09IWT3	09IWT3 human immu	628	44.5	39.7	203	2	09JB97	09jb97 human immu
556	44.5	39.7	171	2	070R20	070R20 human immu	629	44.5	39.7	203	2	09JBC3	09jbc3 human immu
557	44.5	39.7	177	2	0698V0	0698V0 human immu	630	44.5	39.7	204	2	06V7Y0	06v7y0 human immu
558	44.5	39.7	178	2	08UPR4	08UPR4 human immu	631	44.5	39.7	204	2	06V7Y9	06v7y9 human immu
559	44.5	39.7	178	2	08UPR6	08UPR6 human immu	632	44.5	39.7	204	2	06V7Z0	06v7z0 human immu
560	44.5	39.7	178	2	08UPR8	08UPR8 human immu	633	44.5	39.7	204	2	06V7Z4	06v7z4 human immu
561	44.5	39.7	178	2	08UPR1	08UPR1 human immu	634	44.5	39.7	204	2	07ZNH0	07znh0 human immu
562	44.5	39.7	179	2	070CM9	070CM9 human immu	635	44.5	39.7	204	2	09OQ01	09oq01 human immu
563	44.5	39.7	186	2	090RS9	090RS9 human immu	636	44.5	39.7	204	2	09YKX0	09yxc0 human immu
564	44.5	39.7	188	2	092963	092963 human immu	637	44.5	39.7	204	2	09YKX8	09yxc8 human immu
565	44.5	39.7	188	2	09DVH3	09DVH3 human immu	638	44.5	39.7	206	2	071852	071852 human immu
566	44.5	39.7	194	2	092254	092254 human immu	639	44.5	39.7	206	2	08AL78	08al78 human immu
567	44.5	39.7	194	2	070QM0	070QM0 human immu	640	44.5	39.7	206	2	09JBE1	09jbe1 human immu
568	44.5	39.7	195	2	0681E4	0681E4 human immu	641	44.5	39.7	206	2	09YRM7	09yrm7 human immu
569	44.5	39.7	195	2	09DVH9	09DVH9 human immu	642	44.5	39.7	207	2	0681E3	0681e3 human immu
570	44.5	39.7	196	2	07SKV3	07SKV3 human immu	643	44.5	39.7	207	2	09JBA2	09jba2 human immu
571	44.5	39.7	196	2	09JBI9	09JBI9 human immu	644	44.5	39.7	207	2	09JBB0	09jbb0 human immu
572	44.5	39.7	196	2	09JBI3	09JBI3 human immu	645	44.5	39.7	207	2	09JBB3	09jbb3 human immu
573	44.5	39.7	196	2	09JBI4	09JBI4 human immu	646	44.5	39.7	209	2	09JBB4	09jbb4 human immu
574	44.5	39.7	196	2	09JBI6	09JBI6 human immu	647	44.5	39.7	210	2	076528	076528 human immu
575	44.5	39.7	196	2	09JBE2	09JBE2 human immu	648	44.5	39.7	211	2	070QJ4	070qj4 human immu
576	44.5	39.7	196	2	09JBE5	09JBE5 human immu	649	44.5	39.7	212	2	078YH4	078yh4 human immu
577	44.5	39.7	197	2	06SUT4	06SUT4 human immu	650	44.5	39.7	213	2	075119	075119 human immu
578	44.5	39.7	198	2	08QAA4	08QAA4 human immu	651	44.5	39.7	214	2	090AP2	090a2 human immu
579	44.5	39.7	198	2	06SY26	06SY26 human immu	652	44.5	39.7	214	2	090AP3	090a3 human immu
580	44.5	39.7	198	2	06SY27	06SY27 human immu	653	44.5	39.7	214	2	090AP5	090a5 human immu
581	44.5	39.7	198	2	06SY28	06SY28 human immu	654	44.5	39.7	214	2	090AP5	090a5 human immu
582	44.5	39.7	198	2	06SY29	06SY29 human immu	655	44.5	39.7	214	2	070QK9	070qk9 human immu
583	44.5	39.7	198	2	07ZNH2	07ZNH2 human immu	656	44.5	39.7	216	2	09YKX9	09yxc9 human immu
584	44.5	39.7	198	2	09JBI1	09JBI1 human immu	657	44.5	39.7	217	2	073094	073094 human immu
585	44.5	39.7	198	2	09JBI2	09JBI2 human immu	658	44.5	39.7	217	2	073095	073095 human immu
586	44.5	39.7	198	2	090P28	090P28 human immu	659	44.5	39.7	217	2	073097	073097 human immu
587	44.5	39.7	199	2	08ALG7	08ALG7 human immu	660	44.5	39.7	217	2	073106	073106 human immu
588	44.5	39.7	200	2	06V7Y5	06V7Y5 human immu	661	44.5	39.7	217	2	073108	073108 human immu
589	44.5	39.7	200	2	06V7Z1	06V7Z1 human immu	662	44.5	39.7	217	2	073109	073109 human immu
590	44.5	39.7	200	2	06V7Z2	06V7Z2 human immu	663	44.5	39.7	219	2	06DWCO	06dwc0 human immu
591	44.5	39.7	200	2	06V7Z3	06V7Z3 human immu	664	44.5	39.7	219	2	070Q58	070q58 human immu
592	44.5	39.7	200	2	06V7Z5	06V7Z5 human immu	665	44.5	39.7	219	2	073096	073096 human immu
593	44.5	39.7	200	2	09JBA7	09JBA7 human immu	666	44.5	39.7	219	2	073098	073098 human immu
594	44.5	39.7	200	2	09JBB2	09JBB2 human immu	667	44.5	39.7	219	2	073110	073110 human immu
595	44.5	39.7	200	2	09Q4D0	09Q4D0 human immu	668	44.5	39.7	219	2	073111	073111 human immu
596	44.5	39.7	201	2	06V7Y3	06V7Y3 human immu	669	44.5	39.7	219	2	073112	073112 human immu
597	44.5	39.7	201	2	06V7Y6	06V7Y6 human immu	670	44.5	39.7	219	2	073113	073113 human immu
598	44.5	39.7	201	2	09JB99	09JB99 human immu	671	44.5	39.7	219	2	073114	073114 human immu
599	44.5	39.7	201	2	09JBA0	09JBA0 human immu	672	44.5	39.7	219	2	073115	073115 human immu
600	44.5	39.7	201	2	09JBA3	09JBA3 human immu	673	44.5	39.7	219	2	073116	073116 human immu
601	44.5	39.7	201	2	09JBA4	09JBA4 human immu	674	44.5	39.7	219	2	073117	073117 human immu
602	44.5	39.7	201	2	09JBA5	09JBA5 human immu	675	44.5	39.7	220	2	089555	089555 human immu
603	44.5	39.7	201	2	09JBA6	09JBA6 human immu	676	44.5	39.7	220	2	073090	073090 human immu
604	44.5	39.7	201	2	09JBA9	09JBA9 human immu	677	44.5	39.7	220	2	073087	073087 human immu
605	44.5	39.7	201	2	09JBA1	09JBA1 human immu	678	44.5	39.7	225	2	06RUX1	06rux1 human immu
606	44.5	39.7	201	2	09JBB4	09JBB4 human immu	679	44.5	39.7	225	2	073083	073083 human immu
607	44.5	39.7	201	2	09JBB5	09JBB5 human immu	680	44.5	39.7	225	2	073084	073084 human immu
608	44.5	39.7	201	2	09JBC0	09JBC0 human immu	681	44.5	39.7	225	2	073085	073085 human immu
609	44.5	39.7	202	2	09JBC2	09JBC2 human immu	682	44.5	39.7	225	2	073086	073086 human immu
610	44.5	39.7	202	2	06V7Y1	06V7Y1 human immu	683	44.5	39.7	225	2	073087	073087 human immu
611	44.5	39.7	202	2	06V7Y2	06V7Y2 human immu	684	44.5	39.7	225	2	073088	073088 human immu
612	44.5	39.7	202	2	06V7Y4	06V7Y4 human immu	685	44.5	39.7	227	2	081XY3	081xy3 homo sapien
613	44.5	39.7	202	2	06V7Y7	06V7Y7 human immu	686	44.5	39.7	229	2	056080	056080 human immu
614	44.5	39.7	202	2	06V7Y8	06V7Y8 human immu	687	44.5	39.7	259	2	056085	056085 human immu
615	44.5	39.7	202	2	09JB98	09JB98 human immu	688	44.5	39.7	259	2	056089	056089 human immu

689	44.5	39.7	259	092758	human	immun	092758	human	immun	752	44.5	39.7	455	2	Q7ZB18	Q7Zb18	simian-huma	762	44.5	39.7	455	2	Q7ZB18	Q7Zb18	simian-huma
690	44.5	39.7	259	092759	human	immun	092759	human	immun	753	44.5	39.7	455	2	Q7ZBK0	Q7ZbK0	simian-huma	763	44.5	39.7	455	2	Q7ZBK0	Q7ZbK0	simian-huma
691	44.5	39.7	259	092760	human	immun	092760	human	immun	754	44.5	39.7	455	2	Q7ZBK1	Q7ZbK1	simian-huma	764	44.5	39.7	455	2	Q7ZBK1	Q7ZbK1	simian-huma
692	44.5	39.7	259	09WLY3	human	immun	09WLY3	human	immun	755	44.5	39.7	455	2	Q7ZBK6	Q7ZbK6	simian-huma	765	44.5	39.7	455	2	Q7ZBK6	Q7ZbK6	simian-huma
693	44.5	39.7	259	09WLY4	human	immun	09WLY4	human	immun	756	44.5	39.7	455	2	Q7ZBK7	Q7ZbK7	simian-huma	766	44.5	39.7	455	2	Q7ZBK7	Q7ZbK7	simian-huma
694	44.5	39.7	259	09WLY5	human	immun	09WLY5	human	immun	757	44.5	39.7	455	2	Q7ZBK9	Q7ZbK9	simian-huma	767	44.5	39.7	455	2	Q7ZBK9	Q7ZbK9	simian-huma
695	44.5	39.7	265	09WE23	human	immun	09WE23	human	immun	758	44.5	39.7	455	2	Q7ZBL0	Q7ZbL0	simian-huma	768	44.5	39.7	455	2	Q7ZBL0	Q7ZbL0	simian-huma
696	44.5	39.7	265	09WE27	human	immun	09WE27	human	immun	759	44.5	39.7	455	2	Q7ZBL1	Q7ZbL1	simian-huma	769	44.5	39.7	455	2	Q7ZBL1	Q7ZbL1	simian-huma
697	44.5	39.7	295	09J4F8	human	immun	09J4F8	human	immun	770	44.5	39.7	455	2	Q7ZBL2	Q7ZbL2	simian-huma	770	44.5	39.7	455	2	Q7ZBL2	Q7ZbL2	simian-huma
698	44.5	39.7	311	09TNJ1	haplomitri	u	09TNJ1	haplomitri	u	771	44.5	39.7	455	2	Q7ZBL5	Q7ZbL5	simian-huma	771	44.5	39.7	455	2	Q7ZBL5	Q7ZbL5	simian-huma
699	44.5	39.7	311	071332	human	immun	071332	human	immun	772	44.5	39.7	455	2	Q7ZBL6	Q7ZbL6	simian-huma	772	44.5	39.7	455	2	Q7ZBL6	Q7ZbL6	simian-huma
700	44.5	39.7	311	072513	human	immun	072513	human	immun	773	44.5	39.7	455	2	Q7ZBL7	Q7ZbL7	simian-huma	773	44.5	39.7	455	2	Q7ZBL7	Q7ZbL7	simian-huma
701	44.5	39.7	322	07ZQG3	human	immun	07ZQG3	human	immun	774	44.5	39.7	456	2	Q7ZBL9	Q7ZbL9	simian-huma	774	44.5	39.7	456	2	Q7ZBL9	Q7ZbL9	simian-huma
702	44.5	39.7	325	07ZQF7	human	immun	07ZQF7	human	immun	775	44.5	39.7	456	2	Q7ZBU0	Q7ZbU0	simian-huma	775	44.5	39.7	456	2	Q7ZBU0	Q7ZbU0	simian-huma
703	44.5	39.7	326	07ZRS6	human	immun	07ZRS6	human	immun	776	44.5	39.7	456	2	Q7ZBU1	Q7ZbU1	simian-huma	776	44.5	39.7	456	2	Q7ZBU1	Q7ZbU1	simian-huma
704	44.5	39.7	328	07ZRS5	human	immun	07ZRS5	human	immun	777	44.5	39.7	456	2	Q7ZBU3	Q7ZbU3	simian-huma	777	44.5	39.7	456	2	Q7ZBU3	Q7ZbU3	simian-huma
705	44.5	39.7	329	07ZRA0	human	immun	07ZRA0	human	immun	778	44.5	39.7	456	2	Q7ZBU4	Q7ZbU4	simian-huma	778	44.5	39.7	456	2	Q7ZBU4	Q7ZbU4	simian-huma
706	44.5	39.7	329	07ZRA1	human	immun	07ZRA1	human	immun	779	44.5	39.7	456	2	Q7ZBJ5	Q7ZbJ5	simian-huma	779	44.5	39.7	456	2	Q7ZBJ5	Q7ZbJ5	simian-huma
707	44.5	39.7	329	07ZRA	human	immun	07ZRA	human	immun	780	44.5	39.7	456	2	Q7ZBJ6	Q7ZbJ6	simian-huma	780	44.5	39.7	456	2	Q7ZBJ6	Q7ZbJ6	simian-huma
708	44.5	39.7	329	07ZRA3	human	immun	07ZRA3	human	immun	781	44.5	39.7	456	2	Q7ZBJ7	Q7ZbJ7	simian-huma	781	44.5	39.7	456	2	Q7ZBJ7	Q7ZbJ7	simian-huma
709	44.5	39.7	329	07ZRA4	human	immun	07ZRA4	human	immun	782	44.5	39.7	456	2	Q7ZBJ8	Q7ZbJ8	simian-huma	782	44.5	39.7	456	2	Q7ZBJ8	Q7ZbJ8	simian-huma
710	44.5	39.7	329	07ZRA5	human	immun	07ZRA5	human	immun	783	44.5	39.7	456	2	Q7ZBJ9	Q7ZbJ9	simian-huma	783	44.5	39.7	456	2	Q7ZBJ9	Q7ZbJ9	simian-huma
711	44.5	39.7	329	07ZRA6	human	immun	07ZRA6	human	immun	784	44.5	39.7	456	2	Q7ZBK2	Q7ZbK2	simian-huma	784	44.5	39.7	456	2	Q7ZBK2	Q7ZbK2	simian-huma
712	44.5	39.7	329	07ZRA7	human	immun	07ZRA7	human	immun	785	44.5	39.7	456	2	Q7ZBK3	Q7ZbK3	simian-huma	785	44.5	39.7	456	2	Q7ZBK3	Q7ZbK3	simian-huma
713	44.5	39.7	329	07ZRA8	human	immun	07ZRA8	human	immun	786	44.5	39.7	456	2	Q7ZBK4	Q7ZbK4	simian-huma	786	44.5	39.7	456	2	Q7ZBK4	Q7ZbK4	simian-huma
714	44.5	39.7	329	07ZRA9	human	immun	07ZRA9	human	immun	787	44.5	39.7	456	2	Q7ZBK5	Q7ZbK5	simian-huma	787	44.5	39.7	456	2	Q7ZBK5	Q7ZbK5	simian-huma
715	44.5	39.7	329	07ZRA0	human	immun	07ZRA0	human	immun	788	44.5	39.7	456	2	Q7ZBK6	Q7ZbK6	simian-huma	788	44.5	39.7	456	2	Q7ZBK6	Q7ZbK6	simian-huma
716	44.5	39.7	329	07ZRA2	human	immun	07ZRA2	human	immun	789	44.5	39.7	456	2	Q7ZBK9	Q7ZbK9	simian-huma	789	44.5	39.7	456	2	Q7ZBK9	Q7ZbK9	simian-huma
717	44.5	39.7	329	07ZRA3	human	immun	07ZRA3	human	immun	790	44.5	39.7	456	2	Q7ZBK0	Q7ZbK0	simian-huma	790	44.5	39.7	456	2	Q7ZBK0	Q7ZbK0	simian-huma
718	44.5	39.7	329	07ZRA4	human	immun	07ZRA4	human	immun	791	44.5	39.7	456	2	Q7ZBK1	Q7ZbK1	simian-huma	791	44.5	39.7	456	2	Q7ZBK1	Q7ZbK1	simian-huma
719	44.5	39.7	329	07ZRA6	human	immun	07ZRA6	human	immun	792	44.5	39.7	456	2	Q7ZBK2	Q7ZbK2	simian-huma	792	44.5	39.7	456	2	Q7ZBK2	Q7ZbK2	simian-huma
720	44.5	39.7	329	07ZRA5	human	immun	07ZRA5	human	immun	793	44.5	39.7	456	2	Q7ZBK9	Q7ZbK9	simian-huma	793	44.5	39.7	456	2	Q7ZBK9	Q7ZbK9	simian-huma
721	44.5	39.7	348	09IU99	human	immun	09IU99	human	immun	794	44.5	39.7	457	2	Q7ZBN2	Q7ZbN2	simian-huma	794	44.5	39.7	457	2	Q7ZBN2	Q7ZbN2	simian-huma
722	44.5	39.7	352	09W7W0	human	immun	09W7W0	human	immun	795	44.5	39.7	457	2	Q7ZBN3	Q7ZbN3	simian-huma	795	44.5	39.7	457	2	Q7ZBN3	Q7ZbN3	simian-huma
723	44.5	39.7	359	P87975	human	immun	P87975	human	immun	796	44.5	39.7	457	2	Q7ZBN4	Q7ZbN4	simian-huma	796	44.5	39.7	457	2	Q7ZBN4	Q7ZbN4	simian-huma
724	44.5	39.7	360	08QAX4	human	immun	08QAX4	human	immun	797	44.5	39.7	457	2	Q7ZBN5	Q7ZbN5	simian-huma	797	44.5	39.7	457	2	Q7ZBN5	Q7ZbN5	simian-huma
725	44.5	39.7	379	07ZBM5	simian-huma	Q7Zbm5	simian-huma	Q7Zbm5	simian-huma	798	44.5	39.7	457	2	Q7ZBN6	Q7ZbN6	simian-huma	798	44.5	39.7	457	2	Q7ZBN6	Q7ZbN6	simian-huma
726	44.5	39.7	380	07ZBM3	simian-huma	Q7Zbm3	simian-huma	Q7Zbm3	simian-huma	799	44.5	39.7	457	2	Q7ZBN7	Q7ZbN7	simian-huma	799	44.5	39.7	457	2	Q7ZBN7	Q7ZbN7	simian-huma
727	44.5	39.7	380	07ZBM4	simian-huma	Q7Zbm4	simian-huma	Q7Zbm4	simian-huma	800	44.5	39.7	457	2	Q7ZBN8	Q7ZbN8	simian-huma	800	44.5	39.7	457	2	Q7ZBN8	Q7ZbN8	simian-huma
728	44.5	39.7	380	07ZBM6	simian-huma	Q7Zbm6	simian-huma	Q7Zbm6	simian-huma	801	44.5	39.7	457	2	Q7ZBN9	Q7ZbN9	simian-huma	801	44.5	39.7	457	2	Q7ZBN9	Q7ZbN9	simian-huma
729	44.5	39.7	380	07ZBM8	simian-huma	Q7Zbm8	simian-huma	Q7Zbm8	simian-huma	802	44.5	39.7	457	2	Q7ZBN0	Q7ZbN0	simian-huma	802	44.5	39.7	457	2	Q7ZBN0	Q7ZbN0	simian-huma
730	44.5	39.7	380	07ZBM9	simian-huma	Q7Zbm9	simian-huma	Q7Zbm9	simian-huma	803	44.5	39.7	457	2	Q7ZBP1	Q7ZbP1	simian-huma	803	44.5	39.7	457	2	Q7ZBP1	Q7ZbP1	simian-huma
731	44.5	39.7	380	07ZBN0	simian-huma	Q7Zbn0	simian-huma	Q7Zbn0	simian-huma	804	44.5	39.7	457	2	Q7ZBP2	Q7ZbP2	simian-huma	804	44.5	39.7	457	2	Q7ZBP2	Q7ZbP2	simian-huma
732	44.5	39.7	380	07ZBN1	simian-huma	Q7Zbn1	simian-huma	Q7Zbn1	simian-huma	805	44.5	39.7	457	2	Q7ZBP3	Q7ZbP3	simian-huma	805	44.5	39.7	457	2	Q7ZBP3	Q7ZbP3	simian-huma
733	44.5	39.7	386	040372	human	immun	040372	human	immun	806	44.5	39.7	457	2	Q7ZBP4	Q7ZbP4	simian-huma	806	44.5	39.7	457	2	Q7ZBP4	Q7ZbP4	simian-huma
734	44.5	39.7	386	040426	human	immun	040426	human	immun	807	44.5	39.7	457	2	Q7ZBP5	Q7ZbP5	simian-huma	807	44.5	39.7	457	2	Q7ZBP5	Q7ZbP5	simian-huma
735	44.5	39.7	386	040437	human	immun	040437	human	immun	808	44.5	39.7	457	2	Q7ZBP6	Q7ZbP6	simian-huma	808	44.5	39.7	457	2	Q7ZBP6	Q7ZbP6	simian-huma
736	44.5	39.7	393	06A922	human	immun	06A922	human	immun	809	44.5	39.7	457	2	Q7ZBP7	Q7ZbP7	simian-huma	809	44.5	39.7	457	2	Q7ZBP7	Q7ZbP7	simian-huma
737	44.5	39.7	398	0661E0	human	immun	0661E0	human	immun	810	44.5	39.7	457	2	Q7ZBP8	Q7ZbP8	simian-huma	810	44.5	39.7	457	2	Q7ZBP8	Q7ZbP8	simian-huma
738	44.5	39.7	405	06W2X1	human	immun	06W2X1	human	immun	811	44.5	39.7	457	2	Q7ZBP9	Q7ZbP9	simian-huma	811	44.5	39.7	457	2	Q7ZBP9	Q7ZbP9	simian-huma
739	44.5	39.7	405	06W2X3	human	immun	06W2X3	human	immun	812	44.5	39.7	457	2	Q7ZB00	Q7Zb00	simian-huma	812	44.5	39.7	457	2	Q7ZB00	Q7Zb00	simian-huma
740	44.5	39.7	416	072602	human	immun	072602	human	immun	813	44.5	39.7	457	2	Q7ZBQ1	Q7ZbQ1	simian-huma	813	44.5	39.7	457	2	Q7ZBQ1	Q7ZbQ1	simian-huma
741	44.5	39.7	416	08J513	human	immun	08J513	human	immun	814	44.5	39.7	457	2	Q7ZBQ2	Q7ZbQ2	simian-huma	814	44.5	39.7	457	2	Q7ZBQ2	Q7ZbQ2	simian-huma
742	44.5	39.7	422	09RMP4	xenorthodius	Q9rmp4	xenorthodius	Q9rmp4	xenorthodius	815	44.5	39.7	457	2	Q7ZBQ3	Q7ZbQ3	simian-huma	815	44.5	39.7	457	2	Q7ZBQ3	Q7ZbQ3	simian-huma
743	44.5	39.7	423	07N6Q8	photorhabd	Q7nbq8	photorhabd	Q7nbq8	photorhabd	816	44.5	39.7	457	2	Q7ZBQ4	Q7ZbQ4	simian-huma	816	44.5	39.7	457	2	Q7ZBQ4	Q7ZbQ4	

835	44.5	39.7	843	2	Q7SPU1	Q7SPU1 human immun	908	44	39.3	533	2	Q7XSQ5	Q7XSQ5 oryza sativ
836	44.5	39.7	846	2	Q6H1M3	Q6H1M3 human immun	909	44	39.3	537	2	Q94KU2	Q94KU2 spinacia o
837	44.5	39.7	847	1	ENV_HV1S1	P19550 human immun	910	44	39.3	546	1	CH60_MOLSU	Q7mea3 wolnella s
838	44.5	39.7	847	2	Q6BCO4	Q6BCO4 human immun	911	44	39.3	553	2	Q6YUK1	Q6YUK1 oryza sativ
839	44.5	39.7	847	2	Q6AR21	Q6AR21 human immun	912	44	39.3	553	2	Q9X6V4	Q9X6V4 bacillus ha
840	44.5	39.7	852	2	Q418B3	Q418B3 human immun	913	44	39.3	557	2	Q9XEV7	Q9XEV7 glycine max
841	44.5	39.7	853	2	Q6X6N4	Q6X6N4 human immun	914	44	39.3	559	2	Q7N2L1	Q7N2L1 photorhabdu
842	44.5	39.7	854	2	Q6JYK1	Q6JYK1 human immun	915	44	39.3	571	2	Q668S5	Q668S5 aquifex aeo
843	44.5	39.7	855	2	Q9DL76	Q9DL76 human immun	916	44	39.3	586	2	Q95TL6	Q95TL6 drosophi
844	44.5	39.7	857	2	P90249	P90249 human immun	917	44	39.3	586	2	Q9V4M8	Q9V4M8 drosophi
845	44.5	39.7	857	2	Q9OQJ6	Q9OQJ6 human immun	918	44	39.3	589	2	Q9M4U9	Q9M4U9 cucumis mel
846	44.5	39.7	858	2	Q8QDZ4	Q8QDZ4 human immun	919	44	39.3	603	2	Q87EM5	Q87EM5 xylella fae
847	44.5	39.7	858	2	Q75114	Q75114 human immun	920	44	39.3	603	2	Q9PEP4	Q9PEP4 xylella fae
848	44.5	39.7	861	2	Q9O599	Q9O599 human immun	921	44	39.3	638	1	CH6B_DROME	Q9VPS5 drosophi
849	44.5	39.7	861	2	Q6BC66	Q6BC66 human immun	922	44	39.3	749	2	Q88XEO	Q88XEO lactobacill
850	44.5	39.7	861	2	Q6RRP1	Q6RRP1 human immun	923	44	39.3	744	2	Q9LBI2	Q9LBI2 vibrio para
851	44.5	39.7	868	2	Q6UC35	Q6UC35 human immun	924	44	39.3	744	2	Q87MK4	Q87MK4 vibrio para
852	44.5	39.7	875	2	Q6UF78	Q6UF78 human immun	925	44	39.3	750	1	YKS7_YEAST	P34231 saccharomyc
853	44.5	39.7	897	2	Q91ZG4	Q91ZG4 cache valle	926	44	39.3	919	2	Q9HYE4	Q9HYE4 aquifex aeo
854	44.5	39.7	897	2	Q91ZG4	Q91ZG4 cache valle	927	44	39.3	1019	2	Q66770	Q66770 aquifex aeo
855	44	39.3	100	2	Q9LXZ8	Q9LXZ8 plasmodium	928	44	39.3	1023	2	Q9Q094	Q9Q094 chimpanzee
856	44	39.3	100	2	Q9LXZ8	Q9LXZ8 arabisopsis	929	44	39.3	1031	2	Q9Q273	Q9Q273 chimpanzee
857	44	39.3	143	2	Q961X6	Q961X6 homo sapien	930	44	39.3	1045	2	Q6D7E2	Q6D7E2 erwinia car
858	44	39.3	148	2	Q632M6	Q632M6 bacillus ce	931	44	39.3	1209	2	Q6ZES0	Q6ZES0 synechocyst
859	44	39.3	148	2	Q81KD0	Q81KD0 bacillus ce	932	44	39.3	1210	2	Q8EOJ8	Q8EOJ8 oceanobacill
860	44	39.3	148	2	Q6HC66	Q6HC66 bacillus th	933	44	39.3	1223	2	Q6FUN1	Q6FUN1 candida gla
861	44	39.3	149	2	Q83HU3	Q83HU3 tropheryma	934	44	39.3	1307	2	Q9C093	Q9C093 homo sapien
862	44	39.3	162	2	Q83GD8	Q83GD8 tropheryma	935	44	39.3	1577	2	Q55265	Q55265 streptococ
863	44	39.3	181	2	Q9FL19	Q9FL19 arabisopsis	936	44	39.3	1505	2	Q91823	Q91823 xenopus lae
864	44	39.3	184	2	Q8RKU25	Q8RKU25 uncultured	937	44	39.3	2788	2	Q7WRX9	Q7WRX9 anaerobae cl
865	44	39.3	184	2	Q68H71	Q68H71 clostridium	938	44	39.3	3424	2	Q81DB4	Q81DB4 bacillus ce
866	44	39.3	184	2	Q68H72	Q68H72 clostridium	939	44	39.3	4467	2	Q9J3E9	Q9J3E9 murine hepa
867	44	39.3	186	2	Q6G148	Q6G148 staphylococ	940	44	39.3	4470	2	Q66MN5	Q66MN5 murine hepa
868	44	39.3	190	2	Q6TCJ1	Q6TCJ1 human immun	941	44	39.3	5336	2	Q9R9J0	Q9R9J0 bacillus bu
869	44	39.3	196	2	Q84UJ5	Q84UJ5 oryza sativ	942	44	39.3	7176	1	R1B3_CMAS	P16342 m replicase
870	44	39.3	200	1	COAE_BACAN	Q6heg2 bacillus an	943	44	39.3	7178	2	Q66WN6	Q66WN6 murine hepa
871	44	39.3	200	2	Q633L3	Q633L3 bacillus ce	944	44	39.3	7667	2	Q7QG88	Q7QG88 anopheles g
872	44	39.3	200	2	Q6HCU7	Q6HCU7 bacillus th	945	44	39.3	79	2	Q7Q493	Q7Q493 human immun
873	44	39.3	223	2	Q91NKA	Q91NKA avian infec	946	44	39.3	79	2	Q7Q494	Q7Q494 human immun
874	44	39.3	236	2	Q999E5	Q999E5 human immun	947	44	39.3	84	2	Q7Q496	Q7Q496 human immun
875	44	39.3	258	2	Q97134	Q97134 trypanosoma	948	44	39.3	84	2	Q7Q497	Q7Q497 human immun
876	44	39.3	268	2	Q65U07	Q65U07 manheimia	949	44	39.3	84	2	Q7Q499	Q7Q499 human immun
877	44	39.3	282	2	Q8DRY3	Q8DRY3 streptococ	950	44	39.3	85	2	Q7P612	Q7P612 fusobacteri
878	44	39.3	282	2	Q8B4C0	Q8B4C0 streptococ	951	44	39.3	85	2	Q8REL5	Q8REL5 fusobacteri
879	44	39.3	292	1	N1FH_HERSE	P78723 herbaspiril	952	44	39.3	100	2	Q97767	Q97767 human immun
880	44	39.3	308	1	KDGD_BACSU	P42235 bacillus bu	953	44	39.3	146	2	Q9DBE5	Q9DBE5 human immun
881	44	39.3	341	2	Q7ZG60	Q7ZG60 thermus tne	954	44	39.3	157	2	Q91WS3	Q91WS3 human immun
882	44	39.3	350	2	Q6BRAT	Q6BRAT debaryomyce	955	44	39.3	158	2	Q41878	Q41878 human immun
883	44	39.3	352	2	Q6COK3	Q6COK3 yarrowia li	956	44	39.3	160	2	Q91190	Q91190 human immun
884	44	39.3	357	2	Q89Z29	Q89Z29 bacteroides	957	44	39.3	162	1	G16O_BACSU	P80872 bacillus bu
885	44	39.3	358	2	Q8DKN6	Q8DKN6 synechococ	958	44	39.3	162	2	Q91WS9	Q91WS9 human immun
886	44	39.3	401	1	APGM_THEMEA	Q9XZ95 thermocoga	959	44	39.3	163	2	Q10607	Q10607 human immun
887	44	39.3	410	2	Q6CBL6	Q6CBL6 yarrowia li	960	44	39.3	163	2	Q66N50	Q66N50 human immun
888	44	39.3	413	2	Q93Y13	Q93Y13 cucumis sat	961	44	39.3	163	2	Q66N51	Q66N51 human immun
889	44	39.3	428	2	Q7XT74	Q7XT74 oryza sativ	962	44	39.3	163	2	Q66N54	Q66N54 human immun
890	44	39.3	429	2	Q8DX40	Q8DX40 streptococ	963	44	39.3	163	2	Q66N56	Q66N56 human immun
891	44	39.3	447	1	SRS4_STLSO	Q97677 sulfolobus	964	44	39.3	163	2	Q66N57	Q66N57 human immun
892	44	39.3	468	2	Q8P596	Q8P596 xanthomonas	965	44	39.3	164	2	Q10599	Q10599 human immun
893	44	39.3	473	1	LCB1_HUMAN	Q15269 homo sapien	966	44	39.3	166	2	Q9E2U2	Q9E2U2 human immun
894	44	39.3	480	2	Q7FRX8	Q7FRX8 oryza sativ	967	44	39.3	173	2	Q9E2U4	Q9E2U4 human immun
895	44	39.3	480	2	Q9L100	Q9L100 oryza sativ	968	44	39.3	173	2	Q99F32	Q99F32 human immun
896	44	39.3	483	2	Q6CWM20	Q6CWM20 kluyveromyc	969	44	39.3	173	2	Q9E2V5	Q9E2V5 human immun
897	44	39.3	490	2	Q75CT5	Q75CT5 asahya goss	970	44	39.3	176	2	Q8JEM3	Q8JEM3 human immun
898	44	39.3	495	1	IAIC_AEATH	Q8GY00 arabisopsis	971	44	39.3	177	2	Q8UEW0	Q8UEW0 human immun
899	44	39.3	499	2	Q67C11	Q67C11 human immun	972	44	39.3	178	2	Q99F26	Q99F26 human immun
900	44	39.3	504	1	HUTH_STPAM	P64415 staphylococ	973	44	39.3	178	2	Q9QRM1	Q9QRM1 human immun
901	44	39.3	504	1	HUTH_STPAM	P64416 staphylococ	974	44	39.3	179	2	Q8JEV9	Q8JEV9 human immun
902	44	39.3	504	1	HUTH_STPAM	Q8HYV3 staphylococ	975	44	39.3	179	2	Q9E1R2	Q9E1R2 human immun
903	44	39.3	504	2	Q6GDB2	Q6GDB2 staphylococ	976	44	39.3	181	2	Q8Q3K5	Q8Q3K5 human immun
904	44	39.3	513	2	Q6NUL7	Q6NUL7 homo sapien	977	44	39.3	182	2	Q8Q3K1	Q8Q3K1 human immun
905	44	39.3	514	2	Q9AR15	Q9AR15 cucumis sat	978	44	39.3	183	2	Q8UEU1	Q8UEU1 human immun
906	44	39.3	528	2	Q8YVE7	Q8YVE7 arabisopsis	979	44	39.3	183	2	Q90CRO	Q90CRO human immun
907	44	39.3	528	2	Q9FWP5	Q9FWP5 arabisopsis	980	44	39.3	184	2	Q90CQ5	Q90CQ5 human immun

```
981 43.5 38.8 185 2 Q7ZNM9 human immun
982 43.5 38.8 186 2 Q90CP2 human immun
983 43.5 38.8 186 2 Q90CR3 human immun
984 43.5 38.8 187 2 Q99J34 human immun
985 43.5 38.8 188 2 Q9DYG3 human immun
986 43.5 38.8 190 2 Q8QJ32 human immun
987 43.5 38.8 190 2 Q8QJ36 human immun
988 43.5 38.8 191 2 Q8QJ39 human immun
989 43.5 38.8 192 2 Q8QJ39 human immun
990 43.5 38.8 192 2 Q8QJ38 human immun
991 43.5 38.8 192 2 Q6IXS7 human immun
992 43.5 38.8 192 2 Q7SIR1 human immun
993 43.5 38.8 192 2 Q9DV17 human immun
994 43.5 38.8 194 2 Q9DV51 human immun
995 43.5 38.8 195 2 Q8QA98 human immun
996 43.5 38.8 195 2 Q8QAA3 human immun
997 43.5 38.8 195 2 Q7O525 human immun
998 43.5 38.8 195 2 Q7ZP18 human immun
999 43.5 38.8 195 2 Q9DVC2 human immun
1000 43.5 38.8 196 2 Q6S2J0 human immun
```

## ALIGNMENTS

```
RESULT 1
Q6SR10 PRELIMINARY; PRT; 143 AA.
```

```
ID Q6SR10;
AC Q6SR10;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-PH2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_Taxid=264386;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen H.-Y., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451891; AAS44755.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;
```

```
Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MADNGTIVTEELKQLEQNNLV 22
DB 1 MADNGTIVTEELKQLEQNNLV 22
```

## RESULT 2

```
ID Q6SR14 PRELIMINARY; PRT; 143 AA.
AC Q6SR14;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-PH1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_Taxid=264387;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
```

```
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451890; AAS44755.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;
```

```
Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MADNGTIVTEELKQLEQNNLV 22
DB 1 MADNGTIVTEELKQLEQNNLV 22
```

## RESULT 3

```
ID Q6SR18 PRELIMINARY; PRT; 143 AA.
AC Q6SR18;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_Taxid=264386;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451889; AAS44751.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;
```

```
Query Match 100.0%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MADNGTIVTEELKQLEQNNLV 22
DB 1 MADNGTIVTEELKQLEQNNLV 22
```

## RESULT 4

```
ID Q6SRJ2 PRELIMINARY; PRT; 143 AA.
AC Q6SRJ2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_Taxid=264385;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451888; AAS44747.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
```



SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;  
 Query Match 100.0%; Score 112; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22  
 DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 5  
 Q6SRJ6 PRELIMINARY; PRT; 143 AA.  
 AC Q6SRJ6  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DE Membrane glycoprotein M (Fragment).  
 OS SARS coronavirus TW-YM2.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
 OX NCBI\_TaxId=264384;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY451887; AAS44743.1; -  
 DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
 DR InterPro; IPR002574; Corona\_M.  
 DR Pfam; PF01635; Corona\_M; 1.  
 DR NON TER 143  
 FT SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22  
 DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 6  
 Q6SRK4 PRELIMINARY; PRT; 143 AA.  
 AC Q6SRK4  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DE Membrane glycoprotein M (Fragment).  
 OS SARS coronavirus TW-GD5.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
 OX NCBI\_TaxId=264382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY451885; AAS44735.1; -  
 DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
 DR InterPro; IPR002574; Corona\_M.  
 DR Pfam; PF01635; Corona\_M; 1.  
 DR NON TER 143  
 FT SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22

DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 7  
 Q6SRK8 PRELIMINARY; PRT; 143 AA.  
 AC Q6SRK8  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DE Membrane glycoprotein M (Fragment).  
 OS SARS coronavirus TW-GD4.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
 OX NCBI\_TaxId=264381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY451884; AAS44731.1; -  
 DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
 DR InterPro; IPR002574; Corona\_M.  
 DR Pfam; PF01635; Corona\_M; 1.  
 DR NON TER 143  
 FT SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22  
 DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 8  
 Q6SR12 PRELIMINARY; PRT; 143 AA.  
 AC Q6SR12  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DE Membrane glycoprotein M (Fragment).  
 OS SARS coronavirus TW-GD3.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
 OX NCBI\_TaxId=264380;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY451883; AAS44727.1; -  
 DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
 DR InterPro; IPR002574; Corona\_M.  
 DR Pfam; PF01635; Corona\_M; 1.  
 DR NON TER 143  
 FT SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22  
 DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 9  
 Q6SR16 PRELIMINARY; PRT; 143 AA.

AC Q6SR16; 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-GD2.  
OC Coronavirus; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
NCBI\_TaxID=264379;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
Yan Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451882; AAS44723.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON\_TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;  
  
Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MADNGTITVEELKQLLEQWNLV 22  
DB 1 MADNGTITVEELKQLLEQWNLV 22  
  
RESULT 10  
Q6SRM0 PRELIMINARY; PRT; 143 AA.  
ID Q6SRM0; 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-GD1.  
OC Coronavirus; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
NCBI\_TaxID=264378;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
Yan Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451881; AAS44719.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON\_TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;  
  
Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MADNGTITVEELKQLLEQWNLV 22  
DB 1 MADNGTITVEELKQLLEQWNLV 22  
  
RESULT 11  
Q6SRM4 PRELIMINARY; PRT; 143 AA.  
ID Q6SRM4; 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-KC3.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;

OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
NCBI\_TaxID=264377;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
Yan Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451880; AAS44715.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON\_TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;  
  
Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MADNGTITVEELKQLLEQWNLV 22  
DB 1 MADNGTITVEELKQLLEQWNLV 22  
  
RESULT 12  
Q6SRM8 PRELIMINARY; PRT; 143 AA.  
ID Q6SRM8; 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-KC1.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
NCBI\_TaxID=264376;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
Yan Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451879; AAS44711.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON\_TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;  
  
Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MADNGTITVEELKQLLEQWNLV 22  
DB 1 MADNGTITVEELKQLLEQWNLV 22  
  
RESULT 13  
Q6SRN2 PRELIMINARY; PRT; 143 AA.  
ID Q6SRN2; 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-JC2.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
NCBI\_TaxID=264375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
Yan Y.-Y., Chen H.-Y., Chen Y.-M.Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY451878; AAS44707.1; -;  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
FT NON TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22  
Db 1 MADNGTITVEELKQLEQNNLV 22

## RESULT 14

OC O6SRN6 PRELIMINARY; PRT; 143 AA.  
AC O6SRN6;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-HP4.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_Taxid=264374;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M. Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY451877; AAS44703.1; -;  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
FT NON TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22  
Db 1 MADNGTITVEELKQLEQNNLV 22

## RESULT 15

OC O6SRP0 PRELIMINARY; PRT; 143 AA.  
AC O6SRP0;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-HP3.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_Taxid=264373;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M. Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY451876; AAS44699.1; -;  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
FT NON TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22  
Db 1 MADNGTITVEELKQLEQNNLV 22

## RESULT 16

OC O6SRP4 PRELIMINARY; PRT; 143 AA.  
AC O6SRP4;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-HP2.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_Taxid=264372;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M. Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY451875; AAS44695.1; -;  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
FT NON TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22  
Db 1 MADNGTITVEELKQLEQNNLV 22

## RESULT 17

OC O6SRP8 PRELIMINARY; PRT; 143 AA.  
AC O6SRP8;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-HP1.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_Taxid=264371;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M. Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY451874; AAS44691.1; -;  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
FT NON TER 143 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 100.0%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADNGTITVEELKQLEQNNLV 22  
Db 1 MADNGTITVEELKQLEQNNLV 22

RESULT 18  
VME1\_CVHSA STANDARD; PRT; 221 AA.  
ID VME1\_CVHSA STANDARD; PRT; 221 AA.  
AC P59596; O6885; Q77608; Q776R1; Q776R5; Q776S0; Q776S3; Q77726;  
AC Q77756; Q77756; Q77A12;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).  
GN Name=M;  
OS Human coronavirus (strain SARS) (HCoV-SARS) (SARS-CoV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=227859;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Urbani;  
RX MEDLINE=22660724; PubMed=12730500; DOI=10.1126/science.1085952;  
RA Rota P.A., Oberste M.S., Monroe S.S., Nix W.A., Campagnoli R.,  
RA Icenogle J.P., Penaranda S., Bankamp B., Maher K., Chen M.-H.,  
RA Tong S., Tamin A., Lowe L., Frace M., Derisi J.L., Chen Q., Wang D.,  
RA Erdman D.D., Peret T.C.T., Burns C., Ksiazek T.G., Rollin P.E.,  
RA Sanchez A., Liffick S., Holloway B., Limor J., McCausland K.,  
RA Olsen-Rasmussen M., Fouchier R., Gueuther S., Osterhaus A.D.M.E.,  
RA Drosen C., Pallansch M.A., Anderson L.J., Bellini W.J.;  
RT "Characterization of a novel coronavirus associated with severe acute  
RT respiratory syndrome."; Science 300:1394-1399(2003).  
RL Science 300:1394-1399(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Tor2;  
RX MEDLINE=22660725; PubMed=12730501; DOI=10.1126/science.1085953;  
RA Marra M.A., Jones S.J.M., Astell C.R., Holt R.A., Brooks-Wilson A.,  
RA Butcherfield Y.S.N., Khatri A., Asano J.K., Barber S.A., Chan S.Y.,  
RA Cloutier A., Coughlin S.M., Freeman D., Glin N., Griffith O.L.,  
RA Leach S.R., Mayo M., McDonald H., Montgomery S.B., Pandoh P.K.,  
RA Petrescu A.S., Robertson A.G., Schein J.E., Siddiqui A., Small N.,  
RA Stott J.M., Yang G.S., Plummer F., Andonov A., Atsosh H., Bastien N.,  
RA Bernard K., Booth T.F., Bowness D., Czud M., Drebot M., Fernandez L.,  
RA Flick R., Garbutt M., Gray M., Grolla A., Jones S., Feldmann H.,  
RA Meyers A., Kabani A., Li Y., Normand S., Stricker U., Tipples G.A.,  
RA Tyler S., Vogt R., Ward D., Watson B., Brunham R.C., Krajden M.,  
RA Petric M., Skowronski D.M., Upton C., Roper R.L.;  
RT "The genome sequence of the SARS-associated coronavirus."; Science 300:1399-1404(2003).  
RL Science 300:1399-1404(2003).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate CUHK-Su10, and Isolate CUHK-W1;  
RX MEDLINE=22737955; PubMed=12853594; DOI=10.1056/NEJM200307103490216;  
RA Tsui S.K.W., Chim S.S.C., Lo Y.M.D.;  
RT "Coronavirus genomic-sequence variations and the epidemiology of the  
RT severe acute respiratory syndrome."; N. Engl. J. Med. 349:187-188(2003).  
RL N. Engl. J. Med. 349:187-188(2003).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate GZ50, and Isolate HKU-36871;  
RX MEDLINE=22913660; PubMed=12958366; DOI=10.1126/science.1087139;  
RA Guan Y., Zheng B.J., He Y.Q., Liu X.L., Zhuang Z.X., Cheung C.L.,  
RA Luo S.W., Li P.H., Zhang L.D., Guan Y.J., But K.M., Wong K.L.,  
RA Chan K.W., Lim W., Shortridge K.F., Yuen K.Y., Peiris J.S.M.,  
RA Poon L.L.M.;  
RT "Isolation and characterization of viruses related to the SARS  
RT coronavirus from animals in southern China."; Science 302:276-278(2003).  
RL Science 302:276-278(2003).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate HKU-39849;  
RX MEDLINE=22758472; PubMed=12876307;  
RA Zeng F.Y., Chan C.W., Chan M.N., Chen J.D., Chow K.Y.C., Hon C.C.C.,  
RA Hui R.K.H., Li J., Li V.Y.Y., Wang C.Y., Wang P.Y., Guan Y., Zheng B.,  
RA Poon L.L.M., Chan K.H., Yuen K.Y., Peiris J.S.M., Leung F.C.;

RT "The complete genome sequence of severe acute respiratory syndrome  
RT coronavirus strain HKU-39849 (HK-39)."; Exp. Biol. Med. 228:866-873(2003).  
RL Exp. Biol. Med. 228:866-873(2003).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Sin2500, Isolate Sin2677, Isolate Sin2679,  
RC Isolate Sin2748, and Isolate Sin2774;  
RX MEDLINE=22667074; PubMed=12781537; DOI=10.1016/S0140-6736(03)13414-9;  
RA Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,  
RA Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,  
RA Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,  
RA Liu E.T.;  
RT "Comparative full-length genome sequence analysis of 14 SARS  
RT coronavirus isolates and common mutations associated with putative  
RT origins of infection."; Lancet 361:1779-1785(2003).  
RL Lancet 361:1779-1785(2003).  
RN [7]  
RP ERRATUM  
RX PubMed=12781581;  
RA Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,  
RA Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,  
RA Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,  
RA Liu E.T.;  
RL Lancet 361:1832-1832(2003).  
RN [8]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate BJ01, Isolate BJ02, Isolate BJ03, Isolate BJ04, and  
RC Isolate GD01;  
RX PubMed=12781581;  
RA Qiu E., Zhu Q., Yu M., Fan B., Chang G., Si B., Yang B., Peng W.,  
RA Jiang T., Liu B., Deng Y., Liu H., Zhang Y., Wang C., Li Y., Gan Y.,  
RA Li X., Lu F., Tan G., Yang R., Cao W.S., Wang J., Chen W., Cong L.,  
RA Deng Y., Dong W., Han Y., Hu W., Lei M., Li C., Li G., Li H.,  
RA Li S., Li S., Li W., Li W., Lin W., Liu J., Liu Z., Lu H., Ni P.,  
RA Li Q., Sun Y., Wang L., Tong Z., Wang J., Wang X., Wu Q., Xi Y.,  
RA Xu Z., Yang L., Ye C., Ye J., Zhang B., Zhang F., Zhang X.,  
RA Zhou J., Yang H.;  
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate TW1;  
RX Yeh S.-H., Kao C.-L., Tsai C.-Y., Liu C.-J., Chen D.-S., Chen P.-J.;  
RT "The complete genome of SARS coronavirus clone TW1."; Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate FRA;  
RX Rickmann M., Becker S., Klenk H.-D., Doerr H.W., Stadler K.,  
RA Censini S., Guidotti S., Maignani V., Scarselli M., Mora M.,  
RA Donati C., Han J., Song H.C., Abbrignani S., Covacci A., Rappuoli R.;  
RT "SARS virus is a close relative of type II coronaviruses."; Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Frankfurt 1;  
RX Thiel V., Hertzog T., Putics A., Ivanov K.A., Schelle B., Bayer S.,  
RA Scheiner B., Weiland H., Weissdich B., Ziehr J.;  
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Shanghai OXC1;  
RX Yuan Z., Zhang X., Hu Y., Lan S., Wang H., Zhou Z., Wen Y.,  
RA "Analysis of SARS coronavirus genome in Shanghai isolates."; Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.  
RL Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate ZJ01;  
RX Cong L.-M., Ding G.-Q., Lu Y.-Y., Yan J.-Q., Meng J.-Q., Cheng S.-Y.,  
RA Zhang Y.-J., Mei L.-L., Wang Z.-G., Hu N., Mo J., Yao J., Zhu H.-P.,  
RA Lu Q.-Y., Li M.-H., Gong L.-M., Shi W.;  
RL Submitted (Jun-2003) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate TWC;

RA Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee S.C., Lin Y.-C.,  
 RA Hsu C.-K., Chen H.-Y., Chang J.-G., Chen P.-J., Su I.-J.;  
 RT "Genomic sequence of SARS isolate from the first fatal case in  
 RT Taiwan."; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RN (15)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Isolate Taiwan TC1, Isolate Taiwan TC2, and Isolate Taiwan TC3;  
 RA Chang J.-G.C., Lin T.-H., Chen C.-M., Lin C.-S., Chan W.-L.,  
 RA Shih M.-C.; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RN (16)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Isolate TWK, Isolate TWJ, Isolate TWK, Isolate TWS, and  
 RC Isolate TWY; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RA Shu H.-Y., Wu K.M., Tsai S.F.; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RN (17)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Isolate HSR 1; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RA Canducci F., Clementi M., Poli G., Vicenzi E.; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RN (18)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Isolate TW2, and Isolate TW3;  
 RA Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee H.-C., Lin Y.-C.,  
 RA Yao C.-W., Chien T.-S., Lu J.-J., Chen A., Hsu C.-K., Chen H.-Y.,  
 RA Chen P.-J., Su I.-J.; Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 RN (19)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Isolate AS;  
 RA Balotta C., Corvase S., Violin M., Galli M., Moroni M.,  
 RA Vigeant G.M., Ruan Y.J., Salemi M.; Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Component of the viral envelope that plays a central  
 CC role in virus morphogenesis and assembly via its interactions with  
 CC other viral proteins (By similarity).  
 CC SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: Belongs to the coronavirus M protein family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: AY278741; AAP13444.1; -;  
 DR EMBL: AY274119; AAP13441.1; -;  
 DR EMBL: AY278554; AAP13571.1; -;  
 DR EMBL: AY282752; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AY304492; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AY304495; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AY278491; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AY283794; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AY283795; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AY283795; -; NOT\_ANNOTATED\_CDS.  
 Query Match 100.0%; Score 112; DB 1; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADNGTITVEBLKQLEQNNLV 22  
 DB 1 MADNGTITVEBLKQLEQNNLV 22  
 RESULT 19  
 Q66VB9 PRELIMINARY; PRT; 221 AA.  
 AC O66VB9;  
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)

DT 25-OCT-2004 (T-EMBLrel. 28, last sequence update)  
 DT 25-OCT-2004 (T-EMBLrel. 28, last annotation update)  
 DE M protein.  
 OS SARS coronavirus GD322.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=291613;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hu Z., Zhao W., Yan H.;  
 RT "The analyses of M genes' variation rules of SARS-CoV and their  
 RT influence upon the possible B cell epitopes of M genes.";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY702026; AAU07933.1; -;  
 DR InterPro: IPR002574; Corona\_M.  
 DR Pfam: PF01635; Corona\_M; 1.  
 DR Pfam: PF01635; Corona\_M; 1.  
 SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;  
 Query Match 100.0%; Score 112; DB 2; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADNGTITVEBLKQLEQNNLV 22  
 DB 1 MADNGTITVEBLKQLEQNNLV 22  
 RESULT 20  
 Q66Y07 PRELIMINARY; PRT; 221 AA.  
 AC O66Y07;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, last annotation update)  
 DE Hypothetical protein M.  
 GN ORFNames=SARSCoVSP08;  
 OS SARS coronavirus LdJ-2004.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=273522;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Li J., Wei W., Xiao W., Wang M., Wang J., Zhao J., Sun Z., Pei Y.,  
 RA Chen Y.; Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AY595412; AAT52332.1; -;  
 DR EMBL: AY595412; AAT52332.1; -;  
 DR GO: GO:0019058; P: viral infectious cycle; IEA.  
 DR InterPro: IPR002574; Corona\_M.  
 DR Pfam: PF01635; Corona\_M; 1.  
 DR Pfam: PF01635; Corona\_M; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;  
 Query Match 100.0%; Score 112; DB 2; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MADNGTITVEBLKQLEQNNLV 22  
 DB 1 MADNGTITVEBLKQLEQNNLV 22  
 RESULT 21  
 Q6CH34 PRELIMINARY; PRT; 221 AA.  
 ID Q6CH34;  
 AC Q6CH34;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, last annotation update)  
 DE Membrane protein.  
 OS SARS coronavirus Sin03-11.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=255729;  
 NCB1\_TaxID=255729;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sin03-11;
RA Jin W.W., Peng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
RA Gao H., Ning Y., Zhang J.S., Li N., Yin W.D.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY485278; AAR23256.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEBLKQLEQWNLV 22
DB 1 MADNGTITVEBLKQLEQWNLV 22

RESULT 22
Q6RH42 PRELIMINARY; PRT; 221 AA.
ID Q6RH42;
AC Q6RH42;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane protein.
OS SARS coronavirus Sin01-11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=255730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sin01-11;
RA Jin W.W., Peng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
RA Gao H., Ning Y., Zhang J.S., Li N., Yin W.D.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY485277; AAR23248.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEBLKQLEQWNLV 22
DB 1 MADNGTITVEBLKQLEQWNLV 22

RESULT 23
Q6R7Y2 PRELIMINARY; PRT; 221 AA.
ID Q6R7Y2;
AC Q6R7Y2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Membrane protein M.
OS SARS coronavirus NS-1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=260743;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS-1;
RA Guo H., Chen J., Wei W., Li J., Zhang Y., Wang X., Sun Y., Jiao J.,
RA Wang Y., Zhou C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
```

```

DR EMBL; AY508724; AAR91590.1; -
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25069 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEBLKQLEQWNLV 22
DB 1 MADNGTITVEBLKQLEQWNLV 22

RESULT 24
Q6RCW1 PRELIMINARY; PRT; 221 AA.
ID Q6RCW1;
AC Q6RCW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW9.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258972;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502932; AAR87604.1; -
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEBLKQLEQWNLV 22
DB 1 MADNGTITVEBLKQLEQWNLV 22

RESULT 25
Q6RCX2 PRELIMINARY; PRT; 221 AA.
ID Q6RCX2;
AC Q6RCX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW8.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258971;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
```

```

RA Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502931; AAR87593.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ ENVELOPE protein.
KW SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 26
Q6RCY3 PRELIMINARY; PRT; 221 AA.
AC Q6RCY3;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW7.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=258970;
RX [1] SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502930; AAR87582.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 27
Q6RCZ4 PRELIMINARY; PRT; 221 AA.
AC Q6RCZ4;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW6.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=258969;
RX [1] SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
```

```

RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502929; AAR87571.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 28
Q6RD05 PRELIMINARY; PRT; 221 AA.
AC Q6RD05;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW5.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=258968;
RX [1] SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502928; AAR87560.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 29
Q6RD16 PRELIMINARY; PRT; 221 AA.
AC Q6RD16;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=258967;
RX [1] SEQUENCE FROM N.A.
```

```

RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502927; AAR87549.1; -.
DR GO; GO:0019031; C:Viral infectious cycle; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 30
Q6RD27 PRELIMINARY; PRT; 221 AA.
ID 06RD27;
AC 06RD27;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258966;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502926; AAR87538.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 31
Q6RD38 PRELIMINARY; PRT; 221 AA.
ID 06RD38;
AC 06RD38;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
```

```

OX NCBI_TaxID=258965;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502925; AAR87527.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 32
Q6RD49 PRELIMINARY; PRT; 221 AA.
ID 06RD49;
AC 06RD49;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TW11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258964;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502924; AAR87516.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
KW Envelope protein.
SQ SEQUENCE 221 AA; 25006 MW; DBEBBCOABAD77B7D CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNNLV 22
DB 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 33
Q6RD60 PRELIMINARY; PRT; 221 AA.
ID 06RD60;
AC 06RD60;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative envelope protein M.
```



```
OS SARS coronavirus TW10.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258963;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
  Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
  genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502923; AAR87505.1; -.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0019058; P: viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 66586529297478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 34
06S8D3 PRELIMINARY; PRT; 221 AA.
AC 06S8D3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE complete genome.
OS SARS coronavirus ShanghaiQXC2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258508;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ShanghaiQXC2;
RA Yuan Z., Zhang X., Hu Y., Ian S., Zhou Z., Wang H., Wen Y.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY463060; AAR86779.1; -.
DR GO; GO:0019058; P: viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25044 MW; 51875ABE9BAE04FC CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 35
06T1D8 PRELIMINARY; PRT; 221 AA.
AC 06T1D8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M.
OS SARS coronavirus CUHK-12.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
```

```
OX NCBI_TaxID=260550;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14709660;
RA Chim S.S.C., Tong Y.K., Hung E.C.W., Chiu R.W.K., Lo Y.M.D.;
RT "Genomic sequencing of a SARS coronavirus isolate that predated the
  Metropole Hotel case cluster in Hong Kong.";
RL Clin. Chem. 50:231-233(2004).
DR EMBL; AY443095; AAS01068.1; -.
DR GO; GO:0019058; P: viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 36
06TPE4 PRELIMINARY; PRT; 221 AA.
AC 06TPE4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Matrix protein.
OS SARS coronavirus GZ02.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=256753;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou X., Hou J., He M., Ding Y., Wang Z., Li J., Liu Z., Ma S.,
  Zhang K., Pan W., Zhang J., He J., Wang Y., Xu Y., Wang X.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY390556; AAS00007.1; -.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR GO; GO:0019058; P: viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 37
06UZE9 PRELIMINARY; PRT; 221 AA.
AC 06UZE9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative M protein.
OS SARS coronavirus PUMC03.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=253435;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,
  Zhou X., Zhang W., Yu Z., Qin C., Liu X., Shen Y., Ni A., Qiang B.;
```

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY357076; AAR14812.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M\_1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 38  
ID Q6UZF3 PRELIMINARY; PRT; 221 AA.  
AC Q6UZF3;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Putative M protein.  
OS SARS coronavirus PUMC02.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxId=253434;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,  
RA Zhou X., Zhang W., Yu Z., Qin C., Liu X., Shen Y., Ni A., Qiang B.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY357075; AAR14808.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M\_1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 39  
ID Q6V584 PRELIMINARY; PRT; 221 AA.  
AC Q6V584;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Putative M protein.  
OS SARS coronavirus PUMC01.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxId=253433;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,  
RA Zhou X., Zhang W., Yu Z., Fan Z., Peng X., Qin C., Liu X., Shen Y.,  
RA Ni A., Qiang B.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY350750; AAR14804.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M\_1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;

Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 40  
ID Q6VA74 PRELIMINARY; PRT; 221 AA.  
AC Q6VA74;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Putative M protein.  
OS SARS coronavirus CUHK-AG03.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxId=239243;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.W.,  
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,  
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,  
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,  
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,  
RA Mong C.H., Yiu W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;  
RT "Genomic characterisation of the SARS-coronavirus of the Amoy Gardens outbreak in Hong Kong."  
RL Lancet 362:1807-1808(2003).  
DR EMBL; AY345988; AAP94763.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M\_1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22

RESULT 41  
ID Q6VA85 PRELIMINARY; PRT; 221 AA.  
AC Q6VA85;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Putative M protein.  
OS SARS coronavirus CUHK-AG02.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxId=239242;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.W.,  
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,  
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,  
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,  
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,  
RA Wong C.H., Yiu W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;  
RT "Genomic characterisation of the SARS-coronavirus of the Amoy Gardens outbreak in Hong Kong."  
RL Lancet 362:1807-1808(2003).  
DR EMBL; AY345987; AAP94752.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M\_1.

SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;  
Query Match 100.0%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22  
RESULT 42  
Q6VA96 PRELIMINARY; PRT; 221 AA.  
AC Q6VA96; 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE Putative M protein.  
OS SARS coronavirus CUHK-AG01.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=239241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chim S.S.C., Teui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.W.,  
Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,  
Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,  
Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,  
Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,  
Wong C.H., Yiu W.H., Lee N., Mu A., Tee C.H., Chan L.Y.S., Lo Y.M.D.,  
"Genomic characterisation of the SARS-coronavirus of the Amoy Gardens  
outbreak in Hong Kong";  
RT Lancet 362:1807-1808(2003).  
RL EMBL; AY345986; AAP94741.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;  
Query Match 100.0%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22  
RESULT 43  
Q692E0 PRELIMINARY; PRT; 221 AA.  
AC Q692E0; 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DE Membrane glycoprotein.  
OS SARS coronavirus TUF.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=284672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chen W., Yan M., Liu M.,  
"Isolation and identification of Viruses Related to the SARS  
RT Coronavirus from swine in China";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY54424; AAT76152.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25059 MW; 439CD30C104CBFAC CRC64;

Query Match 96.4%; Score 108; DB 2; Length 221;  
Best Local Similarity 95.5%; Pred. No. 1.4e-06;  
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22  
RESULT 44  
Q6QJ38 PRELIMINARY; PRT; 221 AA.  
AC Q6QJ38; 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE Membrane protein.  
OS SARS coronavirus BJ01.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=228407;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li T., Li X., Chang Z., Liu L.,  
"Identification of SARS-CoV RNA leader sequence";  
RT Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY536759; AAS48455.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25059 MW; 439CD30C104CBFAC CRC64;  
Query Match 96.4%; Score 108; DB 2; Length 221;  
Best Local Similarity 95.5%; Pred. No. 1.4e-06;  
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22  
RESULT 45  
Q6SRK0 PRELIMINARY; PRT; 143 AA.  
AC Q6SRK0; 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-YM1.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_TaxID=264383;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ian Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
Yang J.-Y., Chen H.-Y., Chen Y.-M., Arthur J.,  
"Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451886; AAS44739.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON\_TER 143  
SQ SEQUENCE 143 AA; 16435 MW; 2694FA8363B971F7 CRC64;  
Query Match 94.6%; Score 106; DB 2; Length 143;  
Best Local Similarity 95.5%; Pred. No. 1.6e-06;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MADNGTITVEELKQLEQNNLV 22  
DB 1 MADNGTITVEELKQLEQNNLV 22

```

RESULT 46
HOSC_THET2
ID HOSC_THET2 STANDARD; PRT; 376 AA.
AC 087198;
DT 30-MAY-2000 (Rel. 39, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homocitrate synthase (EC 2.3.3.14).
GN Name=lye20; OrderedLocustNames=TTCl550;
OS Thermus thermophilus (Strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
NCBI_TaxID=262724;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99085673; PubMed=9868782;
RX Kosuge T., Hoshino T.;
RT "Lysine is synthesized through the alpha-aminoadipate pathway in
RT Thermus thermophilus";
RL FEMS Microbiol. Lett. 169:361-367(1998).
[2]
RN SEQUENCE FROM N.A.
RX PubMed=15064768; DOI=10.1038/nbt956;
RA Henne A., Brueggemann H., Raasch C., Wlezer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkvienne V., Schlenzcek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus";
RL Nat. Biotechnol. 22:547-553(2004).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + 2-oxoglutarate = 2-
CC hydroxybutyrate-1,2,4-tricarboxylate + CoA.
CC -1- PATHWAY: Lysine biosynthesis; alpha-aminoadipic acid pathway;
CC first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate
CC synthase family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AB018379; BAA33785.1; -.
DR EMBL; AB017306; AAS81892.1; -.
DR PIR; T51170; T51170.
DR InterPro; IPR002034; AIPM/HcIt_synth.
DR InterPro; IPR000891; HMGU-like.
DR Pfam; PF00682; HMGU-like; 1.
DR PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
DR PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
DR PROSITE; PS50991; PYR_CT; 1.
DR Complete proteome; Lysine biosynthesis; Transferase.
FT CONFLICT 104 104 A -> P (in Ref. 1).
SQ SEQUENCE 376 AA; 42159 MW; 1B8BEA63C82FCF06 CRC64;
Query Match 51.8%; Score 58; DB 1; Length 376;
Best Local Similarity 47.4%; Pred. No. 15;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 MADNGTIVVEELKQLEQW 19
DB 355 LADRGQLTLEELDRILREW 373
RESULT 47
Q8PLJ9 PRELIMINARY; PRT; 409 AA.

```

```

AC 08PLJ9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Two-component system sensor protein.
GN Name=regS; OrderedLocustNames=XAC1798;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=306 / ATCC 13902 / XV 101;
RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Camarvan F., Cardozo J., Chambergro F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira L.A.F., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola H.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitejima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AB018182; AAM3666.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0001055; P:two-component sensor molecule activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR005467; His_Kinase.
DR InterPro; IPR003661; His_kin_N.
DR InterPro; IPR009082; His_kin_homodim.
DR Pfam; PF02518; HATPase_c1; 1.
DR Pfam; PF00512; HSKA; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HSKA; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR Complete proteome; Kinase; Phosphorylation; Sensory transduction;
DR Transferase.
SQ SEQUENCE 409 AA; 44065 MW; F481A6B6FA570BE CRC64;
Query Match 49.6%; Score 55.5; DB 2; Length 409;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 12; Conservative 5; Mismatches 4; Indels 1; Gaps 1;
QY 2 ADNGTIVVE-ELKQLEQWNV 22
DB 258 ADNGHLSREVAVKEVLEQWRLV 279
RESULT 48
Q9LRN6 PRELIMINARY; PRT; 229 AA.
AC Q9LRN6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:MU18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC  
 RT clones.";  
 RL DNA Res. 7:131-135(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB028621; BAB01352.1; -.  
 DR HSP; P06787; IFS5.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR010983; EF\_Hand\_Like.  
 DR Pfam; PF00036; ehand; 4.  
 DR ProDom; PD000012; EF-hand; 1.  
 DR SMART; SM00054; Eph; 2.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN 1.  
 SQ SEQUENCE 229 AA; 26266 MW; 94C011172CA33740 CRC64;  
 Query Match 49.1%; Score 55; DB 2; Length 229;  
 Best Local Similarity 61.1%; Pred. No. 23;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Oy 4 NGTITVEELKQLLEQWNL 21  
 DB 70 NGTIDIEELKCKCHELKL 87  
 RESULT 49  
 OXSE24 PRELIMINARY; PRT; 512 AA.  
 AC OXSE24;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Calcium-dependent protein kinase.  
 GN Name=CDPK5;  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cheong Y.H., Moon B.C., Cho M.U.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF194414; AAF23901.2; -.  
 DR HSSP; PA9137; INXK.  
 DR Gramene; OXSE24; -.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001751; CABP\_S100.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR010983; EF\_Hand\_Like.  
 DR InterPro; IPR011009; Kinase\_Like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_kinase.  
 DR Pfam; PF00036; ehand; 4.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD003407; CABP\_S100; 1.  
 DR ProDom; PD000012; EF-hand; 2.

DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00054; Eph; 4.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00018; EF\_HAND; 4.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Calcium; Calcium-binding; Kinase;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 512 AA; 57584 MW; 89E38CFB9537F6 CRC64;  
 Query Match 47.8%; Score 53.5; DB 2; Length 512;  
 Best Local Similarity 57.1%; Pred. No. 82;  
 Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;  
 Oy 4 NGTITVEELKQLLEQWNL 21  
 DB 372 NGTISLEELKQALKQVPMRL 392  
 RESULT 50  
 OXRCJ0 PRELIMINARY; PRT; 279 AA.  
 AC OXRCJ0;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE PspQ protein (CpsQ).  
 GN Name=pspQ; Synonyms=cpsQ;  
 OS Streptococcus thermophilus.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1308;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CNR2368;  
 RX MEDLINE=98325267; PubMed=9657932; DOI=10.1006/plas.1998.1337;  
 RA Bourgoin F., Guedon G., Gintz B., Decaris B.;  
 RT "Characterization of a novel insertion sequence, IS1194, in  
 RT Streptococcus thermophilus.";  
 RL Plasmid 40:44-49(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CNR2368;  
 RX MEDLINE=99307153; PubMed=10375631; DOI=10.1016/S0378-1119(99)00144-4;  
 RA Bourgoin F., Pluvinet A., Gintz B., Decaris B., Guedon G.;  
 RT "Are horizontal transfers involved in the evolution of the  
 RT Streptococcus thermophilus exopolysaccharide synthesis loci?";  
 RL Gene 233:151-161(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CNR2368;  
 RA Schmitt C., Guedon G., Pegulier S., Pebay M., Panis C., Decaris B.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MR-1C;  
 RX PubMed=12647947;  
 RA Broadbent J.R., McMahon D.J., Welker D.L., Oberg C.J., Moineau S.;  
 RT "Biochemistry, genetics, and applications of exopolysaccharide  
 RT production in Streptococcus thermophilus: a review.";  
 RL J. Dairy Sci. 86:407-423(2003).  
 DR EMBL; Z98171; CAB52237.1; -.  
 DR EMBL; AF448249; AAM93399.1; -.  
 DR InterPro; IPR001173; Glyco\_trans\_2.  
 DR Pfam; PF00535; Glycoe\_transf\_2; 1.  
 SQ SEQUENCE 279 AA; 32049 MW; 070D0978EF507A0B CRC64;  
 Query Match 47.3%; Score 53; DB 2; Length 279;  
 Best Local Similarity 50.0%; Pred. No. 52;  
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 Oy 1 MADNGTITVEELKQLLEQWNL 20

Db :||:|:|:|:|  
33 LVDNCGNVDKGLNQN 52

Search completed: May 11, 2005, 21:27:03  
Job time : 132.255 secs

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 21:16:44 ; Search time 28.5532 Seconds  
(without alignments)  
57.516 Million cell updates/sec

Title: US-10-712-812-5  
Perfect score: 112  
Sequence: 1 MADNGRTVEELKQLLEQNNLV 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51.5	46.0	855	4 US-09-206-551-11	Sequence 11, Appl
2	51.5	46.0	855	4 US-09-206-551-12	Sequence 12, Appl
3	51	45.5	205	2 US-08-531-525-31	Sequence 31, Appl
4	51	45.5	205	2 US-08-718-270A-31	Sequence 31, Appl
5	51	45.5	206	3 US-09-078-317-15	Sequence 15, Appl
6	51	45.5	206	3 US-09-454-818-15	Sequence 15, Appl
7	51	45.5	206	3 US-09-709-103-48	Sequence 48, Appl
8	51	45.5	206	4 US-09-439-410A-48	Sequence 48, Appl
9	49	43.8	123	4 US-09-266-965-132	Sequence 132, Appl
10	49	43.8	218	4 US-09-538-092-241	Sequence 241, Appl
11	48	42.9	300	4 US-09-538-092-241	Sequence 241, Appl
12	48	42.9	462	4 US-09-538-092-769	Sequence 769, Appl
13	47	42.0	159	4 US-09-538-092-266	Sequence 266, Appl
14	46	41.1	100	4 US-09-513-999C-6125	Sequence 6125, Appl
15	46	41.1	149	4 US-09-270-767-45884	Sequence 45884, Appl
16	46	41.1	216	4 US-09-710-279-2624	Sequence 2624, Appl
17	46	41.1	274	4 US-09-134-001C-5279	Sequence 5279, Appl
18	46	41.1	300	4 US-09-648-004-26	Sequence 26, Appl
19	46	41.1	300	4 US-10-272-419-26	Sequence 26, Appl
20	46	41.1	415	4 US-09-248-796A-14232	Sequence 14232, Appl
21	46	41.1	532	4 US-09-489-039A-10011	Sequence 10011, Appl
22	46	41.1	536	2 US-08-940-332-2	Sequence 2, Appl
23	46	41.1	537	4 US-09-543-681A-4729	Sequence 4729, Appl
24	46	41.1	537	4 US-09-949-016-7536	Sequence 7536, Appl
25	45	40.2	119	4 US-09-540-236-2256	Sequence 2256, Appl
26	45	40.2	292	4 US-09-248-796A-21680	Sequence 21680, Appl
27	45	40.2	534	1 US-07-872-644-27	Sequence 27, Appl

28	45	40.2	534	1 US-08-297-494-27	Sequence 27, Appl
29	45	40.2	534	1 US-08-297-510-27	Sequence 27, Appl
30	45	40.2	534	1 US-08-479-532-27	Sequence 27, Appl
31	45	40.2	534	1 US-08-455-526-27	Sequence 27, Appl
32	45	40.2	534	1 US-08-455-525-27	Sequence 27, Appl
33	45	40.2	534	3 US-09-139-491-27	Sequence 27, Appl
34	45	40.2	534	3 US-09-883-825-27	Sequence 27, Appl
35	45	40.2	534	5 PCT-US92-03222-27	Sequence 27, Appl
36	45	40.2	714	4 US-09-248-796A-18997	Sequence 18997, Appl
37	45	40.2	1052	3 US-09-255-502-7	Sequence 7, Appl
38	45	40.2	1052	3 US-09-360-237-1	Sequence 1, Appl
39	45	40.2	1052	3 US-09-560-237-3	Sequence 3, Appl
40	45	40.2	1052	4 US-09-255-501-208	Sequence 208, Appl
41	45	40.2	1052	4 US-09-060-854B-7	Sequence 7, Appl
42	45	40.2	1052	4 US-09-891-711-4	Sequence 4, Appl
43	45	40.2	1052	4 US-09-891-711-6	Sequence 6, Appl
44	45	40.2	1052	4 US-09-949-016-6413	Sequence 6413, Appl
45	45	40.2	1052	4 US-09-060-872A-208	Sequence 208, Appl
46	45	40.2	1052	4 US-09-500-135C-208	Sequence 208, Appl
47	45	40.2	1058	4 US-09-949-016-10687	Sequence 10687, Appl
48	44.5	39.7	847	4 US-09-476-242-2	Sequence 2, Appl
49	44	39.3	93	4 US-09-621-976-4009	Sequence 4009, Appl
50	44	39.3	114	4 US-09-107-532A-6600	Sequence 6600, Appl
51	44	39.3	473	4 US-09-949-016-9820	Sequence 9820, Appl
52	44	39.3	545	4 US-09-544-683-2	Sequence 2, Appl
53	44	39.3	545	4 US-09-192-419-2	Sequence 2, Appl
54	44	39.3	952	4 US-09-252-991A-17515	Sequence 17515, Appl
55	44	39.3	1577	2 US-08-793-824-2	Sequence 2, Appl
56	43.5	38.8	434	4 US-09-107-532A-4075	Sequence 4075, Appl
57	43.5	38.8	540	4 US-09-543-681A-5987	Sequence 5987, Appl
58	43.5	38.8	726	4 US-09-902-540-10385	Sequence 10385, Appl
59	43.5	38.8	770	4 US-09-248-796A-17215	Sequence 17215, Appl
60	43	38.4	162	4 US-09-543-681A-6627	Sequence 6627, Appl
61	43	38.4	229	4 US-09-270-767-41871	Sequence 41871, Appl
62	43	38.4	229	4 US-09-270-767-57115	Sequence 57115, Appl
63	43	38.4	259	4 US-09-248-796A-20877	Sequence 20877, Appl
64	43	38.4	490	4 US-08-956-171E-5212	Sequence 5212, Appl
65	43	38.4	490	4 US-08-781-986A-5212	Sequence 5212, Appl
66	43	38.4	597	4 US-09-107-532A-7053	Sequence 7053, Appl
67	43	38.4	3200	4 US-09-328-352-5486	Sequence 5486, Appl
68	42.5	37.9	226	3 US-09-134-001C-5494	Sequence 5494, Appl
69	42.5	37.9	429	3 US-08-411-768B-4	Sequence 4, Appl
70	42.5	37.9	429	4 US-09-543-681A-5233	Sequence 5233, Appl
71	42.5	37.9	431	2 US-08-401-068-4	Sequence 4, Appl
72	42.5	37.9	431	2 US-08-846-338-4	Sequence 4, Appl
73	42.5	37.9	447	2 US-09-489-039A-13287	Sequence 13287, Appl
74	42.5	37.9	596	2 US-08-592-806A-2	Sequence 2, Appl
75	42.5	37.9	596	3 US-09-257-490-2	Sequence 2, Appl
76	42	37.5	115	4 US-09-328-352-5509	Sequence 5509, Appl
77	42	37.5	128	4 US-09-302-540-15331	Sequence 15331, Appl
78	42	37.5	129	4 US-09-134-000C-4841	Sequence 4841, Appl
79	42	37.5	152	4 US-09-248-796A-22337	Sequence 22337, Appl
80	42	37.5	208	4 US-09-489-039A-7411	Sequence 7411, Appl
81	42	37.5	268	4 US-09-328-352-8118	Sequence 8118, Appl
82	42	37.5	275	4 US-09-248-796A-20934	Sequence 20934, Appl
83	42	37.5	295	4 US-09-270-767-62384	Sequence 62384, Appl
84	42	37.5	298	4 US-09-370-767-58159	Sequence 58159, Appl
85	42	37.5	328	4 US-09-134-000C-4243	Sequence 4243, Appl
86	42	37.5	407	4 US-09-248-796A-17916	Sequence 17916, Appl
87	42	37.5	504	4 US-09-370-767-46764	Sequence 46764, Appl
88	42	37.5	540	4 US-09-302-540-15331	Sequence 9824, Appl
89	42	37.5	542	4 US-09-270-767-42841	Sequence 42841, Appl
90	42	37.5	637	4 US-09-248-796A-16272	Sequence 16272, Appl
91	42	37.5	1297	3 US-09-540-245A-17	Sequence 17, Appl
92	42	37.5	2517	4 US-09-502-540-15380	Sequence 15380, Appl
93	41.5	37.1	517	4 US-09-248-796A-15304	Sequence 15304, Appl
94	41.5	37.1	639	3 US-09-347-801-17	Sequence 17, Appl
95	41.5	37.1	639	4 US-09-854-731-17	Sequence 17, Appl
96	41	36.6	71	1 US-08-606-789-6	Sequence 6, Appl
97	41	36.6	71	2 US-09-111-348-6	Sequence 6, Appl
98	41	36.6	71	5 PCT-US95-06406A-2	Sequence 2, Appl
99	41	36.6	83	4 US-09-513-999C-5324	Sequence 5324, Appl
100	41	36.6	106	4 US-09-543-681A-7810	Sequence 7810, Appl

101	41	36.6	123	4	US-09-248-796A-23998	Sequence 23998, A	174	40	35.7	207	3	US-09-216-386-1	Sequence 1, Appl1
102	41	36.6	140	4	US-09-601-729-9	Sequence 9, Appl1	175	40	35.7	207	4	US-09-252-991A-31339	Sequence 31339, A
103	41	36.6	164	3	US-08-765-381-2	Sequence 2, Appl1	176	40	35.7	208	2	US-08-844-120-1	Sequence 1, Appl1
104	41	36.6	164	4	US-09-443-218-2	Sequence 2, Appl1	177	40	35.7	208	3	US-09-213-394-1	Sequence 1, Appl1
105	41	36.6	164	4	US-09-443-218-4	Sequence 4, Appl1	178	40	35.7	208	4	US-09-888-982-1	Sequence 1, Appl1
106	41	36.6	164	4	US-09-443-218-5	Sequence 5, Appl1	179	40	35.7	214	4	US-09-853-450-34	Sequence 34, Appl1
107	41	36.6	164	4	US-09-443-218-7	Sequence 7, Appl1	180	40	35.7	230	2	US-09-022-940-3	Sequence 3, Appl1
108	41	36.6	194	4	US-09-489-039A-12868	Sequence 12868, A	181	40	35.7	230	2	US-09-216-386-3	Sequence 3, Appl1
109	41	36.6	208	3	US-09-134-001C-4449	Sequence 4449, Ap	182	40	35.7	248	2	US-08-867-087B-17	Sequence 17, Appl1
110	41	36.6	211	4	US-09-248-796A-22054	Sequence 22054, A	183	40	35.7	252	4	US-09-252-991A-3813	Sequence 3813, A
111	41	36.6	235	4	US-09-270-767-42965	Sequence 42965, A	184	40	35.7	265	3	US-09-199-637A-31	Sequence 31, Appl1
112	41	36.6	329	4	US-09-602-787A-306	Sequence 306, App	185	40	35.7	272	4	US-09-543-681A-4816	Sequence 4816, Ap
113	41	36.6	345	4	US-09-248-796A-14637	Sequence 14637, A	186	40	35.7	276	4	US-09-489-039A-9658	Sequence 9658, Ap
114	41	36.6	376	4	US-09-328-352-5970	Sequence 5970, Ap	187	40	35.7	319	4	US-09-107-532A-5542	Sequence 5542, Ap
115	41	36.6	397	4	US-09-252-991A-22719	Sequence 22719, A	188	40	35.7	345	4	US-09-543-681A-4540	Sequence 4540, Ap
116	41	36.6	459	4	US-09-602-787A-302	Sequence 302, App	189	40	35.7	358	4	US-09-328-352-6375	Sequence 6375, Ap
117	41	36.6	469	4	US-09-252-991A-227869	Sequence 227869, A	190	40	35.7	390	4	US-09-107-532A-5668	Sequence 5668, Ap
118	41	36.6	490	3	US-09-252-149B-26	Sequence 26, Appl1	191	40	35.7	391	4	US-09-198-452A-921	Sequence 921, App
119	41	36.6	509	4	US-09-248-796A-17566	Sequence 17566, A	192	40	35.7	391	4	US-09-438-185A-855	Sequence 855, Appl1
120	41	36.6	510	4	US-08-249-112-3	Sequence 3, Appl1	193	40	35.7	403	4	US-09-248-796A-14239	Sequence 14239, A
121	41	36.6	510	5	PCT-US95-06556-3	Sequence 3, Appl1	194	40	35.7	462	3	US-09-189-527-13	Sequence 13, Appl1
122	41	36.6	544	2	US-08-387-156-10	Sequence 10, Appl1	195	40	35.7	486	4	US-09-252-991A-19636	Sequence 19636, A
123	41	36.6	544	2	US-08-694-865-10	Sequence 10, Appl1	196	40	35.7	544	2	US-08-467-822-33	Sequence 33, Appl1
124	41	36.6	544	2	US-08-878-748-10	Sequence 10, Appl1	197	40	35.7	544	2	US-08-432-697-33	Sequence 33, Appl1
125	41	36.6	544	2	US-09-124-491-10	Sequence 10, Appl1	198	40	35.7	544	3	US-08-466-248-33	Sequence 33, Appl1
126	41	36.6	544	4	US-09-383-912-10	Sequence 10, Appl1	199	40	35.7	544	4	US-09-198-4452A-153	Sequence 153, Appl1
127	41	36.6	579	4	US-09-470-667-6	Sequence 6, Appl1	200	40	35.7	544	4	US-09-809-745-3	Sequence 3, Appl1
128	41	36.6	699	2	US-08-694-865-16	Sequence 16, Appl1	201	40	35.7	555	4	US-09-438-185A-136	Sequence 136, App
129	41	36.6	699	3	US-09-124-491-16	Sequence 16, Appl1	202	40	35.7	572	4	US-09-702-705-1815	Sequence 1815, Ap
130	41	36.6	699	4	US-09-383-912-16	Sequence 16, Appl1	203	40	35.7	572	4	US-09-736-457-1815	Sequence 1815, Ap
131	41	36.6	780	4	US-09-252-991A-32892	Sequence 32892, A	204	40	35.7	622	4	US-09-671-325-1815	Sequence 1815, Ap
132	41	36.6	890	4	US-09-583-110-4739	Sequence 4739, Ap	205	40	35.7	622	4	US-09-949-016-10606	Sequence 10606, A
133	41	36.6	924	3	US-08-619-812-8	Sequence 8, Appl1	206	40	35.7	631	4	US-09-134-000C-6175	Sequence 6175, Ap
134	41	36.6	926	1	US-07-908-253-2	Sequence 2, Appl1	207	40	35.7	651	4	US-09-902-540-11066	Sequence 11066, A
135	41	36.6	926	1	US-08-455-970A-2	Sequence 2, Appl1	208	40	35.7	774	1	US-07-731-157A-7	Sequence 7, Appl1
136	41	36.6	926	1	US-08-387-156-6	Sequence 6, Appl1	209	40	35.7	774	2	US-08-541-780-7	Sequence 7, Appl1
137	41	36.6	926	2	US-08-694-865-6	Sequence 6, Appl1	210	40	35.7	919	4	US-09-248-796A-19408	Sequence 19408, A
138	41	36.6	926	2	US-08-878-748-6	Sequence 6, Appl1	211	40	35.7	1019	4	US-09-543-681A-4447	Sequence 4447, Ap
139	41	36.6	926	2	US-08-535-837-2	Sequence 2, Appl1	212	40	35.7	1024	4	US-09-562-737-41	Sequence 41, Appl1
140	41	36.6	926	3	US-09-124-491-6	Sequence 6, Appl1	213	40	35.7	1024	4	US-09-562-737-44	Sequence 44, Appl1
141	41	36.6	926	4	US-09-383-912-6	Sequence 2, Appl1	214	40	35.7	1052	4	US-09-949-016-11508	Sequence 11508, A
142	41	36.6	926	4	US-08-976-566-2	Sequence 2, Appl1	215	40	35.7	1231	4	US-09-107-532A-5150	Sequence 5150, Ap
143	41	36.6	926	6	5476657-3	Patent No. 5476657	216	40	35.7	2472	4	US-09-538-092-1312	Sequence 1312, Ap
144	41	36.6	926	6	5476657-3	Patent No. 5476657	217	40	35.7	2509	4	US-09-452-991A-16642	Sequence 16642, A
145	41	36.6	936	1	US-08-455-970A-12	Sequence 12, Appl1	218	40	35.7	2509	4	US-09-252-991A-25753	Sequence 25753, A
146	41	36.6	936	4	US-08-976-566-12	Sequence 12, Appl1	219	39.5	35.3	112	4	US-09-603-208A-38	Sequence 38, Appl1
147	41	36.6	943	1	US-08-455-970A-10	Sequence 10, Appl1	220	39.5	35.3	247	4	US-09-328-352-5648	Sequence 5648, Ap
148	41	36.6	943	1	US-08-976-566-10	Sequence 10, Appl1	221	39.5	35.3	329	3	US-09-308-003-14	Sequence 14, Appl1
149	41	36.6	951	1	US-08-455-970A-14	Sequence 14, Appl1	222	39.5	35.3	528	3	US-08-889-841B-44	Sequence 44, Appl1
150	41	36.6	951	4	US-08-976-566-14	Sequence 14, Appl1	223	39.5	35.3	528	4	US-09-419-362-44	Sequence 44, Appl1
151	41	36.6	977	1	US-08-387-156-8	Sequence 8, Appl1	224	39.5	35.3	587	4	US-09-646-028-50	Sequence 50, Appl1
152	41	36.6	977	2	US-08-694-865-8	Sequence 8, Appl1	225	39.5	35.3	595	4	US-09-646-028-56	Sequence 56, Appl1
153	41	36.6	977	2	US-08-878-748-8	Sequence 8, Appl1	226	39.5	35.3	601	4	US-09-646-028-52	Sequence 52, Appl1
154	41	36.6	977	3	US-09-124-491-8	Sequence 8, Appl1	227	39.5	35.3	608	4	US-09-603-208A-36	Sequence 36, Appl1
155	41	36.6	977	4	US-09-383-912-8	Sequence 8, Appl1	228	39.5	35.3	844	4	US-09-991-258-19	Sequence 19, Appl1
156	41	36.6	1069	1	US-07-777-715-9	Sequence 9, Appl1	229	39.5	35.3	855	1	US-08-022-835-6	Sequence 6, Appl1
157	41	36.6	1069	3	US-08-170-126-4	Sequence 4, Appl1	230	39.5	35.3	855	1	US-08-388-809-6	Sequence 6, Appl1
158	41	36.6	1069	3	US-08-954-418-4	Sequence 4, Appl1	231	39.5	35.3	855	2	US-08-647-714-6	Sequence 6, Appl1
159	41	36.6	1098	1	US-07-777-715-7	Sequence 7, Appl1	232	39	34.8	14	1	US-07-872-644-28	Sequence 28, Appl1
160	41	36.6	1098	1	US-08-170-126-2	Sequence 2, Appl1	233	39	34.8	14	1	US-08-297-494-28	Sequence 28, Appl1
161	41	36.6	1098	3	US-08-954-418-2	Sequence 2, Appl1	234	39	34.8	14	1	US-08-297-510-28	Sequence 28, Appl1
162	41	36.6	2188	4	US-09-328-352-7763	Sequence 7763, Ap	235	39	34.8	14	1	US-08-479-532-28	Sequence 28, Appl1
163	41	36.6	2188	4	US-09-134-000C-3589	Sequence 3589, Ap	236	39	34.8	14	1	US-08-455-528-28	Sequence 28, Appl1
164	41	36.6	291	4	US-09-107-532A-6390	Sequence 6390, Ap	237	39	34.8	14	1	US-08-455-528-28	Sequence 28, Appl1
165	40.5	36.2	838	2	US-08-868-786A-4	Sequence 4, Appl1	238	39	34.8	14	3	US-09-139-497-28	Sequence 28, Appl1
166	40.5	36.2	840	4	US-09-252-991A-19561	Sequence 19561, A	239	39	34.8	14	4	US-09-883-832-28	Sequence 28, Appl1
167	40.5	36.2	3666	2	US-08-222-617A-12	Sequence 12, Appl1	240	39	34.8	14	5	PCT-US92-03222-28	Sequence 28, Appl1
168	40.5	36.2	3727	2	US-08-222-617A-27	Sequence 27, Appl1	241	39	34.8	84	4	US-09-621-976-6554	Sequence 6554, Ap
169	40.5	36.2	3778	2	US-08-222-617A-2	Sequence 2, Appl1	242	39	34.8	87	4	US-09-621-976-4000	Sequence 4000, Ap
170	40	35.7	50	2	US-08-402-804-10	Sequence 10, Appl1	243	39	34.8	93	4	US-09-107-433-3132	Sequence 3132, Ap
171	40	35.7	65	3	US-09-134-001C-4419	Sequence 4419, Ap	244	39	34.8	120	4	US-09-248-796A-28103	Sequence 28103, A
172	40	35.7	206	4	US-09-134-000C-3442	Sequence 3442, Ap	245	39	34.8	136	4	US-09-248-796A-18002	Sequence 18002, A
173	40	35.7	207	2	US-09-022-940-1	Sequence 1, Appl1	246	39	34.8	136	4	US-09-393-627B-26	Sequence 26, Appl1



247	39	34.8	170	4	US-09-134-000C-4756	Sequence 4756, Ap	320	39	34.8	703	3	US-08-910-925-4	Sequence 4, Appl1
248	39	34.8	171	4	US-09-328-352-4783	Sequence 4783, Ap	321	39	34.8	717	3	US-08-910-925-1	Sequence 1, Appl1
249	39	34.8	191	4	US-09-949-016-7105	Sequence 7105, Ap	322	39	34.8	743	3	US-08-910-925-3	Sequence 3, Appl1
250	39	34.8	205	4	US-09-270-767-42795	Sequence 42795, A	323	39	34.8	743	4	US-09-949-016-6261	Sequence 6261, Ap
251	39	34.8	229	4	US-09-270-767-32080	Sequence 32080, A	324	39	34.8	768	2	US-08-222-617A-5	Sequence 5, Appl1
252	39	34.8	229	4	US-09-270-767-47307	Sequence 47307, A	325	39	34.8	972	4	US-09-710-092-2	Sequence 2, Appl1
253	39	34.8	220	3	US-09-516-143A-6	Sequence 6, Appl1	326	39	34.8	983	3	US-09-412-554A-8	Sequence 2, Appl1
254	39	34.8	230	3	US-09-984-205-6	Sequence 6, Appl1	327	39	34.8	989	4	US-09-902-540-15948	Sequence 15948, A
255	39	34.8	241	3	US-08-896-933-32	Sequence 32, Appl1	328	39	34.8	1018	4	US-10-101-464A-909	Sequence 909, App
256	39	34.8	241	3	US-09-314-235-32	Sequence 32, Appl1	329	39	34.8	1056	4	US-09-710-092-6	Sequence 6, Appl1
257	39	34.8	241	4	US-09-708-008B-32	Sequence 32, Appl1	330	39	34.8	1173	4	US-09-543-681A-7865	Sequence 7865, Ap
258	39	34.8	244	4	US-09-710-279-994	Sequence 994, App	331	39	34.8	1270	4	US-09-710-092-10	Sequence 10, Appl1
259	39	34.8	250	2	US-08-879-561-8	Sequence 8, Appl1	332	39	34.8	1426	4	US-09-710-092-14	Sequence 14, Appl1
260	39	34.8	261	4	US-09-949-016-11398	Sequence 11398, A	333	39	34.8	1430	3	US-09-008-1371-2	Sequence 2, Appl1
261	39	34.8	262	4	US-09-857-498A-6	Sequence 6, Appl1	334	39	34.8	1430	3	US-09-210-361-6	Sequence 6, Appl1
262	39	34.8	276	4	US-09-107-532A-6200	Sequence 6200, Ap	335	39	34.8	1430	4	US-09-710-274-6	Sequence 6, Appl1
263	39	34.8	276	4	US-09-134-000C-4646	Sequence 4646, Ap	336	39	34.8	1630	4	US-09-302-540-15591	Sequence 15591, A
264	39	34.8	286	4	US-09-270-767-46126	Sequence 46126, A	337	39	34.8	54	4	US-09-536-977-16	Sequence 16, Appl1
265	39	34.8	301	4	US-09-248-796A-26282	Sequence 26282, A	338	38.5	34.4	121	4	US-09-248-796A-19888	Sequence 19888, A
266	39	34.8	320	2	US-09-027-013-1	Sequence 1, Appl1	339	38.5	34.4	124	4	US-09-536-977-44	Sequence 44, Appl1
267	39	34.8	330	3	US-09-244-233-1	Sequence 1, Appl1	340	38.5	34.4	210	3	US-09-247-378A-46	Sequence 46, Appl1
268	39	34.8	321	4	US-09-328-352-4883	Sequence 4883, Ap	341	38.5	34.4	218	4	US-09-583-110-4540	Sequence 4540, Ap
269	39	34.8	326	4	US-09-489-039A-7348	Sequence 7348, Ap	342	38.5	34.4	222	4	US-09-107-433-4007	Sequence 4007, Ap
270	39	34.8	359	4	US-09-107-532A-4033	Sequence 4033, Ap	343	38.5	34.4	227	4	US-09-328-352-6938	Sequence 6938, Ap
271	39	34.8	358	4	US-09-248-796A-19081	Sequence 19081, A	344	38.5	34.4	324	4	US-09-543-681A-6167	Sequence 6167, Ap
272	39	34.8	360	4	US-09-710-279-2150	Sequence 2150, Ap	345	38.5	34.4	358	3	US-09-500-569-18	Sequence 18, Appl1
273	39	34.8	367	3	US-09-134-001C-3678	Sequence 3678, Ap	346	38.5	34.4	358	4	US-09-971-823B-18	Sequence 18, Appl1
274	39	34.8	376	4	US-09-710-279-2106	Sequence 2106, Ap	347	38.5	34.4	365	3	US-09-500-569-4	Sequence 4, Appl1
275	39	34.8	380	4	US-09-248-796A-17151	Sequence 17151, A	348	38.5	34.4	365	4	US-09-971-823B-4	Sequence 4, Appl1
276	39	34.8	408	1	US-07-951-715A-21	Sequence 21, Appl1	349	38.5	34.4	425	4	US-09-536-977-46	Sequence 46, Appl1
277	39	34.8	408	2	US-08-459-448A-21	Sequence 21, Appl1	350	38.5	34.4	425	4	US-09-536-977-48	Sequence 48, Appl1
278	39	34.8	408	3	US-08-459-459A-21	Sequence 21, Appl1	351	38.5	34.4	425	4	US-09-536-977-50	Sequence 50, Appl1
279	39	34.8	408	3	US-08-459-504B-21	Sequence 21, Appl1	352	38.5	34.4	425	4	US-09-536-977-52	Sequence 52, Appl1
280	39	34.8	408	3	US-08-459-444-21	Sequence 21, Appl1	353	38.5	34.4	450	4	US-09-252-991A-24440	Sequence 24440, A
281	39	34.8	408	3	US-07-577-422-21	Sequence 21, Appl1	354	38.5	34.4	476	4	US-09-536-977-74	Sequence 74, Appl1
282	39	34.8	408	3	US-09-988-462-21	Sequence 21, Appl1	355	38.5	34.4	494	4	US-09-452-996A-28022	Sequence 28022, A
283	39	34.8	426	3	US-08-676-444-40	Sequence 40, Appl1	356	38.5	34.4	575	4	US-09-248-796A-17643	Sequence 17643, A
284	39	34.8	453	4	US-09-543-681A-7700	Sequence 7700, Ap	357	38.5	34.4	602	4	US-09-540-236-3263	Sequence 3263, Ap
285	39	34.8	457	4	US-09-248-796A-23295	Sequence 23295, A	358	38.5	34.4	635	4	US-09-536-977-68	Sequence 68, Appl1
286	39	34.8	463	1	US-07-951-715A-25	Sequence 25, Appl1	359	38.5	34.4	657	3	US-09-256-194-2	Sequence 2, Appl1
287	39	34.8	463	2	US-08-459-448A-25	Sequence 25, Appl1	360	38.5	34.4	665	2	US-08-448-603A-32	Sequence 32, Appl1
288	39	34.8	463	3	US-08-459-595A-25	Sequence 25, Appl1	361	38.5	34.4	665	3	US-09-134-075-32	Sequence 32, Appl1
289	39	34.8	463	3	US-08-459-504B-25	Sequence 25, Appl1	362	38.5	34.4	665	3	US-09-492-739-32	Sequence 32, Appl1
290	39	34.8	463	3	US-08-459-444-25	Sequence 0, Appl1	363	38.5	34.4	665	4	US-09-966-931A-32	Sequence 32, Appl1
291	39	34.8	463	3	US-09-547-422-25	Sequence 0, Appl1	364	38.5	34.4	675	3	US-09-134-001C-5219	Sequence 5219, Ap
292	39	34.8	463	4	US-09-988-462-25	Sequence 25, Appl1	365	38.5	34.4	687	4	US-09-536-977-70	Sequence 70, Appl1
293	39	34.8	464	1	US-07-951-715A-22	Sequence 22, Appl1	366	38.5	34.4	715	4	US-09-328-352-6830	Sequence 6830, Ap
294	39	34.8	464	2	US-08-459-448A-22	Sequence 22, Appl1	367	38.5	34.4	820	4	US-09-536-977-72	Sequence 72, Appl1
295	39	34.8	464	3	US-08-459-595A-22	Sequence 22, Appl1	368	38.5	34.4	857	2	US-08-448-603A-30	Sequence 30, Appl1
296	39	34.8	464	3	US-08-459-504B-22	Sequence 22, Appl1	369	38.5	34.4	857	3	US-09-492-739-30	Sequence 30, Appl1
297	39	34.8	464	3	US-08-459-444-22	Sequence 0, Appl1	370	38.5	34.4	857	3	US-09-492-739-30	Sequence 30, Appl1
298	39	34.8	464	3	US-09-547-422-22	Sequence 0, Appl1	371	38.5	34.4	857	4	US-09-966-931A-30	Sequence 30, Appl1
299	39	34.8	464	4	US-09-988-462-22	Sequence 22, Appl1	372	38.5	34.4	1048	4	US-08-887-534A-85	Sequence 85, Appl1
300	39	34.8	464	4	US-09-949-016-7399	Sequence 7399, Ap	373	38.5	34.4	1048	4	US-09-527-431A-85	Sequence 85, Appl1
301	39	34.8	491	4	US-09-489-039A-9206	Sequence 9206, Ap	374	38.5	34.4	1048	4	US-09-446-861-85	Sequence 85, Appl1
302	39	34.8	545	2	US-08-467-822-30	Sequence 30, Appl1	375	38	33.9	37	3	US-08-974-549A-68	Sequence 68, Appl1
303	39	34.8	545	3	US-08-432-697-30	Sequence 30, Appl1	376	38	33.9	37	3	US-08-974-549A-210	Sequence 210, App
304	39	34.8	545	3	US-08-462-248-30	Sequence 30, Appl1	377	38	33.9	37	3	US-08-912-951-68	Sequence 68, Appl1
305	39	34.8	545	4	US-09-604-957-4	Sequence 4, Appl1	378	38	33.9	37	4	US-09-402-181B-68	Sequence 68, Appl1
306	39	34.8	546	3	US-08-470-260-6	Sequence 6, Appl1	379	38	33.9	37	4	US-09-402-181B-210	Sequence 210, App
307	39	34.8	546	3	US-08-471-491-6	Sequence 6, Appl1	380	38	33.9	37	4	US-09-721-456-68	Sequence 68, Appl1
308	39	34.8	546	3	US-08-466-662-6	Sequence 6, Appl1	381	38	33.9	37	4	US-09-721-456-210	Sequence 210, App
309	39	34.8	546	4	US-08-256-847C-1	Sequence 1, Appl1	382	38	33.9	40	1	US-08-444-005-27	Sequence 27, Appl1
310	39	34.8	546	4	US-08-256-847C-7	Sequence 7, Appl1	383	38	33.9	45	2	US-08-219-237B-10	Sequence 10, Appl1
311	39	34.8	555	1	US-08-039-777-3	Sequence 3, Appl1	384	38	33.9	54	3	US-08-851-843A-21	Sequence 21, Appl1
312	39	34.8	555	1	US-08-611-361A-3	Sequence 3, Appl1	385	38	33.9	54	3	US-08-854-050-21	Sequence 21, Appl1
313	39	34.8	551	1	US-09-640-305-2	Sequence 2, Appl1	386	38	33.9	54	3	US-09-430-323-21	Sequence 21, Appl1
314	39	34.8	561	1	US-08-360-673-2	Sequence 2, Appl1	387	38	33.9	54	4	US-09-766-253-21	Sequence 21, Appl1
315	39	34.8	604	4	US-09-949-016-6585	Sequence 6585, Ap	388	38	33.9	63	3	US-08-894-626A-5	Sequence 1, Appl1
316	39	34.8	604	4	US-09-949-016-10250	Sequence 10250, A	389	38	33.9	64	4	US-09-248-796A-24105	Sequence 24105, A
317	39	34.8	637	4	US-09-949-016-10426	Sequence 10426, A	390	38	33.9	65	2	US-08-867-087B-31	Sequence 31, Appl1
318	39	34.8	657	4	US-09-949-016-6174	Sequence 6174, Ap	391	38	33.9	68	3	US-09-527-236A-22	Sequence 22, Appl1
319	39	34.8	678	4	US-09-949-016-10001	Sequence 10001, A	392	38	33.9	68	4	US-09-756-854-22	Sequence 22, Appl1

393	38	33.9	70	4	US-09-159-277A-5	Sequence 5, Appl1	466	38	33.9	314	1	US-08-152-443A-19	Sequence 19, Appl1
394	38	33.9	70	4	US-08-844-691A-5	Sequence 5, Appl1	467	38	33.9	314	2	US-08-389-459A-6	Sequence 6, Appl1
395	38	33.9	72	4	US-09-583-110-4899	Sequence 4899, Ap	468	38	33.9	314	3	US-08-987-867A-6	Sequence 6, Appl1
396	38	33.9	72	4	US-09-107-433-2938	Sequence 2938, Ap	469	38	33.9	314	5	PCT-US95-1708B-4	Sequence 4, Appl1
397	38	33.9	77	4	US-08-828-683A-24	Sequence 24, Appl1	470	38	33.9	327	3	US-09-134-001C-3339	Sequence 3339, Ap
398	38	33.9	84	4	US-09-069-827A-119	Sequence 119, App	471	38	33.9	327	3	US-08-679-493A-71	Sequence 71, Appl
399	38	33.9	85	1	US-09-042-785A-26	Sequence 26, Appl1	472	38	33.9	327	4	US-08-679-493A-72	Sequence 72, Appl
400	38	33.9	95	1	US-07-987-272A-9	Sequence 9, Appl1	473	38	33.9	327	4	US-09-585-858-53	Sequence 53, Appl
401	38	33.9	97	4	US-09-461-912A-48	Sequence 48, Appl1	474	38	33.9	327	4	US-10-270-878-53	Sequence 53, Appl
402	38	33.9	99	4	US-09-270-767-31885	Sequence 31885, A	475	38	33.9	321	2	US-08-564-972-9	Sequence 9, Appl1
403	38	33.9	99	4	US-09-270-767-47102	Sequence 47102, A	476	38	33.9	321	4	US-09-086-483A-3	Sequence 3, Appl1
404	38	33.9	120	1	US-08-233-788A-57	Sequence 57, Appl1	477	38	33.9	321	4	US-09-580-212-3	Sequence 3, Appl1
405	38	33.9	124	4	US-09-328-352-5521	Sequence 5521, Ap	478	38	33.9	331	4	US-09-769-402-3	Sequence 3, Appl1
406	38	33.9	127	4	US-09-614-912-146	Sequence 146, App	479	38	33.9	335	1	US-07-947-130-2	Sequence 2, Appl1
407	38	33.9	134	4	US-10-000-489-2	Sequence 2, Appl1	480	38	33.9	335	1	US-08-421-822-2	Sequence 2, Appl1
408	38	33.9	137	3	US-09-446-504-34	Sequence 34, Appl1	481	38	33.9	335	1	US-08-421-823-2	Sequence 2, Appl1
409	38	33.9	137	3	US-09-712-266-34	Sequence 34, Appl1	482	38	33.9	335	2	US-08-219-237B-2	Sequence 2, Appl1
410	38	33.9	143	4	US-09-328-352-7316	Sequence 7316, Ap	483	38	33.9	335	2	US-08-409-338-1	Sequence 1, Appl1
411	38	33.9	151	1	US-08-233-788A-59	Sequence 59, Appl1	484	38	33.9	335	3	US-08-815-469-6	Sequence 6, Appl1
412	38	33.9	152	4	US-09-248-796A-15593	Sequence 15593, A	485	38	33.9	335	3	US-09-290-640-2	Sequence 2, Appl1
413	38	33.9	153	4	US-09-107-532A-5159	Sequence 5159, Ap	486	38	33.9	335	3	US-09-006-633A-7	Sequence 7, Appl1
414	38	33.9	156	4	US-09-710-379-2848	Sequence 2848, Ap	487	38	33.9	335	3	US-08-468-560C-2	Sequence 2, Appl1
415	38	33.9	165	4	US-09-540-236-3123	Sequence 3123, Ap	488	38	33.9	335	3	US-09-180-100-20	Sequence 20, Appl
416	38	33.9	167	4	US-09-710-279-408	Sequence 408, App	489	38	33.9	335	4	US-09-565-918-3	Sequence 3, Appl1
417	38	33.9	174	2	US-08-564-972-62	Sequence 62, App	490	38	33.9	335	4	US-09-573-986-7	Sequence 7, Appl1
418	38	33.9	175	4	US-09-107-433-3909	Sequence 3909, Ap	491	38	33.9	335	4	US-09-665-615B-2	Sequence 2, Appl1
419	38	33.9	189	4	US-09-270-767-31816	Sequence 31816, A	492	38	33.9	335	4	US-09-557-908-6	Sequence 6, Appl1
420	38	33.9	189	4	US-09-270-767-47033	Sequence 47033, A	493	38	33.9	335	4	US-09-874-138-4	Sequence 4, Appl1
421	38	33.9	192	4	US-09-107-532A-6870	Sequence 6870, A	494	38	33.9	335	4	US-09-333-966-6	Sequence 6, Appl1
422	38	33.9	200	2	US-08-531-525-33	Sequence 33, Appl1	495	38	33.9	335	4	US-09-849-016-5877	Sequence 5877, Ap
423	38	33.9	200	2	US-08-718-270A-33	Sequence 33, Appl1	496	38	33.9	335	5	PCT-US95-1708B-2	Sequence 2, Appl1
424	38	33.9	205	4	US-09-107-532A-4830	Sequence 4830, Ap	497	38	33.9	338	4	US-09-248-796A-15934	Sequence 15934, A
425	38	33.9	208	3	US-09-134-001C-4697	Sequence 4697, Ap	498	38	33.9	345	3	US-09-120-365-73	Sequence 73, Appl
426	38	33.9	215	4	US-09-902-540-11802	Sequence 11802, A	499	38	33.9	345	3	US-09-515-039-73	Sequence 73, Appl
427	38	33.9	222	3	US-09-134-001C-4254	Sequence 4264, Ap	500	38	33.9	345	3	US-08-827-171B-7	Sequence 7, Appl1
428	38	33.9	223	4	US-09-543-681A-5667	Sequence 5667, Ap	501	38	33.9	345	4	US-09-598-062-7	Sequence 7, Appl1
429	38	33.9	228	4	US-09-710-279-31190	Sequence 3190, Ap	502	38	33.9	347	4	US-09-543-681A-5515	Sequence 5515, Ap
430	38	33.9	230	2	US-08-844-120-3	Sequence 3, Appl1	503	38	33.9	351	1	US-09-500-651-2	Sequence 2, Appl1
431	38	33.9	230	2	US-09-022-940-5	Sequence 5, Appl1	504	38	33.9	351	2	US-08-813-591-2	Sequence 2, Appl1
432	38	33.9	230	3	US-09-216-001-3	Sequence 3, Appl1	505	38	33.9	354	4	US-09-489-039A-12174	Sequence 12174, A
433	38	33.9	230	3	US-09-216-001-3	Sequence 3, Appl1	506	38	33.9	361	4	US-09-252-991A-30426	Sequence 30426, A
434	38	33.9	230	3	US-08-878-862-5	Sequence 5, Appl1	507	38	33.9	365	4	US-09-270-767-58705	Sequence 58705, A
435	38	33.9	230	3	US-09-213-394-3	Sequence 3, Appl1	508	38	33.9	369	4	US-09-328-352-5957	Sequence 5957, Ap
436	38	33.9	230	3	US-09-988-982-3	Sequence 3, Appl1	509	38	33.9	375	4	US-09-107-532A-3754	Sequence 3754, Ap
437	38	33.9	234	3	US-09-503-39A-122	Sequence 22, Appl1	510	38	33.9	377	2	US-08-839-581A-31	Sequence 31, Appl
438	38	33.9	236	4	US-09-489-039A-11850	Sequence 11850, A	511	38	33.9	377	3	US-09-023-591A-31	Sequence 31, Appl
439	38	33.9	246	3	US-09-451-117-2	Sequence 2, Appl1	512	38	33.9	383	3	US-09-134-001C-3701	Sequence 3701, Ap
440	38	33.9	246	4	US-09-888-555-2	Sequence 2, Appl1	513	38	33.9	383	4	US-09-710-279-3110	Sequence 3110, Ap
441	38	33.9	246	4	US-09-888-501-2	Sequence 2, Appl1	514	38	33.9	384	4	US-09-452-991A-19333	Sequence 19333, A
442	38	33.9	248	4	US-09-902-540-16288	Sequence 16288, A	515	38	33.9	386	4	US-09-248-796A-15067	Sequence 15067, A
443	38	33.9	250	2	US-08-867-087B-13	Sequence 13, Appl1	516	38	33.9	387	4	US-09-949-016-7720	Sequence 2, Appl1
444	38	33.9	254	4	US-09-270-767-33738	Sequence 33738, A	517	38	33.9	388	2	US-08-382-505-2	Sequence 2, Appl1
445	38	33.9	254	4	US-09-270-767-48955	Sequence 48955, A	518	38	33.9	396	1	US-07-757-390-14	Sequence 14, Appl
446	38	33.9	259	4	US-09-248-796A-16308	Sequence 16308, A	519	38	33.9	396	1	US-08-442-282-14	Sequence 14, Appl
447	38	33.9	261	4	US-09-248-796A-26725	Sequence 26725, A	520	38	33.9	396	1	US-08-442-281-14	Sequence 14, Appl
448	38	33.9	261	6	5320958-3	Patent No. 5320958	521	38	33.9	396	2	US-08-939-727-14	Sequence 14, Appl
449	38	33.9	261	6	5320958-3	Patent No. 5320958	522	38	33.9	397	4	US-09-270-767-44356	Sequence 44356, A
450	38	33.9	265	4	US-09-710-379-174	Sequence 174, App	523	38	33.9	420	1	US-07-757-390-13	Sequence 13, Appl
451	38	33.9	266	3	US-08-815-809-5	Sequence 5, Appl1	524	38	33.9	420	1	US-08-442-282-13	Sequence 13, Appl
452	38	33.9	272	4	US-09-270-767-31963	Sequence 31963, A	525	38	33.9	420	1	US-08-442-281-13	Sequence 13, Appl
453	38	33.9	272	4	US-09-270-767-47180	Sequence 47180, A	526	38	33.9	420	2	US-08-939-727-13	Sequence 13, Appl
454	38	33.9	273	4	US-09-248-796A-16521	Sequence 16521, A	527	38	33.9	420	4	US-09-886-319A-24	Sequence 24, Appl
455	38	33.9	280	2	US-08-816-155B-43	Sequence 43, Appl1	528	38	33.9	420	4	US-09-494-016-5958	Sequence 5958, Ap
456	38	33.9	280	2	US-09-079-587-43	Sequence 43, Appl1	529	38	33.9	424	4	US-09-198-452A-45	Sequence 45, Appl1
457	38	33.9	294	4	US-09-328-352-7430	Sequence 7430, Ap	530	38	33.9	425	4	US-09-109-204-31	Sequence 31, Appl
458	38	33.9	306	4	US-09-583-110-2708	Sequence 2708, Ap	531	38	33.9	425	4	US-09-490-032-31	Sequence 31, Appl
459	38	33.9	309	4	US-09-538-092-405	Sequence 105, App	532	38	33.9	427	3	US-09-690-265-1	Sequence 1, Appl1
460	38	33.9	313	3	US-08-836-561-106	Sequence 106, App	533	38	33.9	427	4	US-09-949-016-8614	Sequence 8614, Ap
461	38	33.9	313	4	US-09-434-122-106	Sequence 126, App	534	38	33.9	427	4	US-09-949-016-8620	Sequence 8620, Ap
462	38	33.9	313	4	US-09-252-991A-32836	Sequence 32836, A	535	38	33.9	437	3	US-09-134-001C-5342	Sequence 5342, Ap
463	38	33.9	314	1	US-08-589-446-6	Sequence 6, Appl1	536	38	33.9	441	4	US-09-134-000C-6563	Sequence 6563, Ap
464	38	33.9	314	1	US-08-444-882-6	Sequence 6, Appl1	537	38	33.9	454	4	US-09-248-796A-14748	Sequence 14748, A
465	38	33.9	314	1	US-08-444-231-19	Sequence 19, Appl1	538	38	33.9	460	4	US-09-759-595-1	Sequence 1, Appl1

539	38	33.9	471	4	US-09-583-110-3667	Sequence 3667, Ap	612	37.5	33.5	92	2	US-08-448-603A-14	Sequence 14, Appl
540	38	33.9	471	4	US-08-378-213-2	Sequence 2, Appl	613	37.5	33.5	92	3	US-09-134-075-14	Sequence 14, Appl
541	38	33.9	471	4	US-08-378-213-4	Sequence 4, Appl	614	37.5	33.5	92	3	US-09-492-739-14	Sequence 14, Appl
542	38	33.9	471	4	US-08-378-213-5	Sequence 5, Appl	615	37.5	33.5	92	4	US-09-966-931A-14	Sequence 14, Appl
543	38	33.9	471	4	US-08-378-213-6	Sequence 6, Appl	616	37.5	33.5	166	4	US-09-252-991A-2467	Sequence 2467, A
544	38	33.9	471	4	US-09-120-043-3	Sequence 3, Appl	617	37.5	33.5	172	4	US-09-248-196A-2166	Sequence 2166, A
545	38	33.9	471	4	US-09-120-044-4	Sequence 4, Appl	618	37.5	33.5	196	4	US-09-448-196A-2166	Sequence 1811, A
546	38	33.9	471	4	US-09-107-433-3566	Sequence 3566, Ap	619	37.5	33.5	213	2	US-08-437-013-2	Sequence 2, Appl
547	38	33.9	471	4	US-08-840-713-39	Sequence 39, Appl	620	37.5	33.5	213	4	US-09-375-506A-2	Sequence 2, Appl
548	38	33.9	502	4	US-09-710-279-2880	Sequence 3136, Ap	621	37.5	33.5	217	4	US-09-348-796A-21994	Sequence 21994, A
549	38	33.9	509	4	US-09-710-279-2880	Sequence 2880, Ap	622	37.5	33.5	259	4	US-08-737-319-2	Sequence 2, Appl
550	38	33.9	511	4	US-09-107-532A-6171	Sequence 6171, Ap	623	37.5	33.5	293	1	US-08-524-125-15	Sequence 15, Appl
551	38	33.9	513	3	US-09-134-001C-4386	Sequence 4386, Ap	624	37.5	33.5	293	4	US-08-937-155-15	Sequence 15, Appl
552	38	33.9	513	3	US-09-134-001C-4629	Sequence 4629, Ap	625	37.5	33.5	293	4	US-09-323-998A-15	Sequence 15, Appl
553	38	33.9	535	2	US-08-564-972-1	Sequence 1, Appl	626	37.5	33.5	305	4	US-09-323-998A-43	Sequence 43, Appl
554	38	33.9	535	3	US-09-171-969-9	Sequence 9, Appl	627	37.5	33.5	305	1	US-08-524-125-14	Sequence 14, Appl
555	38	33.9	535	4	US-09-250-131-2	Sequence 2, Appl	628	37.5	33.5	305	4	US-08-937-155-14	Sequence 14, Appl
556	38	33.9	540	4	US-09-107-532A-5314	Sequence 5314, Ap	629	37.5	33.5	305	4	US-09-323-998A-14	Sequence 14, Appl
557	38	33.9	555	4	US-09-107-532A-4722	Sequence 4722, Ap	630	37.5	33.5	305	4	US-09-323-998A-44	Sequence 44, Appl
558	38	33.9	560	4	US-10-205-641-1	Sequence 1, Appl	631	37.5	33.5	375	4	US-09-533-029-12	Sequence 12, Appl
559	38	33.9	561	4	US-09-489-039A-11625	Sequence 11625, A	632	37.5	33.5	389	4	US-09-800-170-18	Sequence 18, Appl
560	38	33.9	562	4	US-09-117-217-14	Sequence 14, Appl	633	37.5	33.5	406	4	US-09-543-681A-6072	Sequence 6072, Ap
561	38	33.9	562	4	US-09-735-487-14	Sequence 14, Appl	634	37.5	33.5	427	4	US-09-328-352-4720	Sequence 4720, Ap
562	38	33.9	567	4	US-09-639-245-4	Sequence 4, Appl	635	37.5	33.5	477	4	US-09-802-540-12554	Sequence 12554, A
563	38	33.9	572	4	US-09-949-016-6070	Sequence 6070, Ap	636	37.5	33.5	495	3	US-08-889-841B-28	Sequence 28, Appl
564	38	33.9	572	4	US-09-902-540-13770	Sequence 13770, A	637	37.5	33.5	495	3	US-08-889-841B-25	Sequence 25, Appl
565	38	33.9	573	4	US-09-643-657-18	Sequence 18, Appl	638	37.5	33.5	495	4	US-09-419-362-25	Sequence 28, Appl
566	38	33.9	578	4	US-09-949-016-11503	Sequence 11503, A	639	37.5	33.5	495	4	US-09-419-362-28	Sequence 28, Appl
567	38	33.9	592	4	US-09-328-352-5499	Sequence 5499, Ap	640	37.5	33.5	501	2	US-08-448-603A-2	Sequence 2, Appl
568	38	33.9	615	4	US-08-840-713-35	Sequence 35, Appl	641	37.5	33.5	501	3	US-09-134-075-2	Sequence 2, Appl
569	38	33.9	617	4	US-08-840-713-37	Sequence 37, A	642	37.5	33.5	501	3	US-09-492-739-2	Sequence 2, Appl
570	38	33.9	619	4	US-09-270-767-42558	Sequence 42558, A	643	37.5	33.5	501	4	US-09-966-931A-2	Sequence 1, Appl
571	38	33.9	622	5	US-08-132-990A-4	Sequence 4, Appl	644	37.5	33.5	511	2	US-08-448-603A-1	Sequence 1, Appl
572	38	33.9	622	5	PCT-US92-09382-4	Sequence 4, Appl	645	37.5	33.5	511	3	US-09-134-075-1	Sequence 1, Appl
573	38	33.9	629	2	US-08-132-990A-8	Sequence 8, Appl	646	37.5	33.5	511	3	US-08-889-841B-41	Sequence 41, Appl
574	38	33.9	629	5	PCT-US92-09382-8	Sequence 8, Appl	647	37.5	33.5	511	3	US-09-492-739-1	Sequence 1, Appl
575	38	33.9	644	4	US-09-949-016-9507	Sequence 9507, Ap	648	37.5	33.5	511	3	US-09-419-362-41	Sequence 41, Appl
576	38	33.9	658	4	US-09-538-092-1190	Sequence 1190, Ap	649	37.5	33.5	511	4	US-09-134-000C-5413	Sequence 5413, Ap
577	38	33.9	669	3	US-09-013-895A-3	Sequence 3, Appl	650	37.5	33.5	511	4	US-09-966-931A-1	Sequence 1, Appl
578	38	33.9	669	4	US-09-448-868-3	Sequence 3, Appl	651	37.5	33.5	605	1	US-08-190-802A-49	Sequence 49, Appl
579	38	33.9	682	1	US-08-441-139-2	Sequence 2, Appl	652	37.5	33.5	605	3	US-09-063-950A-5	Sequence 5, Appl
580	38	33.9	740	4	US-09-134-000C-6441	Sequence 6441, Ap	653	37.5	33.5	605	3	US-08-477-346-49	Sequence 49, Appl
581	38	33.9	812	3	US-09-150-460B-8	Sequence 8, Appl	654	37.5	33.5	605	3	US-08-473-089-49	Sequence 49, Appl
582	38	33.9	812	4	US-09-166-350-12	Sequence 12, Appl	655	37.5	33.5	605	4	US-08-487-072A-49	Sequence 49, Appl
583	38	33.9	813	4	US-09-328-352-7421	Sequence 7421, Ap	656	37.5	33.5	605	4	US-09-538-092-1087	Sequence 1087, Ap
584	38	33.9	825	4	US-09-438-185A-29	Sequence 29, Appl	657	37.5	33.5	615	2	US-08-525-742-10	Sequence 10, Appl
585	38	33.9	850	4	US-09-952-060-2	Sequence 2, Appl	658	37.5	33.5	615	4	US-09-949-016-10995	Sequence 10995, A
586	38	33.9	850	4	US-09-952-060-4	Sequence 4, Appl	659	37.5	33.5	651	4	US-09-107-532A-4902	Sequence 4902, Ap
587	38	33.9	875	3	US-09-150-460B-7	Sequence 7, Appl	660	37.5	33.5	651	4	US-09-134-000C-5569	Sequence 5569, Ap
588	38	33.9	875	4	US-09-952-060-6	Sequence 6, Appl	661	37.5	33.5	651	4	US-08-56-200-96	Sequence 96, Appl
589	38	33.9	875	4	US-09-952-060-8	Sequence 8, Appl	662	37.5	33.5	684	4	US-09-448-796A-15264	Sequence 15264, A
590	38	33.9	879	4	US-09-949-016-8492	Sequence 8492, Ap	663	37.5	33.5	884	4	US-09-328-352-4598	Sequence 4598, Ap
591	38	33.9	900	4	US-09-107-532A-5284	Sequence 5284, Ap	664	37.5	33.5	3224	2	US-08-705-660-34	Sequence 34, Appl
592	38	33.9	913	2	US-07-743-357-22	Sequence 22, Appl	665	37.5	33.5	3224	3	US-08-989-045-34	Sequence 34, Appl
593	38	33.9	921	3	US-09-514-599-2	Sequence 2, Appl	666	37.5	33.5	3224	4	US-09-338-092-1161	Sequence 1161, Ap
594	38	33.9	921	4	US-09-996-024-2	Sequence 2, Appl	667	37.5	33.0	3224	4	US-09-315-355A-34	Sequence 34, Appl
595	38	33.9	923	4	US-09-352-991A-28964	Sequence 28964, A	668	37.5	33.0	20	2	US-08-564-972-33	Sequence 33, Appl
596	38	33.9	1005	2	US-07-743-357-1	Sequence 1, Appl	669	37.5	33.0	21	6	5164481-9	Patent No. 5164481
597	38	33.9	1010	3	US-09-134-001C-5178	Sequence 5178, Ap	670	37.5	33.0	21	6	5164481-9	Patent No. 5164481
598	38	33.9	1015	3	US-08-463-210-9	Sequence 9, Appl	671	37.5	33.0	30	3	US-08-456-747C-44	Sequence 44, Appl
599	38	33.9	1015	3	US-09-124-900-3	Sequence 3, Appl	672	37.5	33.0	30	3	US-08-834-130A-44	Sequence 44, Appl
600	38	33.9	1015	4	US-08-463-028-9	Sequence 9, Appl	673	37.5	33.0	45	1	US-08-056-200-95	Sequence 95, Appl
601	38	33.9	1016	2	US-07-743-357-2	Sequence 2, Appl	674	37.5	33.0	45	2	US-08-056-200-96	Sequence 96, Appl
602	38	33.9	1016	2	US-07-743-357-4	Sequence 4, Appl	675	37.5	33.0	45	2	US-08-600-644-95	Sequence 95, Appl
603	38	33.9	1016	2	US-07-743-357-5	Sequence 5, Appl	676	37.5	33.0	45	2	US-08-600-644-96	Sequence 96, Appl
604	38	33.9	1024	4	US-09-562-737-47	Sequence 47, Appl	677	37.5	33.0	55	4	US-09-270-767-60822	Sequence 60822, A
605	38	33.9	1058	4	US-09-489-039A-11177	Sequence 11177, A	678	37.5	33.0	67	4	US-09-770-767-60567	Sequence 60567, A
606	38	33.9	1287	4	US-09-252-991A-29606	Sequence 29606, A	679	37.5	33.0	67	4	US-09-033-524A-9	Sequence 9, Appl
607	38	33.9	1290	3	US-09-150-460B-6	Sequence 6, Appl	680	37.5	33.0	69	4	US-09-621-976-6824	Sequence 6824, Ap
608	38	33.9	1291	3	US-09-150-460B-10	Sequence 10, Appl	681	37.5	33.0	75	4	US-09-328-352-6180	Sequence 6180, Ap
609	38	33.9	1291	3	US-09-220-641-5	Sequence 5, Appl	682	37.5	33.0	75	4	US-09-489-039A-11726	Sequence 11726, Ap
610	38	33.9	1350	4	US-09-952-060-35	Sequence 35, Appl	683	37.5	33.0	78	4	US-09-107-532A-5623	Sequence 5623, Ap
611	38	33.9	1735	4	US-09-902-540-14547	Sequence 14547, A	684	37.5	33.0	79	4	US-09-134-000C-6715	Sequence 6715, Ap

685	37	33.0	82	1	US-07-881-075-19	Sequence 19, Appl	758	37	33.0	344	4	US-09-809-665A-101	Sequence 101, App
686	37	33.0	82	1	US-08-120-827-19	Sequence 19, Appl	759	37	33.0	347	4	US-09-543-681A-6950	Sequence 6950, Ap
687	37	33.0	82	1	US-08-478-675-19	Sequence 19, Appl	760	37	33.0	352	4	US-08-630-915A-12	Sequence 12, Appl
688	37	33.0	108	4	US-09-270-767-45324	Sequence 45324, A	761	37	33.0	352	4	US-09-648-004-24	Sequence 24, Appl
689	37	33.0	113	4	US-09-107-532A-4396	Sequence 4396, Ap	762	37	33.0	352	4	US-09-879-957-12	Sequence 12, Appl
690	37	33.0	113	4	US-09-270-767-46286	Sequence 46286, A	763	37	33.0	352	4	US-10-272-419-24	Sequence 24, Appl
691	37	33.0	113	4	US-09-270-767-61866	Sequence 61866, A	764	37	33.0	352	4	US-09-949-016-6302	Sequence 6302, Ap
692	37	33.0	116	4	US-09-328-352-5161	Sequence 5161, Ap	765	37	33.0	355	4	US-09-248-796A-14612	Sequence 14612, A
693	37	33.0	123	4	US-09-540-236-2571	Sequence 2571, Ap	766	37	33.0	356	4	US-09-538-092-353	Sequence 353, App
694	37	33.0	126	4	US-09-107-532A-6790	Sequence 6790, Ap	767	37	33.0	359	1	US-07-881-075-51	Sequence 2, Appl
695	37	33.0	136	4	US-09-248-796A-20550	Sequence 20550, A	768	37	33.0	359	1	US-08-120-827-2	Sequence 2, Appl
696	37	33.0	136	4	US-09-902-540-12878	Sequence 12878, A	769	37	33.0	359	1	US-08-478-675-2	Sequence 2, Appl
697	37	33.0	137	4	US-09-270-767-33796	Sequence 33796, A	770	37	33.0	360	2	US-08-531-927B-2	Sequence 2, Appl
698	37	33.0	137	4	US-09-270-767-49013	Sequence 49013, A	771	37	33.0	360	4	US-09-041-886-13	Sequence 13, Appl
699	37	33.0	137	4	US-09-949-016-10576	Sequence 10576, A	772	37	33.0	360	4	US-09-538-092-1207	Sequence 1207, Ap
700	37	33.0	137	4	US-09-949-016-10577	Sequence 10577, A	773	37	33.0	362	4	US-09-248-796A-20105	Sequence 20105, A
701	37	33.0	141	4	US-09-543-681A-7686	Sequence 7686, Ap	774	37	33.0	366	4	US-09-949-016-9429	Sequence 9429, Ap
702	37	33.0	142	4	US-09-601-729-5	Sequence 5, Appl	775	37	33.0	367	4	US-09-949-016-9627	Sequence 9627, Ap
703	37	33.0	142	4	US-09-601-729-11	Sequence 11, Appl	776	37	33.0	380	1	US-07-881-075-51	Sequence 51, Appl
704	37	33.0	146	3	US-08-792-013-7	Sequence 7, Appl	777	37	33.0	380	1	US-08-120-827-51	Sequence 51, Appl
705	37	33.0	146	4	US-09-107-532A-7088	Sequence 7088, Ap	778	37	33.0	380	1	US-08-478-675-51	Sequence 51, Appl
706	37	33.0	147	1	US-08-171-385-5	Sequence 5, Appl	779	37	33.0	380	1	US-09-538-092-1017	Sequence 1017, Ap
707	37	33.0	147	3	US-08-361-441B-5	Sequence 5, Appl	780	37	33.0	380	4	US-09-949-016-7165	Sequence 7165, Ap
708	37	33.0	147	3	US-08-361-441B-42	Sequence 42, Appl	781	37	33.0	380	4	US-09-949-016-7167	Sequence 7167, Ap
709	37	33.0	147	3	US-09-049-672A-27	Sequence 27, Appl	782	37	33.0	393	4	US-09-489-032A-7842	Sequence 7842, Ap
710	37	33.0	147	3	US-08-792-013-4	Sequence 4, Appl	783	37	33.0	404	4	US-09-248-796A-18878	Sequence 18878, A
711	37	33.0	147	3	US-08-792-013-6	Sequence 6, Appl	784	37	33.0	405	4	US-09-252-991A-15148	Sequence 15148, A
712	37	33.0	151	4	US-09-543-681A-8097	Sequence 8097, Ap	785	37	33.0	406	4	US-09-942-577-2	Sequence 2, Appl
713	37	33.0	151	4	US-09-543-681A-8326	Sequence 8326, Ap	786	37	33.0	413	3	US-08-942-577-2	Sequence 2, Appl
714	37	33.0	156	4	US-09-513-999C-7983	Sequence 7983, Ap	787	37	33.0	413	4	US-09-614-066-13	Sequence 13, Appl
715	37	33.0	172	4	US-09-513-999C-7983	Sequence 7983, Ap	788	37	33.0	413	4	US-09-614-066-14	Sequence 14, Appl
716	37	33.0	174	4	US-09-710-279-1938	Sequence 1938, Ap	789	37	33.0	413	4	US-09-821-802A-7	Sequence 7, Appl
717	37	33.0	187	4	US-09-107-532A-4940	Sequence 4940, Ap	790	37	33.0	413	4	US-09-821-802A-8	Sequence 8, Appl
718	37	33.0	190	1	US-08-393-985-25	Sequence 19162, A	791	37	33.0	416	3	US-08-852-936C-1	Sequence 1, Appl
719	37	33.0	190	4	US-09-134-000C-6075	Sequence 25, Appl	792	37	33.0	416	3	US-09-257-721-2	Sequence 2, Appl
720	37	33.0	203	3	US-08-852-936C-4	Sequence 6075, Ap	793	37	33.0	416	3	US-09-311-760-2	Sequence 2, Appl
721	37	33.0	203	3	US-09-300-328-4	Sequence 4, Appl	794	37	33.0	416	3	US-09-300-328-1	Sequence 1, Appl
722	37	33.0	209	4	US-09-902-540-12992	Sequence 12992, A	795	37	33.0	416	3	US-09-069-023-23	Sequence 23, Appl
723	37	33.0	222	4	US-09-508-710-14	Sequence 14, Appl	796	37	33.0	416	3	US-09-561-756-30	Sequence 30, Appl
724	37	33.0	228	4	US-09-710-279-970	Sequence 970, App	797	37	33.0	416	3	US-09-227-721-30	Sequence 30, Appl
725	37	33.0	231	4	US-09-248-796A-25146	Sequence 25146, A	798	37	33.0	416	4	US-08-865-579-2	Sequence 2, Appl
726	37	33.0	234	3	US-09-134-001C-3195	Sequence 3195, A	799	37	33.0	416	4	US-10-059-749-2	Sequence 2, Appl
727	37	33.0	234	4	US-09-134-000C-6036	Sequence 6036, Ap	800	37	33.0	416	4	US-09-954-697-30	Sequence 30, Appl
728	37	33.0	254	4	US-09-949-016-10670	Sequence 10670, A	801	37	33.0	416	4	US-09-851-877-102	Sequence 102, App
729	37	33.0	259	4	US-09-509-738C-25	Sequence 25, Appl	802	37	33.0	416	4	US-09-328-352-7726	Sequence 7726, Ap
730	37	33.0	263	1	US-08-393-985-23	Sequence 23, Appl	803	37	33.0	418	4	US-09-107-532A-5939	Sequence 5939, A
731	37	33.0	263	4	US-09-902-540-11627	Sequence 11627, A	804	37	33.0	444	4	US-09-248-796A-16216	Sequence 16216, A
732	37	33.0	271	4	US-09-809-665A-6	Sequence 6, Appl	805	37	33.0	445	4	US-09-328-352-6114	Sequence 6114, Ap
733	37	33.0	273	4	US-09-134-000C-3441	Sequence 3441, Ap	806	37	33.0	445	4	US-09-538-092-123	Sequence 123, App
734	37	33.0	277	6	5164481-2	Sequence 3441, Ap	807	37	33.0	465	4	US-09-252-991A-23099	Sequence 23099, A
735	37	33.0	277	6	5164481-2	Patent No. 5164481	808	37	33.0	469	4	US-09-538-092-244	Sequence 244, App
736	37	33.0	285	1	US-08-393-985-2	Sequence 2, Appl	809	37	33.0	469	4	US-09-538-092-245	Sequence 245, App
737	37	33.0	285	4	US-08-311-731A-34	Sequence 34, Appl	810	37	33.0	479	4	US-09-543-681A-6605	Sequence 6605, Ap
738	37	33.0	285	4	US-08-311-731A-36	Sequence 36, Appl	811	37	33.0	490	2	US-08-687-916-24	Sequence 24, Appl
739	37	33.0	286	1	US-09-370-767-44940	Sequence 44940, A	812	37	33.0	490	3	US-09-138-61A-24	Sequence 24, Appl
740	37	33.0	288	4	US-08-337-602-4	Sequence 4, Appl	813	37	33.0	493	4	US-09-252-991A-30722	Sequence 30722, A
741	37	33.0	288	3	US-08-558-135-4	Sequence 4, Appl	814	37	33.0	497	3	US-08-882-164D-32	Sequence 32, Appl
742	37	33.0	288	3	US-08-819-286-3	Sequence 3, Appl	815	37	33.0	499	3	US-09-090-793-11	Sequence 11, Appl
743	37	33.0	291	2	US-08-531-927B-4	Sequence 4, Appl	816	37	33.0	508	4	US-09-231-899-11	Sequence 11, Appl
744	37	33.0	296	4	US-09-902-540-14392	Sequence 14392, A	817	37	33.0	508	4	US-09-270-767-44071	Sequence 44071, A
745	37	33.0	298	4	US-09-134-001C-4569	Sequence 4569, Ap	818	37	33.0	512	4	US-09-902-540-13924	Sequence 13924, A
746	37	33.0	300	4	US-09-248-796A-14770	Sequence 14770, A	819	37	33.0	522	4	US-09-538-092-1096	Sequence 1096, Ap
747	37	33.0	303	4	US-09-352-991A-28605	Sequence 28605, A	820	37	33.0	525	1	US-08-375-709-19	Sequence 19, Appl
748	37	33.0	307	3	US-09-475-316A-70	Sequence 70, Appl	821	37	33.0	525	1	US-08-752-929-19	Sequence 19, Appl
749	37	33.0	307	4	US-09-704-640-70	Sequence 70, Appl	822	37	33.0	530	3	US-08-979-608A-8	Sequence 8, Appl
750	37	33.0	309	3	US-09-475-316A-72	Sequence 72, Appl	823	37	33.0	530	4	US-09-517-848-8	Sequence 8, Appl
751	37	33.0	309	4	US-09-134-001C-4952	Sequence 4952, Ap	824	37	33.0	530	4	US-09-616-288-8	Sequence 8, Appl
752	37	33.0	309	4	US-09-704-640-72	Sequence 72, Appl	825	37	33.0	532	4	US-09-710-279-546	Sequence 546, Appl
753	37	33.0	325	4	US-09-949-016-9168	Sequence 9168, Ap	826	37	33.0	533	4	US-09-252-991A-20633	Sequence 20633, A
754	37	33.0	325	4	US-09-949-016-9169	Sequence 9169, Ap	827	37	33.0	543	1	US-08-375-709-17	Sequence 17, Appl
755	37	33.0	339	4	US-09-107-532A-5514	Sequence 5514, Ap	828	37	33.0	543	1	US-08-752-929-17	Sequence 17, Appl
756	37	33.0	341	4	US-09-710-279-226	Sequence 226, App	829	37	33.0	543	3	US-09-090-793-10	Sequence 10, Appl
757	37	33.0	342	4	US-09-991-258-10	Sequence 10, Appl	830	37	33.0	543	4	US-09-231-899-10	Sequence 10, Appl

831	37	33.0	544	4	US-09-248-796A-18637	Sequence 18637, A	904	37	33.0	1533	3	US-09-534-242-9	Sequence 9, Appl1
832	37	33.0	546	4	US-09-616-289-44	Sequence 44, Appl1	905	37	33.0	1533	3	US-09-454-854-9	Sequence 9, Appl1
833	37	33.0	548	4	US-09-902-540-12604	Sequence 12604, A	906	37	33.0	1533	3	US-09-164-671-9	Sequence 9, Appl1
834	37	33.0	553	4	US-09-902-540-9807	Sequence 9807, Ap	907	37	33.0	1533	4	US-09-182-113-9	Sequence 9, Appl1
835	37	33.0	557	3	US-08-979-608A-5	Sequence 5, Appl1	908	37	33.0	1533	4	US-08-862-442-9	Sequence 1033, Ap
836	37	33.0	557	3	US-09-517-849-5	Sequence 5, Appl1	909	37	33.0	1533	4	US-09-538-092-1033	Sequence 45587, A
837	37	33.0	557	4	US-09-616-289-5	Sequence 16908, A	910	37	33.0	1565	4	US-09-970-767-45587	Sequence 15978, A
838	37	33.0	558	4	US-09-252-991A-16908	Sequence 20658, A	911	37	33.0	1803	4	US-09-902-540-15978	Sequence 94, Appl1
839	37	33.0	559	4	US-09-347-801-19	Sequence 19, Appl1	912	37	33.0	1898	1	US-08-056-200-94	Sequence 94, Appl1
840	37	33.0	566	3	US-09-854-731-19	Sequence 19, Appl1	913	37	33.0	1898	2	US-09-538-092-1280	Sequence 1280, Ap
841	37	33.0	576	4	US-09-554-731-19	Sequence 439, App	914	37	33.0	1959	2	US-08-822-445-2	Sequence 2, Appl1
842	37	33.0	653	4	US-09-198-452A-439	Sequence 6748, Ap	915	37	33.0	2186	2	US-09-396-540-2	Sequence 4, Appl1
843	37	33.0	661	4	US-09-328-352-6748	Sequence 6983, Ap	916	37	33.0	2471	3	US-09-112-450-4	Sequence 4, Appl1
844	37	33.0	665	4	US-09-328-352-6983	Sequence 421, App	917	37	33.0	2471	4	US-09-419-291A-4	Sequence 4, Appl1
845	37	33.0	674	3	US-09-160-119-2	Sequence 421, App	918	37	33.0	2771	4	US-10-116-046-4	Sequence 4, Appl1
846	37	33.0	674	4	US-09-438-185A-421	Sequence 22481, A	919	37	33.0	2771	4	US-10-116-046-4	Sequence 23, Appl1
847	37	33.0	694	4	US-09-252-991A-22481	Sequence 24140, A	920	36.5	32.6	59	3	US-08-468-011A-23	Sequence 23, Appl1
848	37	33.0	706	3	US-09-408-820-2	Sequence 2, Appl1	921	36.5	32.6	200	4	US-09-236-468A-23	Sequence 4217, Ap
849	37	33.0	716	4	US-09-248-796A-24140	Sequence 1178, Ap	922	36.5	32.6	248	1	US-08-500-125-4	Sequence 4, Appl1
850	37	33.0	741	4	US-09-710-279-1178	Sequence 2921, Ap	923	36.5	32.6	248	1	US-08-500-125-4	Sequence 4, Appl1
851	37	33.0	751	4	US-09-540-236-2921	Sequence 3689, Ap	924	36.5	32.6	248	2	US-07-779-704B-4	Sequence 4, Appl1
852	37	33.0	766	3	US-09-134-001C-3689	Sequence 5192, Ap	925	36.5	32.6	251	4	US-09-270-767-44812	Sequence 44812, A
853	37	33.0	775	4	US-09-248-796A-17675	Sequence 17675, A	926	36.5	32.6	266	3	US-09-134-001C-5453	Sequence 5453, Ap
854	37	33.0	784	4	US-09-583-110-5192	Sequence 2, Appl1	927	36.5	32.6	295	3	US-09-134-001C-2850	Sequence 2850, Ap
855	37	33.0	787	3	US-09-721-383-2	Sequence 2, Appl1	928	36.5	32.6	307	4	US-09-197-970B-3	Sequence 3, Appl1
856	37	33.0	787	3	US-09-721-377-2	Sequence 2, Appl1	929	36.5	32.6	326	4	US-09-583-110-4330	Sequence 4330, Ap
857	37	33.0	787	4	US-09-121-251-2	Sequence 2, Appl1	930	36.5	32.6	335	4	US-09-222-938A-4	Sequence 4, Appl1
858	37	33.0	787	4	US-10-114-764-2	Sequence 2, Appl1	931	36.5	32.6	335	4	US-09-222-938A-4	Sequence 4, Appl1
859	37	33.0	787	4	US-09-107-433-4612	Sequence 4612, Ap	932	36.5	32.6	336	1	US-07-641-143B-2	Sequence 2, Appl1
860	37	33.0	823	4	US-09-252-991A-17457	Sequence 17457, A	933	36.5	32.6	336	1	US-08-124-290-2	Sequence 2, Appl1
861	37	33.0	860	4	US-09-936-989A-2	Sequence 2, Appl1	934	36.5	32.6	336	3	US-08-696-372A-2	Sequence 2, Appl1
862	37	33.0	886	4	US-09-543-681A-4302	Sequence 4302, Ap	935	36.5	32.6	336	3	US-08-235-836C-52	Sequence 52, Appl1
863	37	33.0	911	4	US-09-252-991A-25237	Sequence 25237, A	936	36.5	32.6	336	3	US-08-235-836C-54	Sequence 128, App
864	37	33.0	925	4	US-09-936-989A-6	Sequence 6, Appl1	937	36.5	32.6	336	3	US-08-235-836C-18	Sequence 34, Appl1
865	37	33.0	944	4	US-09-437-568A-39	Sequence 39, Appl1	938	36.5	32.6	345	3	US-08-858-003-34	Sequence 34, Appl1
866	37	33.0	950	4	US-09-543-681A-5997	Sequence 5997, Ap	939	36.5	32.6	345	3	US-09-078-166-34	Sequence 34, Appl1
867	37	33.0	953	4	US-09-252-991A-21559	Sequence 21559, A	940	36.5	32.6	345	3	US-08-997-467-34	Sequence 34, Appl1
868	37	33.0	971	3	US-09-112-450-2	Sequence 2, Appl1	941	36.5	32.6	348	4	US-09-107-433-4918	Sequence 4918, Ap
869	37	33.0	971	4	US-09-419-291A-2	Sequence 2, Appl1	942	36.5	32.6	393	4	US-09-328-352-7167	Sequence 7167, Ap
870	37	33.0	971	4	US-10-116-048-2	Sequence 2, Appl1	943	36.5	32.6	433	4	US-09-252-991A-22241	Sequence 29241, A
871	37	33.0	975	4	US-09-540-236-2304	Sequence 2304, Ap	944	36.5	32.6	494	4	US-09-517-779-2	Sequence 2, Appl1
872	37	33.0	992	1	US-08-127-499A-1	Sequence 1, Appl1	945	36.5	32.6	498	1	US-08-500-125-2	Sequence 2, Appl1
873	37	33.0	992	1	US-08-482-847-1	Sequence 1, Appl1	946	36.5	32.6	498	1	US-08-500-125-2	Sequence 2, Appl1
874	37	33.0	998	4	US-09-248-796A-19450	Sequence 20908, A	947	36.5	32.6	499	2	US-07-779-704B-2	Sequence 7370, Ap
875	37	33.0	1000	4	US-09-562-737-43	Sequence 43, Appl1	948	36.5	32.6	500	4	US-09-248-796A-18166	Sequence 18166, A
876	37	33.0	1024	4	US-09-562-737-46	Sequence 46, Appl1	949	36.5	32.6	513	3	US-08-472-240A-14	Sequence 14, Appl1
877	37	33.0	1024	4	US-09-562-737-48	Sequence 48, Appl1	950	36.5	32.6	514	3	US-09-370-098-2	Sequence 31, Appl1
878	37	33.0	1024	4	US-09-562-737-50	Sequence 50, Appl1	951	36.5	32.6	536	4	US-09-595-857B-31	Sequence 31, Appl1
879	37	33.0	1024	1	US-08-093-453B-3	Sequence 3, Appl1	952	36.5	32.6	539	4	US-08-468-011A-2	Sequence 2, Appl1
880	37	33.0	1063	1	US-08-127-499A-8	Sequence 8, Appl1	953	36.5	32.6	541	3	US-09-236-468A-2	Sequence 2, Appl1
881	37	33.0	1063	1	US-08-482-847-8	Sequence 18666, A	954	36.5	32.6	541	5	PCT-US95-0708B-2	Sequence 2, Appl1
882	37	33.0	1068	4	US-09-248-796A-18666	Sequence 7696, Ap	955	36.5	32.6	545	4	US-09-489-039A-11980	Sequence 11980, A
883	37	33.0	1086	4	US-09-543-681A-7696	Sequence 8890, Ap	956	36.5	32.6	550	2	US-08-417-210A-140	Sequence 140, App
884	37	33.0	1107	4	US-09-489-039A-8890	Sequence 6, Appl1	957	36.5	32.6	550	4	US-09-136-159A-143	Sequence 143, App
885	37	33.0	1151	3	US-08-840-006-6	Sequence 5, Appl1	958	36.5	32.6	550	4	US-09-417-210A-140	Sequence 140, App
886	37	33.0	1200	3	US-08-840-006-5	Sequence 24, Appl1	959	36.5	32.6	550	4	US-09-631-603-20	Sequence 20, Appl1
887	37	33.0	1214	4	US-10-164-595-24	Sequence 15, Appl1	960	36.5	32.6	550	4	US-09-826-509-565	Sequence 565, App
888	37	33.0	1296	3	US-08-728-603-15	Sequence 15, Appl1	961	36.5	32.6	551	2	US-08-417-210A-137	Sequence 137, App
889	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	962	36.5	32.6	606	3	US-09-257-490-6	Sequence 6, Appl1
890	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	963	36.5	32.6	606	3	US-09-257-490-6	Sequence 6, Appl1
891	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	964	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
892	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	965	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
893	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	966	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
894	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	967	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
895	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	968	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
896	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	969	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
897	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	970	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
898	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	971	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
899	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	972	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
900	37	33.0	1497	3	US-09-534-242-7	Sequence 7, Appl1	973	36.5	32.6	636	4	US-09-720-524-7	Sequence 7, Appl1
901	37	33.0	1533	1	US-08-623-679-9	Sequence 9, Appl1	974	36.5	32.6	856	1	US-08-388-809-2	Sequence 2, Appl1
902	37	33.0	1533	3	US-08-933-774-9	Sequence 9, Appl1	975	36.5	32.6	856	1	US-08-388-809-2	Sequence 2, Appl1
903	37	33.0	1533	3	US-09-181-030-9	Sequence 9, Appl1	976	36.5	32.6	856	2	US-08-647-714-2	Sequence 2, Appl1

977 36.5 32.6 856 3 US-07-956-483-11 Sequence 11, Appl  
978 36.5 32.6 857 1 US-08-022-835-4 Sequence 4, Appl  
979 36.5 32.6 857 1 US-08-388-809-4 Sequence 4, Appl  
980 36.5 32.6 857 2 US-08-647-714-4 Sequence 4, Appl  
981 36.5 32.6 875 4 US-09-206-551-14 Sequence 14, Appl  
982 36.5 32.6 887 3 US-08-472-240A-2 Sequence 2, Appl  
983 36.5 32.6 1005 1 US-08-089-986-3 Sequence 3, Appl  
984 36.5 32.6 1005 1 US-08-478-585-3 Sequence 3, Appl  
985 36.5 32.6 1005 1 US-08-717-312-3 Sequence 3, Appl  
986 36.5 32.6 1005 2 US-08-266-408-3 Sequence 3, Appl  
987 36.5 32.6 1005 5 PCT-US94-07886-3 Sequence 3, Appl  
988 36.5 32.6 1279 4 US-09-538-092-976 Sequence 976, Ap  
989 36.5 32.6 1769 4 US-09-949-016-8280 Sequence 8280, Ap  
990 36.5 32.6 1769 4 US-09-949-016-8281 Sequence 8281, Ap  
991 36.5 32.6 1769 4 US-09-949-016-8282 Sequence 8282, Ap  
992 36.5 32.6 1784 3 US-09-040-738-2 Sequence 2, Appl  
993 36.5 32.6 1784 3 US-08-652-426A-2 Sequence 2, Appl  
994 36.5 32.6 1813 4 US-09-949-016-8283 Sequence 8283, Ap  
995 36.5 32.6 1813 4 US-09-949-016-8284 Sequence 8284, Ap  
996 36.5 32.6 1813 4 US-09-949-016-8285 Sequence 8285, Ap  
997 36.5 32.6 2050 2 US-08-347-594A-2 Sequence 2, Appl  
998 36.5 32.6 2713 5 PCT-US96-01735-1 Sequence 1, Appl  
999 36.5 32.6 2749 4 US-09-385-222A-4 Sequence 4, Appl  
1000 36.5 32.6 2813 4 US-09-381-261A-1 Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-09-206-551-11  
; Sequence 11, Application US/09206551B  
; Patent No. 6521739  
; GENERAL INFORMATION:  
; APPLICANT: Hahn, Beatrice H.  
; APPLICANT: Gao, Feng  
; APPLICANT: Marx, Preston A.  
; APPLICANT: Shaw, George M.  
; APPLICANT: Smith, Stephen M.  
; APPLICANT: Georges-Courbot, Marie Claude  
; APPLICANT: Lu, Chang Yong  
; TITLE OF INVENTION: Complete Genome Sequences of a Simian  
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped  
; TITLE OF INVENTION: Mangabey  
; FILE REFERENCE: D6286  
; CURRENT APPLICATION NUMBER: US/09/206,551B  
; CURRENT FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 11  
; LENGTH: 855  
; TYPE: PRF  
; ORGANISM: Simian immunodeficiency virus  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of homologous region of  
; OTHER INFORMATION: A\_U455 lentiviral env protein  
US-09-206-551-11

Query Match 46.0%; Score 51.5; DB 4; Length 855;  
Best Local Similarity 43.5%; Pred. No. 31;  
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 MADNGTIVE-ELKQLEQNMV 22  
DB 401 MGPNGTITLCRIKQIINMQRV 423

RESULT 2  
US-09-206-551-12  
; Sequence 12, Application US/09206551B  
; Patent No. 6521739  
; GENERAL INFORMATION:  
; APPLICANT: Hahn, Beatrice H.  
; APPLICANT: Gao, Feng

; APPLICANT: Marx, Preston A.  
; APPLICANT: Shaw, George M.  
; APPLICANT: Smith, Stephen M.  
; APPLICANT: Georges-Courbot, Marie Claude  
; APPLICANT: Lu, Chang Yong  
; TITLE OF INVENTION: Complete Genome Sequences of a Simian  
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped  
; FILE REFERENCE: D6286  
; CURRENT APPLICATION NUMBER: US/09/206,551B  
; CURRENT FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 12  
; LENGTH: 855  
; TYPE: PRF  
; ORGANISM: Simian immunodeficiency virus  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of homologous region of  
; OTHER INFORMATION: B\_HXB2R lentiviral env protein  
US-09-206-551-12

Query Match 46.0%; Score 51.5; DB 4; Length 855;  
Best Local Similarity 43.5%; Pred. No. 31;  
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 MADNGTIVE-ELKQLEQNMV 22  
DB 401 MGPNGTITLCRIKQIINMQRV 423

RESULT 3  
US-08-531-525-31  
; Sequence 31, Application US/08531525  
; Patent No. 5840683  
; GENERAL INFORMATION:  
; APPLICANT: Hlavka, Joseph J.  
; APPLICANT: Pincus, Matthew R.  
; APPLICANT: No. 58406831e, John F.  
; APPLICANT: Adajian, Henry B.  
; APPLICANT: Kende, Andrew S.  
; TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action  
; TITLE OF INVENTION: of P21 Ras  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/531,525  
; FILING DATE: 21-SEP-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 37-94  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 205 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-531-525-31

Query Match 45.5%; Score 51; DB 2; Length 205;  
Best Local Similarity 42.9%; Pred. No. 7.3;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQWNL 21  
DB 131 LEDKQVSVBEAKRAEQWNV 151

## RESULT 4

US-08-718-270A-31  
Sequence 31, Application US/08718270A  
Patent No. 5910478  
GENERAL INFORMATION:  
APPLICANT: Hlavka, Joseph J.  
APPLICANT: Pincus, Matthew R.  
APPLICANT: No. 59104781e, John F.  
APPLICANT: Absajian, Henry B.  
TITLE OF INVENTION: Peptidomimetics Inhibiting  
TITLE OF INVENTION: the Oncogenic Action of p21 Ras  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/718,270A  
FILING DATE: 20-SEP-1996  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/531,525  
FILING DATE: 21-SEP-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/004,091  
FILING DATE: 21-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 78-95  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-718-270A-31

Query Match 45.5%; Score 51; DB 2; Length 205;  
Best Local Similarity 42.9%; Pred. No. 7.3;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MADNGTIVBELKQLEQWNL 21

DB 131 LEDKQVSVBEAKRAEQWNV 151

RESULT 5  
US-09-078-317-15  
Sequence 15, Application US/09078317  
Patent No. 6017710

## GENERAL INFORMATION:

APPLICANT: Allen, Maxine J.  
APPLICANT: Rutter, Marc  
APPLICANT: Buckler, Alan J.  
TITLE OF INVENTION: RAQ Genes and Their Uses  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bozicevic & Reed, LLP  
STREET: 285 Hamilton Ave, Suite 200  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/078,317  
FILING DATE: 13-MAY-1998  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Francis, Carol L  
REGISTRATION NUMBER: 36,513  
REFERENCE/DOCKET NUMBER: SEQ-18P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-327-3400  
TELEFAX: 650-327-3231  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 206 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6017710e  
US-09-078-317-15

Query Match 45.5%; Score 51; DB 3; Length 206;  
Best Local Similarity 42.9%; Pred. No. 7.4;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQWNL 21  
DB 131 LEDKQVSVBEAKRAEQWNV 151

## RESULT 6

US-09-454-818-15  
Sequence 15, Application US/09454818  
Patent No. 6381792  
GENERAL INFORMATION:  
APPLICANT: Allen, Maxine J.  
APPLICANT: Rutter, Marc  
APPLICANT: Buckler, Alan J.  
TITLE OF INVENTION: RAQ Genes and Their Uses  
FILE REFERENCE: AXYS-018DIV  
CURRENT APPLICATION NUMBER: US/09/454,818  
CURRENT FILING DATE: 1999-12-03  
PRIORITY APPLICATION NUMBER: 09/078,317  
PRIORITY FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 15  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-454-818-15

Query Match 45.5%; Score 51; DB 3; Length 206;  
Best Local Similarity 42.9%; Pred. No. 7.4;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQWNL 21  
DB 131 LEDKROVSYEAKNRAEQWNV 151

RESULT 7  
US-09-709-103-48  
Sequence 48, Application US/09709103  
Patent No. 6733991  
GENERAL INFORMATION:  
APPLICANT: Cismowski, Mary  
APPLICANT: Duzic, Emil  
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor  
FILE REFERENCE: 60388-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/709,103  
CURRENT FILING DATE: 2000-11-08  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 48  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-09-709-103-48

Query Match 45.5%; Score 51; DB 4; Length 206;  
Best Local Similarity 42.9%; Pred. No. 7.4;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQWNL 21  
DB 131 LEDKROVSYEAKNRAEQWNV 151

RESULT 8  
US-09-439-410A-48  
Sequence 48, Application US/09439410A  
Patent No. 6746852  
GENERAL INFORMATION:  
APPLICANT: Cismowski, Mary  
APPLICANT: Duzic, Emil  
TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF  
FILE REFERENCE: 1919/60388-B  
CURRENT APPLICATION NUMBER: US/09/439,410A  
CURRENT FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 48  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-439-410A-48

Query Match 45.5%; Score 51; DB 4; Length 206;  
Best Local Similarity 42.9%; Pred. No. 7.4;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQWNL 21  
DB 131 LEDKROVSYEAKNRAEQWNV 151

RESULT 9  
US-09-266-965-132  
Sequence 132, Application US/09266965  
Patent No. 6495348  
GENERAL INFORMATION:  
APPLICANT: Sherman, D  
APPLICANT: Mao, Y  
APPLICANT: Varoglu, M  
APPLICANT: He, M  
APPLICANT: Sheldon, P  
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
FILE REFERENCE: 600.456US1  
CURRENT APPLICATION NUMBER: US/09/266,965  
CURRENT FILING DATE: 1999-03-12  
EARLIER APPLICATION NUMBER: US 08/624,447  
EARLIER FILING DATE: 1996-08-19  
EARLIER APPLICATION NUMBER: PCT/US94/11279  
EARLIER FILING DATE: 1994-10-06  
EARLIER APPLICATION NUMBER: US 08/133,963  
EARLIER FILING DATE: 1993-10-07  
NUMBER OF SEQ ID NOS: 145  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 132  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Streptomyces lavendulae  
US-09-266-965-132

Query Match 43.8%; Score 49; DB 4; Length 123;  
Best Local Similarity 57.1%; Pred. No. 8.1;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NGTIVTEELKQLE 17  
DB 86 NGTIVTEELKQLE 99

RESULT 10  
US-09-538-092-241  
Sequence 241, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Giot, Loic  
APPLICANT: Mansfield, Traci A.  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538,092  
CURRENT FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CuratPatSeqFormatter Version 0.9  
SEQ ID NO 241  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: Polypeptide Accession Number YER063W  
US-09-538-092-241

Query Match 43.8%; Score 49; DB 4; Length 218;  
Best Local Similarity 52.4%; Pred. No. 15;  
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQWNL 21  
DB 1 MADYSSLTIVVQKDLTKRNL 21



RESULT 11  
US-09-543-681A-7926  
; Sequence 7926, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709, 1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7926  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-7926

Query Match 42.9%; Score 48; DB 4; Length 300;  
Best Local Similarity 45.0%; Pred. No. 31;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MADNGTIVVELKQLLEQNM 20  
DB 60 LTDDGALVYHAKQIQAQFN 79

RESULT 12  
US-09-538-092-769  
; Sequence 769, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Glot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CurataseqFormatter Version 0.9  
; SEQ ID NO 769  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number YPL003W  
US-09-538-092-769

Query Match 42.9%; Score 48; DB 4; Length 462;  
Best Local Similarity 43.8%; Pred. No. 50;  
Matches 7; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 3 DNGTIVVELKQLLEQ 18  
DB 213 NNGRITIDMKKVVDDQ 228

RESULT 13  
US-09-538-092-266  
; Sequence 266, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Glot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CurataseqFormatter Version 0.9  
; SEQ ID NO 266  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number YPL017C  
US-09-538-092-266

Query Match 42.0%; Score 47; DB 4; Length 159;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTTIVVELKQLLEQNM 20  
DB 31 GTTPESFSKIKYWN 46

RESULT 14  
US-09-513-999C-6125  
; Sequence 6125, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclet, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6125  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-6125

Query Match 41.1%; Score 46; DB 4; Length 100;  
Best Local Similarity 60.0%; Pred. No. 18;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVVELKQLLE 17  
DB 47 ENSEINIVELKQVLE 61

RESULT 15  
US-09-270-767-45884  
; Sequence 45884, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; PRIOR FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 45884

LENGTH: 149  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-45884

Query Match 41.1%; Score 46; DB 4; Length 149;  
Best Local Similarity 41.2%; Pred. No. 27;  
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLEOM 19  
DB 92 NKGTISARQRLNLOM 108

RESULT 16  
US-09-710-279-2624  
Sequence 2624, Application US/09710279  
Patent No. 6703492  
GENERAL INFORMATION:  
APPLICANT: KIMBERLY, WILLIAM JOHN  
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
FILE REFERENCE: PU3480US  
CURRENT APPLICATION NUMBER: US/09/710,279  
CURRENT FILING DATE: 2000-11-09  
PRIOR APPLICATION NUMBER: 60/164,258  
PRIOR FILING DATE: 1999-11-09  
NUMBER OF SEQ ID NOS: 4472  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 2624  
LENGTH: 216  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-710-279-2624

Query Match 41.1%; Score 46; DB 4; Length 216;  
Best Local Similarity 60.0%; Pred. No. 42;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTIVEELKQLEO 18  
DB 59 NGMTLEAKYQLE 73

RESULT 17  
US-09-134-001C-5279  
Sequence 5279, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 5279  
LENGTH: 274  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5279

Query Match 41.1%; Score 46; DB 3; Length 274;  
Best Local Similarity 60.0%; Pred. No. 54;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTIVEELKQLEO 18

DB 117 NGMTLEAKYQLE 131

RESULT 18  
US-09-648-004-26  
Sequence 26, Application US/09648004  
Patent No. 6498242  
GENERAL INFORMATION:  
APPLICANT: CHEN, QIONG  
APPLICANT: THOMAS, STUART  
APPLICANT: NAGARAJAN, VASANTHA  
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
FILE REFERENCE: CL-1341-A  
CURRENT APPLICATION NUMBER: US/09/648,004  
CURRENT FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/252,553  
PRIOR FILING DATE: 1999-02-19  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 26  
LENGTH: 300  
TYPE: PRT  
ORGANISM: Acinetobacter sp.  
US-09-648-004-26

Query Match 41.1%; Score 46; DB 4; Length 300;  
Best Local Similarity 25.0%; Pred. No. 60;  
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQLEOM 20  
DB 22 MOENPMTEDEFRSMFDEWH 41

RESULT 19  
US-10-272-419-26  
Sequence 26, Application US/10272419  
Patent No. 6794165  
GENERAL INFORMATION:  
APPLICANT: CHEN, QIONG  
APPLICANT: THOMAS, STUART  
APPLICANT: NAGARAJAN, VASANTHA  
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
FILE REFERENCE: CL1341-A  
CURRENT APPLICATION NUMBER: US/10/272,419  
CURRENT FILING DATE: 2002-10-16  
PRIOR APPLICATION NUMBER: 09/252,553  
PRIOR FILING DATE: 1999-02-19  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 26  
LENGTH: 300  
TYPE: PRT  
ORGANISM: Acinetobacter sp.  
US-10-272-419-26

Query Match 41.1%; Score 46; DB 4; Length 300;  
Best Local Similarity 25.0%; Pred. No. 60;  
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKQLEOM 20  
DB 22 MOENPMTEDEFRSMFDEWH 41

RESULT 20  
US-09-248-796A-14232  
Sequence 14232, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
PRIORITY FILING DATE: 1999-02-12  
PRIORITY APPLICATION NUMBER: US 60/074,725  
PRIORITY FILING DATE: 1998-02-13  
PRIORITY APPLICATION NUMBER: US 60/096,409  
PRIORITY FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 14232  
LENGTH: 415  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-14232

Query Match 41.1%; Score 46; DB 4; Length 415;  
Best Local Similarity 46.7%; Pred. No. 87;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 ITVEBELKQLEQNL 21  
DB 106 ITPKCLKRAIDQWNI 120

RESULT 21  
US-09-489-039A-10011  
Sequence 10011, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
PRIORITY FILING DATE: 2000-01-27  
PRIORITY APPLICATION NUMBER: US 60/117,747  
PRIORITY FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 10011  
LENGTH: 532  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-10011

Query Match 41.1%; Score 46; DB 4; Length 532;  
Best Local Similarity 53.3%; Pred. No. 1,1e+02;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MANGTITVEELKQL 15  
DB 293 MADNGTLFDEIGEL 307

RESULT 22  
US-08-940-332-2  
Sequence 2, Application US/08940332  
Patent No. 5885834  
GENERAL INFORMATION:  
APPLICANT: Epstein, Paul M.  
TITLE OF INVENTION: SYNTHESIS OF ANTISENSE  
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE OF PHOSPHODIESTERASE AND  
TITLE OF INVENTION: INDUCEMENT OF APOPTOSIS IN HUMAN LYMPHOBLASTOID CELLS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ALIX, YALE & RISTAS, LLP  
STREET: 750 MAIN STREET  
CITY: HARTFORD  
STATE: CT  
COUNTRY: USA  
ZIP: 06103-2721  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,332  
FILING DATE: 30-SEP-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,207  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Alix, James B.  
REGISTRATION NUMBER: 20,736  
REFERENCE/DOCKET NUMBER: UCON/137/US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (860)527-9211  
TELEFAX: (860)527-5029  
INFORMATION FOR SEQ ID NOS: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 536 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-940-332-2

Query Match 41.1%; Score 46; DB 2; Length 536;  
Best Local Similarity 60.0%; Pred. No. 1,2e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTITVEELKQLE 17  
DB 47 ENGEMINEELKNLE 61

RESULT 23  
US-09-543-681A-4729  
Sequence 4729, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
PRIORITY FILING DATE: 2000-04-05  
PRIORITY APPLICATION NUMBER: US 60/128,706  
PRIORITY FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 4729  
LENGTH: 537  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-4729

Query Match 41.1%; Score 46; DB 4; Length 537;  
Best Local Similarity 36.8%; Pred. No. 1,2e+02;  
Matches 7; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 3 DNGTITVEELKQLEQNL 21  
DB 114 DNGSASLEDEPHELDKWL 132

RESULT 24  
US-09-949-016-7536  
Sequence 7536, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016

```

RESULT 26
US-09-248-796A-21680
; Sequence 21680, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21680
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-21680

```

RESULT 28  
US-08-297-494-27  
; Sequence 27, Application US/08297494  
; Patent No. 5580771  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.

APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
STREET: Two First National Plaza, 20 South Clark  
Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,494  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 558077land, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-297-494-27

Query Match 40.2%; Score 45; DB 1; Length 534;  
Best Local Similarity 53.3%; Pred. No. 1.6e+02;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLE 17  
DB 46 ENGEVNIIEELKNLE 60

RESULT 29  
US-08-297-510-27  
Sequence 27, Application US/08297510  
Patent No. 5602019  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
STREET: Two First National Plaza, 20 South Clark  
Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,510  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5602019and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-297-510-27

Query Match 40.2%; Score 45; DB 1; Length 534;  
Best Local Similarity 53.3%; Pred. No. 1.6e+02;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLE 17  
DB 46 ENGEVNIIEELKNLE 60

RESULT 30  
US-08-479-532-27  
Sequence 27, Application US/08479532  
Patent No. 576752  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
STREET: Two First National Plaza, 20 South Clark  
Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,532  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:

```

US-08-455-526-27
Query Match          40.2%; Score 45; DB 1; Length 534;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches      8; Conservative      4; Mismatches      3; Indels      0; Gaps      0;

QY      3 DNGTITVEELKNLE 17
      :|: :|||: ||
      46 ENGEVNIEELKNLE 60

Db

RESULT 32
US-08-455-525-27
; Sequence 27, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,525
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5800987and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-455-525-27
Query Match          40.2%; Score 45; DB 1; Length 534;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches      8; Conservative      4; Mismatches      3; Indels      0; Gaps      0;

QY      3 DNGTITVEELKNLE 17
      :|: :|||: ||
      46 ENGEVNIEELKNLE 60

Db

RESULT 33
US-09-139-491-27

```

Sequence 27, Application US/09139491  
Patent No. 6015677  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,491  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,525  
FILING DATE: 31-MAY-1995  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6015677and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 984-9740  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-139-491-27

Query Match 40.2%; Score 45; DB 3; Length 534;  
Best Local Similarity 53.3%; Pred. No. 1.6e+02;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEBKQKLE 17  
DB 46 ENGEVNIIEBKQKLE 60

RESULT 34  
US-09-883-825-27  
Sequence 27, Application US/09883825  
Patent No. 6642040  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/883,825  
FILING DATE: 18-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/123,783  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/297,494  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6642040and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-883-825-27

Query Match 40.2%; Score 45; DB 4; Length 534;  
Best Local Similarity 53.3%; Pred. No. 1.6e+02;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DNGTIVEBKQKLE 17  
DB 46 ENGEVNIIEBKQKLE 60

RESULT 35  
PCT-US92-03222-27  
Sequence 27, Application PC/TUS9203222  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03222
FILING DATE: 19920420
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03222-27

Query Match
Best Local Similarity 53.3%; Score 45; DB 5; Length 534;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 DNGTIVEELKQLEQNL 17
Db 46 ENGEVNEIEELKNLE 60

RESULT 36
US-09-248-796A-18997
Sequence 18997, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18997
LENGTH: 714
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-18997

Query Match
Best Local Similarity 46.7%; Score 45; DB 4; Length 714;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ITVEELKQLEQNL 21
Db 87 ITLENKKGIDKNNI 101

RESULT 37
US-09-255-502-7
Sequence 7, Application US/09255502
Patent No. 6218165
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: Mutant Proteins Having Lower Allergenic Responses in
```

```
TITLE OF INVENTION: Humans and Methods for Constructing, Identifying and
FILE OF INVENTION: Producing Such Proteins
FILE REFERENCE: GC 527-D2
CURRENT APPLICATION NUMBER: US/09/255,502
CURRENT FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: 09/060,872
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1052
TYPE: PRT
ORGANISM: Homo sapiens
US-09-255-502-7

Query Match
Best Local Similarity 38.1%; Score 45; DB 3; Length 1052;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MADNGTIVEELKQLEQNL 21
Db 747 MPDTGANIPALNELLSVNM 767

RESULT 38
US-09-360-237-1
Sequence 1, Application US/09360237
Patent No. 6322962
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: CHENG, DONG
APPLICANT: ESPENSHADE, PETER J.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: RAWSON, ROBERT B.
APPLICANT: SAKAI, JURO
TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
FILE REFERENCE: UTXD:567
CURRENT APPLICATION NUMBER: US/09/360,237
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/096,571
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1052
TYPE: PRT
ORGANISM: Cricetus griseus
US-09-360-237-1

Query Match
Best Local Similarity 40.2%; Score 45; DB 3; Length 1052;
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MADNGTIVEELKQLEQNL 21
Db 747 MPDTGANIPALNELLSVNM 767

RESULT 39
US-09-360-237-3
Sequence 3, Application US/09360237
Patent No. 6322962
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: CHENG, DONG
APPLICANT: ESPENSHADE, PETER J.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: RAWSON, ROBERT B.
APPLICANT: SAKAI, JURO
TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
FILE REFERENCE: UTXD:567
```



CURRENT APPLICATION NUMBER: US/09/360,237  
CURRENT FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: 60/096,571  
EARLIER FILING DATE: 1998-08-14  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1052  
TYPE: PRT  
ORGANISM: Human  
US-09-360-237-3

Query Match 40.2%; Score 45; DB 3; Length 1052;  
Best Local Similarity 38.1%; Pred. No. 3.4e+02;  
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21  
DB 747 MPDTGANIPALNELLSSVNM 767

RESULT 40  
US-09-255-501-208  
Sequence 208, Application US/09255501  
Patent No. 6596525  
GENERAL INFORMATION:  
APPLICANT: Estell, David  
APPLICANT: Harding, Fiona  
TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN  
TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND  
FILE REFERENCE: GC527  
CURRENT APPLICATION NUMBER: US/09/255,501  
CURRENT FILING DATE: 1999-02-23  
NUMBER OF SEQ ID NOS: 211  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 208  
LENGTH: 1052  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-255-501-208

Query Match 40.2%; Score 45; DB 4; Length 1052;  
Best Local Similarity 38.1%; Pred. No. 3.4e+02;  
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21  
DB 747 MPDTGANIPALNELLSSVNM 767

RESULT 41  
US-09-060-854B-7  
Sequence 7, Application US/09060854B  
Patent No. 6642011  
GENERAL INFORMATION:  
APPLICANT: Betell, David Aaron  
TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical  
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. 6642011-H  
FILE REFERENCE: GC532  
CURRENT APPLICATION NUMBER: US/09/060,854B  
CURRENT FILING DATE: 1998-04-15  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 1052  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-060-854B-7

Query Match 40.2%; Score 45; DB 4; Length 1052;  
Best Local Similarity 38.1%; Pred. No. 3.4e+02;

Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;  
QY 1 MADNGTIVEELKOLLEQNL 21  
DB 747 MPDTGANIPALNELLSSVNM 767

RESULT 42  
US-09-891-711-4  
Sequence 4, Application US/09891711  
Patent No. 6723553  
GENERAL INFORMATION:  
APPLICANT: Pharmacia AB  
TITLE OF INVENTION: Promoter Sequences  
FILE REFERENCE: 00130  
CURRENT APPLICATION NUMBER: US/09/891,711  
CURRENT FILING DATE: 2001-06-26  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 1052  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-891-711-4

Query Match 40.2%; Score 45; DB 4; Length 1052;  
Best Local Similarity 38.1%; Pred. No. 3.4e+02;  
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21  
DB 747 MPDTGANIPALNELLSSVNM 767

RESULT 43  
US-09-891-711-6  
Sequence 6, Application US/09891711  
Patent No. 6723553  
GENERAL INFORMATION:  
APPLICANT: Pharmacia AB  
TITLE OF INVENTION: Promoter Sequences  
FILE REFERENCE: 00130  
CURRENT APPLICATION NUMBER: US/09/891,711  
CURRENT FILING DATE: 2001-06-26  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 1052  
TYPE: PRT  
ORGANISM: Cricetus griseus  
US-09-891-711-6

Query Match 40.2%; Score 45; DB 4; Length 1052;  
Best Local Similarity 38.1%; Pred. No. 3.4e+02;  
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVEELKOLLEQNL 21  
DB 747 MPDTGANIPALNELLSSVNM 767

RESULT 44  
US-09-949-016-6413  
Sequence 6413, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6413  
LENGTH: 1052  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6413

Query Match 40.2%; Score 45; DB 4; Length 1052;  
Best Local Similarity 38.1%; Pred. No. 3.4e+02;  
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKOLLEQNL 21  
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 45  
US-09-060-872A-208  
Sequence 208, Application US/09060872A  
Patent No. 683550  
GENERAL INFORMATION:  
APPLICANT: Estell, David  
TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN  
TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND  
FILE REFERENCE: GC527  
CURRENT APPLICATION NUMBER: US/09/060,872A  
CURRENT FILING DATE: 1998-04-15  
NUMBER OF SEQ ID NOS: 211  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 208  
LENGTH: 1052  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-060-872A-208

Query Match 40.2%; Score 45; DB 4; Length 1052;  
Best Local Similarity 38.1%; Pred. No. 3.4e+02;  
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKOLLEQNL 21  
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 46  
US-09-500-135C-208  
Sequence 208, Application US/09500135C  
Patent No. 6838269  
GENERAL INFORMATION:  
APPLICANT: Estell, David A.  
APPLICANT: Harding, Fiona A.  
TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND  
TITLE OF INVENTION: METHODS OF MAKING AND USING THE SAME  
FILE REFERENCE: A-68893/DJB/DAV  
CURRENT APPLICATION NUMBER: US/09/500,135C  
CURRENT FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: US 09/060,872  
PRIOR FILING DATE: 1998-04-15  
NUMBER OF SEQ ID NOS: 236  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 208  
LENGTH: 1052  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-500-135C-208

Query Match 40.2%; Score 45; DB 4; Length 1052;  
Best Local Similarity 38.1%; Pred. No. 3.4e+02;  
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKOLLEQNL 21  
DB 747 MPDTGANIPALNELLSVNM 767

RESULT 47  
US-09-949-016-10687  
Sequence 10687, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10687  
LENGTH: 1058  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-10687

Query Match 40.2%; Score 45; DB 4; Length 1058;  
Best Local Similarity 38.1%; Pred. No. 3.5e+02;  
Matches 8; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKOLLEQNL 21  
DB 753 MPDTGANIPALNELLSVNM 773

RESULT 48  
US-09-476-242-2  
Sequence 2, Application US/09476242  
Patent No. 6889879  
GENERAL INFORMATION:  
APPLICANT: BARNETT, Susan  
APPLICANT: HARTEG, Karin  
APPLICANT: MARTIN, Eric  
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES  
FILE REFERENCE: 1605.002  
CURRENT APPLICATION NUMBER: US/09/476,242  
CURRENT FILING DATE: 1999-12-30  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 847  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus  
US-09-476-242-2

Query Match 39.7%; Score 44.5; DB 4; Length 847;  
Best Local Similarity 45.0%; Pred. No. 3.2e+02;  
Matches 9; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 4 NGTIVBELKOLLEQNL 22  
DB 401 NGTIVBELKOLLEQNL 420

RESULT 49  
US-09-621-976-4009  
Sequence 4009, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jober, S.  
APPLICANT: Giordano, J.V.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO: 4009  
LENGTH: 93  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -58..-1  
US-09-621-976-4009

Query Match  
Best Local Similarity 39.3%; Score 44; DB 4; Length 93;  
Best Local Similarity 37.5%; Pred. No. 32;  
Matches 9; Conservative 7; Mismatches 6; Indels 2; Gaps 1;

QY 1 MADNGTITVEE-LKQLEQNLV 22  
DB 9 LSAQGTVTFFEDVAVKFTQEEML 32

RESULT 50  
US-09-107-532A-6600  
Sequence 6600, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 6600:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...114  
SEQUENCE DESCRIPTION: SEQ ID NO: 6600:  
US-09-107-532A-6600

Query Match  
Best Local Similarity 39.3%; Score 44; DB 4; Length 114;  
Best Local Similarity 42.9%; Pred. No. 40;  
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLEQNL 21  
DB 49 LIDSGAETVGEVSMILDYFNL 69

Search completed: May 11, 2005, 21:27:56  
Job time : 40.5532 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 21:23:25 ; Search time 85.6596 Seconds  
(without alignments)  
85.795 Million cell updates/sec

Title: US-10-712-812-5  
Perfect score: 112  
Sequence: 1 MADNGRTYBELKQLEQNNLV 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 1000 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/prodata/2/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/2/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/2/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/2/pubppa/PCUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/2/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/prodata/2/pubppa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/2/pubppa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/2/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/2/pubppa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/prodata/2/pubppa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/prodata/2/pubppa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/prodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	100.0	221	16	US-10-839-729-6 Sequence 6, Appl1
2	112	100.0	221	16	US-10-839-729-7 Sequence 7, Appl1
3	112	100.0	221	16	US-10-839-729-8 Sequence 8, Appl1
4	112	100.0	221	16	US-10-839-729-9 Sequence 9, Appl1
5	112	100.0	221	17	US-10-699-936-24 Sequence 24, Appl1
6	112	100.0	221	17	US-10-699-936-81 Sequence 81, Appl1
7	112	100.0	221	17	US-10-699-936-82 Sequence 82, Appl1
8	112	100.0	221	17	US-10-699-936-83 Sequence 83, Appl1
9	112	100.0	242	17	US-10-808-187-214 Sequence 214, Appl1
10	73	65.2	15	16	US-10-839-729-46 Sequence 46, Appl1
11	53.5	47.8	336	15	US-10-425-114-69487 Sequence 69487, A
12	53.5	47.8	486	16	US-10-437-963-158994 Sequence 158994, A
13	53.5	47.8	512	16	US-10-437-963-158996 Sequence 158996, A

14	53.5	47.8	523	15	US-10-425-114-57880 Sequence 57880, A
15	51.5	46.0	855	14	US-10-369-294-11 Sequence 11, Appl1
16	51.5	46.0	855	14	US-10-369-294-12 Sequence 12, Appl1
17	51	45.5	54	9	US-09-864-761-39008 Sequence 39008, A
18	51	45.5	206	10	US-09-873-546-10 Sequence 10, Appl1
19	51	45.5	206	10	US-10-153-668-214 Sequence 214, Appl1
20	51	45.5	206	14	US-10-021-660-132 Sequence 132, Appl1
21	51	45.5	206	15	US-10-231-913-64 Sequence 64, Appl1
22	51	45.5	206	15	US-10-211-462-79 Sequence 79, Appl1
23	51	45.5	206	16	US-10-408-765A-2022 Sequence 2022, Ap
24	51	45.5	206	16	US-10-804-491-48 Sequence 48, Appl1
25	51	45.5	209	15	US-10-231-913-66 Sequence 66, Appl1
26	51	45.5	351	15	US-10-282-122A-51593 Sequence 51593, A
27	50	44.6	92	15	US-10-424-599-219887 Sequence 219887, A
28	50	44.6	174	16	US-10-437-963-186189 Sequence 186189, A
29	50	44.6	546	15	US-10-417-700A-49 Sequence 49, Appl1
30	50	44.6	546	15	US-10-424-599-203557 Sequence 203557, A
31	50	44.6	549	15	US-10-425-114-54704 Sequence 54704, A
32	50	44.6	673	15	US-10-282-122A-76721 Sequence 76721, A
33	49	43.8	123	10	US-09-953-348-132 Sequence 132, Appl1
34	49	43.8	123	14	US-10-267-255-132 Sequence 63, Appl1
35	48	42.9	206	15	US-10-231-913-63 Sequence 63, Appl1
36	48	42.9	206	15	US-10-231-913-65 Sequence 65, Appl1
37	48	42.9	206	15	US-10-231-913-67 Sequence 67, Appl1
38	48	42.9	299	16	US-10-437-963-124248 Sequence 124248, A
39	48	42.9	401	15	US-10-369-493-10440 Sequence 10440, A
40	48	42.9	4437	14	US-10-314-657-45 Sequence 45, Appl1
41	48	42.9	4437	17	US-10-473-193-45 Sequence 45, Appl1
42	47	42.0	159	15	US-10-429-812-4 Sequence 30, Appl1
43	47	42.0	159	15	US-10-612-779-30 Sequence 30, Appl1
44	47	42.0	159	17	US-10-823-397-33 Sequence 33, Appl1
45	47	42.0	508	16	US-10-686-947-238 Sequence 238, Appl1
46	47	42.0	508	16	US-10-686-947-266 Sequence 266, Appl1
47	47	42.0	509	16	US-10-686-947-240 Sequence 240, Appl1
48	47	42.0	659	15	US-10-369-493-2600 Sequence 2600, Ap
49	47	42.0	967	14	US-10-156-761-14515 Sequence 14515, A
50	46.5	41.5	428	15	US-10-282-122A-77230 Sequence 77230, A
51	46.5	41.5	849	14	US-09-899-575-23 Sequence 23, Appl1
52	46.5	41.5	849	14	US-10-190-433-148 Sequence 148, Appl1
53	46	41.1	183	15	US-10-425-114-49684 Sequence 49684, A
54	46	41.1	216	17	US-10-760-048B-286 Sequence 286, Appl1
55	46	41.1	224	16	US-10-470-701-39143 Sequence 39143, A
56	46	41.1	300	14	US-10-272-419-26 Sequence 26, Appl1
57	46	41.1	513	16	US-10-437-963-173217 Sequence 173217, A
58	46	41.1	515	17	US-10-781-102-1 Sequence 1, Appl1
59	46	41.1	515	17	US-10-425-114-64587 Sequence 64587, A
60	46	41.1	536	17	US-10-781-102-3 Sequence 3, Appl1
61	46	41.1	536	17	US-10-815-392-1 Sequence 1, Appl1
62	46	41.1	545	15	US-10-282-122A-54546 Sequence 54546, A
63	46	41.1	572	9	US-09-986-632-10 Sequence 10, Appl1
64	46	41.1	792	13	US-10-025-380-1127 Sequence 1127, Ap
65	45.5	40.6	175	15	US-10-425-114-44519 Sequence 44519, A
66	45.5	40.6	202	15	US-10-424-599-213143 Sequence 213143, A
67	45.5	40.6	422	15	US-10-282-122A-78200 Sequence 78200, A
68	45	40.2	60	17	US-10-781-102-13 Sequence 13, Appl1
69	45	40.2	126	15	US-10-424-599-147399 Sequence 147399, A
70	45	40.2	137	15	US-10-425-114-51360 Sequence 51360, A
71	45	40.2	137	15	US-10-424-599-188811 Sequence 188811, A
72	45	40.2	229	15	US-10-424-599-277269 Sequence 277269, A
73	45	40.2	339	14	US-10-029-386-32401 Sequence 32401, A
74	45	40.2	336	15	US-10-424-599-165657 Sequence 165657, A
75	45	40.2	462	15	US-10-282-122A-53097 Sequence 53097, A
76	45	40.2	467	15	US-10-104-047-2347 Sequence 2347, Ap
77	45	40.2	508	16	US-10-686-947-174 Sequence 174, Appl1
78	45	40.2	534	9	US-09-883-825-27 Sequence 27, Appl1
79	45	40.2	534	16	US-10-697-894-27 Sequence 27, Appl1
80	45	40.2	547	16	US-10-437-963-179668 Sequence 179668, A
81	45	40.2	636	15	US-10-282-122A-60575 Sequence 60575, A
82	45	40.2	633	9	US-09-815-242-11334 Sequence 11334, A
83	45	40.2	643	15	US-10-282-122A-58503 Sequence 58503, A
84	45	40.2	666	15	US-10-264-231-2631 Sequence 2631, Ap
85	45	40.2	808	15	US-10-104-047-2324 Sequence 2324, Ap
86	45	40.2	1052	9	US-09-060-8548-7 Sequence 7, Appl1

87	45	40.2	1052	9	US-09-891-711-4	Sequence 4, Appli	160	43	38.4	304	15	US-10-424-599-280749	Sequence 280749,
88	45	40.2	1052	9	US-09-891-711-6	Sequence 6, Appli	161	43	38.4	311	14	US-10-219-810-49	Sequence 49, Appl
89	45	40.2	1052	15	US-10-665-689-6	Sequence 6, Appli	162	43	38.4	325	15	US-10-424-599-198782	Sequence 198782,
90	45	40.2	1052	16	US-10-829-118-4	Sequence 4, Appli	163	43	38.4	394	16	US-10-451-467A-510	Sequence 510, App
91	45	40.2	1052	16	US-10-829-118-6	Sequence 6, Appli	164	43	38.4	407	15	US-10-108-260A-4092	Sequence 4092, Ap
92	45	40.2	1696	16	US-10-408-765A-822	Sequence 822, App	165	43	38.4	453	14	US-10-156-761-12790	Sequence 12790, A
93	45	40.2	1720	15	US-10-161-927-8	Sequence 8, Appli	166	43	38.4	467	15	US-10-417-700A-39	Sequence 39, Appl
94	44.5	39.7	159	15	US-10-425-114-43153	Sequence 43153, A	167	43	38.4	469	15	US-10-369-493-2943	Sequence 2943, Ap
95	44.5	39.7	171	15	US-10-425-114-47363	Sequence 47363, A	168	43	38.4	490	8	US-08-781-986A-5212	Sequence 5212, Ap
96	44.5	39.7	258	15	US-10-424-599-218227	Sequence 218227, A	169	43	38.4	490	15	US-10-329-624-5212	Sequence 5212, Ap
97	44.5	39.7	410	15	US-10-425-114-38139	Sequence 38139, A	170	43	38.4	492	15	US-10-424-599-272777	Sequence 272777, A
98	44.5	39.7	417	15	US-10-369-493-21136	Sequence 21136, A	171	43	38.4	510	15	US-10-369-493-56	Sequence 56, Appl
99	44.5	39.7	484	17	US-10-866-527-128	Sequence 128, App	172	43	38.4	521	15	US-09-820-843A-93	Sequence 93, Appl
100	44.5	39.7	497	15	US-10-424-599-191824	Sequence 191824, A	173	43	38.4	555	15	US-10-282-122A-67921	Sequence 67921, A
101	44.5	39.7	502	15	US-10-425-114-40675	Sequence 40675, A	174	43	38.4	567	15	US-10-425-114-69463	Sequence 69463, A
102	44.5	39.7	542	15	US-10-424-599-218225	Sequence 218225, A	175	43	38.4	587	15	US-10-283-122A-57771	Sequence 57771, A
103	44.5	39.7	549	9	US-09-828-313-39	Sequence 39, Appl	176	43	38.4	594	15	US-10-369-493-3337	Sequence 3337, Ap
104	44.5	39.7	549	16	US-10-768-863A-39	Sequence 39, Appl	177	43	38.4	1883	15	US-10-296-734-399	Sequence 399, App
105	44.5	39.7	619	9	US-09-891-609-4	Sequence 4, Appli	178	43	38.4	1896	15	US-10-326-734-333	Sequence 333, App
106	44.5	39.7	646	9	US-09-891-609-2	Sequence 2, Appli	179	43	38.4	5245	14	US-10-329-079-11	Sequence 11, Appl
107	44.5	39.7	842	14	US-10-190-435-2	Sequence 2, Appli	180	43	38.4	5245	14	US-10-329-079-11	Sequence 405, App
108	44.5	39.7	842	14	US-10-241-009-2	Sequence 2, Appli	181	43	38.4	5747	15	US-10-296-734-405	Sequence 221216
109	44.5	39.7	842	14	US-10-190-434B-2	Sequence 2, Appli	182	42.5	37.9	114	15	US-10-424-599-221216	Sequence 221216
110	44.5	39.7	842	14	US-10-190-305A-2	Sequence 2, Appli	183	42.5	37.9	424	15	US-10-369-493-232	Sequence 232, App
111	44.5	39.7	847	9	US-09-476-242-2	Sequence 2, Appli	184	42.5	37.9	429	9	US-09-815-243-10098	Sequence 10098, A
112	44	39.3	68	15	US-10-424-599-161357	Sequence 161357, A	185	42.5	37.9	429	15	US-10-369-493-770	Sequence 770, App
113	44	39.3	74	15	US-10-424-599-146899	Sequence 146899, A	186	42.5	37.9	429	15	US-10-282-122A-56485	Sequence 56485, A
114	44	39.3	143	11	US-09-978-360A-641	Sequence 641, App	187	42.5	37.9	435	15	US-10-282-122A-59565	Sequence 59565, A
115	44	39.3	157	15	US-10-369-493-2907	Sequence 2907, App	188	42.5	37.9	437	14	US-10-156-761-14620	Sequence 14620, A
116	44	39.3	182	15	US-10-424-599-199507	Sequence 199507, A	189	42.5	37.9	506	17	US-10-866-527-118	Sequence 118, App
117	44	39.3	196	16	US-10-437-963-102544	Sequence 102544, A	190	42.5	37.9	546	11	US-09-764-875-1122	Sequence 832, App
118	44	39.3	196	16	US-10-437-963-200009	Sequence 200009, A	191	42.5	37.9	568	11	US-09-764-875-8122	Sequence 832, App
119	44	39.3	200	15	US-10-424-599-236486	Sequence 236486, A	192	42.5	37.9	883	16	US-10-441-949-2	Sequence 2, Appli
120	44	39.3	206	15	US-10-231-913-6	Sequence 6, Appli	193	42.5	37.9	883	16	US-10-441-949-2	Sequence 2, Appli
121	44	39.3	257	15	US-10-425-114-44806	Sequence 44806, A	194	42	37.5	44	10	US-09-877-843-84	Sequence 84, Appl
122	44	39.3	273	17	US-10-729-571B-48	Sequence 48, Appl	195	42	37.5	78	15	US-10-369-493-20021	Sequence 20021, A
123	44	39.3	277	15	US-10-282-122A-57733	Sequence 57733, A	196	42	37.5	82	15	US-10-424-599-180924	Sequence 180924, A
124	44	39.3	286	16	US-10-437-963-201175	Sequence 201175, A	197	42	37.5	94	15	US-10-424-599-228445	Sequence 228445, A
125	44	39.3	300	15	US-10-424-599-235900	Sequence 235900, A	198	42	37.5	117	15	US-10-335-977-8014	Sequence 8014, Ap
126	44	39.3	308	15	US-10-369-493-23066	Sequence 23066, A	199	42	37.5	127	15	US-10-424-599-161942	Sequence 161942, A
127	44	39.3	316	15	US-10-425-114-55782	Sequence 55782, A	200	42	37.5	155	16	US-10-437-963-166917	Sequence 166917, A
128	44	39.3	331	15	US-10-424-599-276035	Sequence 276035, A	201	42	37.5	163	15	US-10-424-599-148963	Sequence 148963, A
129	44	39.3	428	16	US-10-437-963-141938	Sequence 141938, A	202	42	37.5	169	16	US-10-767-701-52386	Sequence 52386, A
130	44	39.3	473	14	US-10-354-358-96	Sequence 96, Appl	203	42	37.5	189	16	US-10-767-701-32627	Sequence 32627, A
131	44	39.3	476	15	US-10-264-049-2925	Sequence 2925, Ap	204	42	37.5	202	15	US-10-424-599-271745	Sequence 271745, A
132	44	39.3	480	16	US-10-437-963-201442	Sequence 201442, A	205	42	37.5	207	15	US-10-424-599-249257	Sequence 249257, A
133	44	39.3	491	9	US-09-815-242-5671	Sequence 5671, Ap	206	42	37.5	208	16	US-10-767-701-33537	Sequence 33537, A
134	44	39.3	504	9	US-09-815-242-12692	Sequence 12692, A	207	42	37.5	225	15	US-10-282-122A-78029	Sequence 78029, A
135	44	39.3	511	15	US-10-282-122A-44428	Sequence 44428, A	208	42	37.5	244	15	US-10-369-493-6951	Sequence 2951, Ap
136	44	39.3	533	16	US-10-437-963-200006	Sequence 200006, A	209	42	37.5	295	15	US-10-425-114-53449	Sequence 53449, A
137	44	39.3	545	14	US-10-192-419-2	Sequence 2, Appli	210	42	37.5	305	15	US-10-425-114-70080	Sequence 70080, A
138	44	39.3	553	15	US-10-369-493-17467	Sequence 17467, A	211	42	37.5	305	16	US-10-767-701-44602	Sequence 44602, A
139	44	39.3	557	15	US-10-424-599-236485	Sequence 236485, A	212	42	37.5	315	16	US-10-437-963-116503	Sequence 116503, A
140	44	39.3	571	15	US-10-369-493-39	Sequence 39, Appl	213	42	37.5	324	15	US-10-282-122A-57080	Sequence 57080, A
141	44	39.3	1905	11	US-09-964-956-44	Sequence 44, Appl	214	42	37.5	331	15	US-10-424-599-238604	Sequence 238604, A
142	43.5	38.8	107	15	US-10-424-599-244888	Sequence 244888, A	215	42	37.5	347	15	US-10-425-114-38844	Sequence 38844, A
143	43.5	38.8	429	9	US-10-282-122A-75835	Sequence 75835, A	216	42	37.5	351	14	US-10-033-585-7371	Sequence 7371, Ap
144	43.5	38.8	477	9	US-09-815-242-13991	Sequence 13991, A	217	42	37.5	357	15	US-10-424-599-226137	Sequence 226137, A
145	43.5	38.8	500	17	US-10-866-527-38	Sequence 38, Appl	218	42	37.5	397	16	US-10-437-963-143589	Sequence 143589, A
146	43.5	38.8	530	16	US-10-437-963-153480	Sequence 153480, A	219	42	37.5	423	15	US-10-369-493-6746	Sequence 6746, App
147	43.5	38.8	619	15	US-10-369-493-19203	Sequence 19203, A	220	42	37.5	450	15	US-10-282-122A-69508	Sequence 69508, A
148	43.5	38.8	673	14	US-10-156-761-11243	Sequence 11243, A	221	42	37.5	451	15	US-10-282-122A-67651	Sequence 67651, A
149	43.5	38.8	999	16	US-10-437-963-117353	Sequence 117353, A	222	42	37.5	460	15	US-10-417-700A-133	Sequence 133, App
150	43	38.4	42	14	US-10-029-386-31644	Sequence 31644, A	223	42	37.5	464	15	US-10-369-493-7005	Sequence 7005, Ap
151	43	38.4	83	15	US-10-424-599-194945	Sequence 194945, A	224	42	37.5	467	9	US-09-875-573-17	Sequence 17, Appl
152	43	38.4	90	15	US-10-335-977-8761	Sequence 8761, Ap	225	42	37.5	467	9	US-09-875-573-19	Sequence 19, Appl
153	43	38.4	172	15	US-10-369-493-21205	Sequence 21205, A	226	42	37.5	467	9	US-09-875-573-21	Sequence 21, Appl
154	43	38.4	172	15	US-10-282-122A-68573	Sequence 68573, A	227	42	37.5	468	9	US-09-875-573-23	Sequence 23, Appl
155	43	38.4	196	9	US-09-764-877-1830	Sequence 1830, Ap	228	42	37.5	468	9	US-09-875-573-25	Sequence 25, Appl
156	43	38.4	196	15	US-10-242-515-1830	Sequence 1830, Ap	229	42	37.5	468	9	US-09-875-573-27	Sequence 27, Appl
157	43	38.4	210	15	US-10-425-114-40176	Sequence 40176, A	230	42	37.5	481	15	US-10-425-114-53209	Sequence 53209, A
158	43	38.4	210	16	US-10-767-701-36983	Sequence 36983, A	231	42	37.5	481	15	US-10-425-114-59273	Sequence 59273, A
159	43	38.4	263	15	US-10-335-977-8763	Sequence 8763, Ap	232	42	37.5	481	16	US-10-767-701-46495	Sequence 46495, A

233	42	37.5	485	15	US-10-425-114-46975	Sequence 46975, A	306	41	36.6	329	15	US-10-627-476-306	Sequence 306, App
234	42	37.5	485	15	US-10-425-114-47502	Sequence 47502, A	307	41	36.6	336	15	US-10-425-114-38903	Sequence 38903, A
235	42	37.5	485	15	US-10-425-114-47600	Sequence 47600, A	308	41	36.6	367	15	US-10-786-720-48	Sequence 48, Appl
236	42	37.5	485	15	US-10-425-114-53351	Sequence 53351, A	309	41	36.6	416	15	US-10-335-977-8816	Sequence 8816, Ap
237	42	37.5	485	15	US-10-425-114-53175	Sequence 53175, A	310	41	36.6	421	15	US-10-335-977-8817	Sequence 8817, Ap
238	42	37.5	485	15	US-10-425-114-59189	Sequence 59189, A	311	41	36.6	421	15	US-10-335-977-8818	Sequence 8818, Ap
239	42	37.5	485	15	US-10-425-114-55993	Sequence 55993, A	312	41	36.6	430	15	US-10-335-977-3201	Sequence 3201, Ap
240	42	37.5	485	15	US-10-425-114-62688	Sequence 62688, A	313	41	36.6	455	15	US-10-369-493-18160	Sequence 18160, A
241	42	37.5	485	15	US-10-425-114-66115	Sequence 66115, A	314	41	36.6	459	15	US-10-627-476-302	Sequence 302, App
242	42	37.5	485	15	US-10-425-114-72073	Sequence 72073, A	315	41	36.6	465	15	US-10-282-122A-66168	Sequence 66168, A
243	42	37.5	485	15	US-10-425-114-72092	Sequence 72092, A	316	41	36.6	471	15	US-10-425-114-55771	Sequence 55771, A
244	42	37.5	485	15	US-10-425-114-72099	Sequence 72099, A	317	41	36.6	479	15	US-10-335-977-9400	Sequence 9400, Ap
245	42	37.5	490	15	US-10-369-493-16459	Sequence 16459, A	318	41	36.6	479	9	US-09-738-626-3765	Sequence 3765, Ap
246	42	37.5	498	16	US-10-767-701-46009	Sequence 46009, A	319	41	36.6	489	15	US-10-282-122A-45280	Sequence 45280, A
247	42	37.5	518	16	US-10-437-963-195842	Sequence 195842, A	320	41	36.6	490	14	US-10-074-155-26	Sequence 26, Appl
248	42	37.5	531	15	US-10-425-114-70256	Sequence 70256, A	321	41	36.6	495	10	US-09-848-806-1	Sequence 1, Appl
249	42	37.5	537	15	US-10-425-114-70196	Sequence 70196, A	322	41	36.6	495	10	US-10-369-493-6635	Sequence 6635, Ap
250	42	37.5	539	15	US-10-425-114-37249	Sequence 37249, A	323	41	36.6	501	10	US-09-848-806-3	Sequence 3, Appl
251	42	37.5	549	16	US-10-437-963-164372	Sequence 164372, A	324	41	36.6	503	15	US-10-424-559-274943	Sequence 274943, A
252	42	37.5	574	16	US-10-437-963-102998	Sequence 102998, A	325	41	36.6	505	15	US-10-282-122A-46385	Sequence 46385, A
253	42	37.5	608	15	US-10-282-122A-71442	Sequence 71442, A	326	41	36.6	542	16	US-10-437-963-196998	Sequence 196998, A
254	42	37.5	643	15	US-10-282-122A-67033	Sequence 67033, A	327	41	36.6	559	16	US-10-437-963-184089	Sequence 184089, A
255	42	37.5	684	15	US-10-282-122A-47915	Sequence 47915, A	328	41	36.6	579	17	US-10-802-682-6	Sequence 6, Appl
256	42	37.5	689	15	US-10-424-593-187294	Sequence 187294, A	329	41	36.6	581	16	US-10-437-963-197001	Sequence 197001, A
257	42	37.5	698	15	US-10-369-493-13572	Sequence 13572, A	330	41	36.6	585	15	US-10-282-122A-71330	Sequence 71330, A
258	42	37.5	698	15	US-10-369-493-18198	Sequence 18198, A	331	41	36.6	596	9	US-09-815-242-5244	Sequence 5244, Ap
259	42	37.5	703	16	US-10-437-963-166914	Sequence 166914, A	332	41	36.6	604	9	US-09-815-242-12525	Sequence 12525, A
260	42	37.5	722	16	US-10-437-963-166911	Sequence 166911, A	333	41	36.6	604	15	US-10-282-122A-43977	Sequence 43977, A
261	42	37.5	909	17	US-10-826-812-13	Sequence 13, Appl	334	41	36.6	608	16	US-10-148-884-2	Sequence 2, Appl
262	42	37.5	1238	16	US-10-408-765A-2450	Sequence 2450, Ap	335	41	36.6	611	15	US-10-369-493-5204	Sequence 5204, Appl
263	42	37.5	1297	14	US-10-289-776-17	Sequence 17, Appl	336	41	36.6	618	16	US-10-437-963-197005	Sequence 197005, A
264	42	37.5	1297	17	US-10-826-812-6	Sequence 6, Appl	337	41	36.6	630	15	US-10-282-122A-60647	Sequence 60647, A
265	42	37.5	1409	15	US-10-369-493-5387	Sequence 5387, Ap	338	41	36.6	695	10	US-09-305-924-13	Sequence 13, Appl
266	42	37.5	1973	16	US-10-661-809-22	Sequence 22, Appl	339	41	36.6	719	15	US-10-425-114-70174	Sequence 70174, A
267	42	37.5	1973	16	US-10-661-809-24	Sequence 24, Appl	340	41	36.6	754	15	US-10-282-122A-66762	Sequence 66762, A
268	41.5	37.1	98	16	US-10-437-963-162000	Sequence 162000, A	341	41	36.6	831	15	US-10-369-493-18676	Sequence 18676, A
269	41.5	37.1	98	16	US-10-767-701-53086	Sequence 53086, A	342	41	36.6	883	17	US-10-472-928-4222	Sequence 4222, Ap
270	41.5	37.1	122	15	US-10-424-599-146448	Sequence 146448, A	343	41	36.6	887	9	US-09-815-242-12179	Sequence 12179, A
271	41.5	37.1	121	16	US-10-437-963-137765	Sequence 137765, A	344	41	36.6	890	15	US-10-282-122A-74187	Sequence 74187, A
272	41.5	37.1	251	15	US-10-424-599-146446	Sequence 146446, A	345	41	36.6	890	16	US-10-474-776-393	Sequence 393, App
273	41.5	37.1	368	15	US-10-469-993-12	Sequence 12, Appl	346	41	36.6	953	10	US-09-884-696-3	Sequence 3, Appl
274	41.5	37.1	374	16	US-10-437-963-118336	Sequence 118336, A	347	41	36.6	953	16	US-10-148-884-5	Sequence 5, Appl
275	41.5	37.1	425	15	US-10-282-122A-68661	Sequence 68661, A	348	41	36.6	1100	17	US-10-741-849-7239	Sequence 7239, Ap
276	41.5	37.1	470	15	US-10-425-114-70198	Sequence 70198, A	349	41	36.6	1110	16	US-10-437-963-197003	Sequence 197003, A
277	41.5	37.1	472	15	US-10-417-700A-67	Sequence 67, Appl	350	41	36.6	1217	16	US-10-437-963-183891	Sequence 183891, A
278	41.5	37.1	500	16	US-10-437-963-137763	Sequence 137763, A	351	41	36.6	1346	16	US-10-437-963-121131	Sequence 121131, A
279	41.5	37.1	518	16	US-10-437-963-168927	Sequence 168927, A	352	41	36.6	1396	15	US-10-282-122A-69535	Sequence 69535, A
280	41.5	37.1	561	14	US-10-032-585-7306	Sequence 7306, Ap	353	40.5	36.2	111	15	US-10-424-599-265776	Sequence 265776, A
281	41.5	37.1	603	16	US-10-437-963-161888	Sequence 161888, A	354	40.5	36.2	251	15	US-10-369-493-14215	Sequence 14215, A
282	41.5	37.1	639	9	US-09-854-731-17	Sequence 17, Appl	355	40.5	36.2	251	15	US-10-369-493-14944	Sequence 14944, A
283	41	36.6	40	17	US-10-781-102-9	Sequence 9, Appl	356	40.5	36.2	252	15	US-10-369-493-14589	Sequence 14589, A
284	41	36.6	55	15	US-10-424-599-235854	Sequence 235854, A	357	40.5	36.2	257	15	US-10-369-493-11551	Sequence 11551, A
285	41	36.6	60	17	US-10-781-102-8	Sequence 8, Appl	358	40.5	36.2	345	16	US-10-437-963-204556	Sequence 204556, A
286	41	36.6	63	16	US-10-437-963-182278	Sequence 182278, A	359	40.5	36.2	404	16	US-10-437-963-110927	Sequence 110927, A
287	41	36.6	71	9	US-09-982-809-2	Sequence 2, Appl	360	40.5	36.2	459	15	US-10-369-493-2334	Sequence 2334, Ap
288	41	36.6	71	14	US-10-161-941-11	Sequence 11, Appl	361	40.5	36.2	459	15	US-10-369-493-2336	Sequence 2336, Ap
289	41	36.6	99	16	US-10-437-963-168376	Sequence 168376, A	362	40.5	36.2	470	16	US-10-728-195-11	Sequence 17, Appl
290	41	36.6	133	16	US-10-286-421-28	Sequence 28, Appl	363	40.5	36.2	487	17	US-10-866-527-50	Sequence 50, Appl
291	41	36.6	135	16	US-10-767-701-55426	Sequence 55426, A	364	40.5	36.2	493	17	US-10-866-527-130	Sequence 130, App
292	41	36.6	140	15	US-10-335-977-9398	Sequence 9398, Ap	365	40.5	36.2	503	9	US-09-759-841-4	Sequence 4, Appl
293	41	36.6	147	15	US-10-282-122A-77767	Sequence 77767, A	366	40.5	36.2	512	17	US-10-866-527-108	Sequence 108, App
294	41	36.6	148	15	US-10-424-599-155154	Sequence 155154, A	367	40	35.7	39	17	US-10-781-102-11	Sequence 11, Appl
295	41	36.6	149	15	US-10-369-493-2146	Sequence 2146, Ap	368	40	35.7	48	17	US-10-476-447-2	Sequence 2, Appl
296	41	36.6	157	15	US-10-424-599-236576	Sequence 236576, A	369	40	35.7	52	13	US-10-102-265-13	Sequence 13, Appl
297	41	36.6	158	15	US-10-389-566-511	Sequence 511, App	370	40	35.7	53	9	US-09-799-514-16	Sequence 16, Appl
298	41	36.6	160	15	US-10-108-260A-3318	Sequence 3318, Ap	371	40	35.7	71	15	US-10-424-599-176074	Sequence 176074, A
299	41	36.6	161	15	US-10-369-493-22406	Sequence 22406, A	372	40	35.7	90	14	US-10-106-698-5022	Sequence 5022, Ap
300	41	36.6	164	10	US-09-443-218-2	Sequence 2, Appl	373	40	35.7	120	15	US-10-424-599-24339	Sequence 24339, A
301	41	36.6	164	10	US-09-443-218-4	Sequence 4, Appl	374	40	35.7	138	15	US-10-425-114-66012	Sequence 66012, A
302	41	36.6	164	10	US-09-443-218-5	Sequence 5, Appl	375	40	35.7	139	15	US-10-425-114-60512	Sequence 60512, A
303	41	36.6	164	10	US-09-443-218-7	Sequence 7, Appl	376	40	35.7	140	15	US-10-425-114-41418	Sequence 41418, A
304	41	36.6	264	15	US-10-425-114-38904	Sequence 38904, A	377	40	35.7	142	16	US-10-437-963-204004	Sequence 204004, A
305	41	36.6	309	15	US-10-369-493-10903	Sequence 10903, A	378	40	35.7	156	15	US-10-424-599-184133	Sequence 184133, A

379	40	35.7	158	13	US-10-102-265-3	Sequence 3, Appl1
380	40	35.7	158	13	US-10-102-265-6	Sequence 6, Appl1
381	40	35.7	158	13	US-10-424-599-234231	Sequence 234231, A
382	40	35.7	159	13	US-10-102-265-4	Sequence 4, Appl1
383	40	35.7	159	13	US-10-102-265-7	Sequence 7, Appl1
384	40	35.7	159	13	US-10-102-265-1	Sequence 1, Appl1
385	40	35.7	160	15	US-10-424-599-245344	Sequence 245344, A
386	40	35.7	166	14	US-10-237-271-18	Sequence 18, Appl1
387	40	35.7	166	14	US-10-408-765A-2060	Sequence 2060, Ap
388	40	35.7	170	15	US-10-425-114-46390	Sequence 46390, A
389	40	35.7	171	16	US-10-767-701-45361	Sequence 45361, A
390	40	35.7	176	15	US-10-424-599-242860	Sequence 242860, A
391	40	35.7	179	13	US-10-102-265-2	Sequence 2, Appl1
392	40	35.7	179	13	US-10-102-265-5	Sequence 5, Appl1
393	40	35.7	179	13	US-10-102-265-15	Sequence 15, Appl1
394	40	35.7	181	16	US-10-102-265-14	Sequence 14, Appl1
395	40	35.7	181	16	US-10-767-701-34753	Sequence 34753, A
396	40	35.7	187	9	US-09-815-153-3	Sequence 3, Appl1
397	40	35.7	187	9	US-10-428-487-3	Sequence 3, Appl1
398	40	35.7	187	15	US-10-424-599-283060	Sequence 283060, A
399	40	35.7	191	16	US-10-767-701-45179	Sequence 45179, A
400	40	35.7	196	9	US-09-815-153-7	Sequence 7, Appl1
401	40	35.7	197	16	US-10-437-963-144209	Sequence 144209, A
402	40	35.7	198	9	US-09-815-153-5	Sequence 5, Appl1
403	40	35.7	198	15	US-10-428-487-22	Sequence 22, Appl1
404	40	35.7	199	15	US-10-282-122A-52399	Sequence 52399, A
405	40	35.7	203	16	US-10-767-701-37332	Sequence 37332, A
406	40	35.7	206	16	US-10-363-829-311	Sequence 311, App
407	40	35.7	208	9	US-09-988-982-1	Sequence 1, Appl1
408	40	35.7	208	15	US-10-131-487A-185	Sequence 185, App
409	40	35.7	211	16	US-10-767-701-5874	Sequence 5874, A
410	40	35.7	214	9	US-09-853-450-34	Sequence 34, Appl1
411	40	35.7	216	15	US-10-424-599-184045	Sequence 184045, A
412	40	35.7	217	16	US-10-478-245-4	Sequence 4, Appl1
413	40	35.7	218	15	US-10-296-115-772	Sequence 772, App
414	40	35.7	219	14	US-10-106-698-5793	Sequence 5793, Ap
415	40	35.7	222	15	US-10-424-599-254434	Sequence 254434, A
416	40	35.7	223	15	US-10-425-114-42487	Sequence 42487, A
417	40	35.7	224	15	US-10-425-114-36966	Sequence 36966, A
418	40	35.7	224	16	US-10-437-963-200588	Sequence 200588, A
419	40	35.7	230	14	US-10-237-271-17	Sequence 17, Appl1
420	40	35.7	230	15	US-10-210-130-56	Sequence 56, Appl1
421	40	35.7	230	15	US-10-236-417-60	Sequence 60, Appl1
422	40	35.7	230	15	US-10-236-417-64	Sequence 64, Appl1
423	40	35.7	233	16	US-10-699-156-18	Sequence 18, Appl1
424	40	35.7	234	13	US-10-102-265-1	Sequence 1, Appl1
425	40	35.7	234	15	US-10-428-487-1	Sequence 1, Appl1
426	40	35.7	234	15	US-10-302-172-950	Sequence 950, App
427	40	35.7	235	9	US-09-815-153-6	Sequence 6, Appl1
428	40	35.7	235	14	US-10-314-657-27	Sequence 27, Appl1
429	40	35.7	235	15	US-10-428-487-84	Sequence 84, Appl1
430	40	35.7	235	17	US-10-473-193-27	Sequence 27, Appl1
431	40	35.7	244	15	US-10-424-599-210083	Sequence 210083, A
432	40	35.7	244	15	US-10-425-114-39990	Sequence 39990, A
433	40	35.7	247	15	US-10-369-493-448	Sequence 448, App
434	40	35.7	248	16	US-10-437-963-169185	Sequence 169185, A
435	40	35.7	250	15	US-10-282-122A-68953	Sequence 68953, A
436	40	35.7	254	15	US-10-369-493-20963	Sequence 20963, A
437	40	35.7	254	16	US-10-767-701-43819	Sequence 43819, A
438	40	35.7	258	15	US-10-424-599-229486	Sequence 229486, A
439	40	35.7	263	9	US-09-925-899-991	Sequence 991, App
440	40	35.7	263	10	US-09-925-299-991	Sequence 991, App
441	40	35.7	265	15	US-09-975-719-31	Sequence 31, Appl1
442	40	35.7	267	15	US-10-424-599-211068	Sequence 211068, A
443	40	35.7	268	16	US-10-437-963-192778	Sequence 192778, A
444	40	35.7	270	16	US-10-437-963-171875	Sequence 171875, A
445	40	35.7	273	15	US-10-369-493-12865	Sequence 12865, A
446	40	35.7	282	15	US-10-282-122A-62789	Sequence 62789, A
447	40	35.7	282	15	US-10-282-122A-64811	Sequence 64811, A
448	40	35.7	283	16	US-10-437-963-165776	Sequence 165776, A
449	40	35.7	291	9	US-09-864-761-37074	Sequence 37074, A
450	40	35.7	294	15	US-10-369-493-18390	Sequence 18390, A
451	40	35.7	300	15	US-10-424-599-211071	Sequence 211071, A
	40	35.7	314	15	US-10-425-114-65717	Sequence 65717, A
452	40	35.7	316	9	US-09-799-514-11	Sequence 11, Appl1
453	40	35.7	324	15	US-10-094-749-1930	Sequence 1930, Ap
454	40	35.7	326	15	US-10-282-122A-53226	Sequence 53226, A
455	40	35.7	326	15	US-10-425-114-51354	Sequence 51354, A
456	40	35.7	326	15	US-10-316-223-104	Sequence 104, Appl1
457	40	35.7	336	16	US-10-437-963-104617	Sequence 104617, A
458	40	35.7	340	16	US-10-437-963-104617	Sequence 104617, A
459	40	35.7	344	9	US-09-925-300-1360	Sequence 1360, Ap
460	40	35.7	344	15	US-10-369-493-16716	Sequence 16716, A
461	40	35.7	345	14	US-10-033-201B-263	Sequence 263, App
462	40	35.7	351	15	US-10-369-493-17093	Sequence 17093, A
463	40	35.7	357	15	US-10-282-122A-52822	Sequence 52822, A
464	40	35.7	362	15	US-10-425-114-47534	Sequence 47534, A
465	40	35.7	362	15	US-10-425-114-65151	Sequence 65151, A
466	40	35.7	373	15	US-10-424-599-274676	Sequence 274676, A
467	40	35.7	383	15	US-10-425-114-53577	Sequence 53577, A
468	40	35.7	391	15	US-10-289-762-921	Sequence 921, App
469	40	35.7	394	15	US-10-108-260A-2699	Sequence 2699, Ap
470	40	35.7	397	14	US-10-156-761-7779	Sequence 7779, Ap
471	40	35.7	400	16	US-10-437-963-165037	Sequence 165037, A
472	40	35.7	418	15	US-10-282-122A-55471	Sequence 55471, A
473	40	35.7	419	16	US-10-437-963-108808	Sequence 108808, A
474	40	35.7	444	9	US-09-805-020-53	Sequence 53, Appl1
475	40	35.7	446	15	US-10-424-599-151497	Sequence 151497, A
476	40	35.7	450	15	US-10-282-122A-71596	Sequence 71596, A
477	40	35.7	457	16	US-10-437-963-200116	Sequence 200116, A
478	40	35.7	459	15	US-10-424-599-275168	Sequence 275168, A
479	40	35.7	463	13	US-10-037-860-13	Sequence 13, Appl1
480	40	35.7	466	15	US-10-417-700A-51	Sequence 51, Appl1
481	40	35.7	469	16	US-10-322-281-834	Sequence 834, App
482	40	35.7	469	16	US-10-466-406-10	Sequence 10, Appl1
483	40	35.7	478	15	US-10-282-122A-64268	Sequence 64268, A
484	40	35.7	484	15	US-10-282-122A-52836	Sequence 52836, A
485	40	35.7	487	15	US-10-425-114-56442	Sequence 56442, A
486	40	35.7	488	15	US-10-424-599-280137	Sequence 280137, A
487	40	35.7	490	17	US-10-675-086-24	Sequence 24, Appl1
488	40	35.7	491	16	US-10-282-122A-48421	Sequence 48421, A
489	40	35.7	494	16	US-10-437-963-180232	Sequence 180232, A
490	40	35.7	500	15	US-10-424-599-275172	Sequence 275172, A
491	40	35.7	505	15	US-10-425-114-47312	Sequence 47312, A
492	40	35.7	508	16	US-10-437-963-155126	Sequence 155126, A
493	40	35.7	509	14	US-10-097-559-11	Sequence 11, Appl1
494	40	35.7	511	15	US-10-424-599-202766	Sequence 202766, A
495	40	35.7	521	16	US-10-437-963-200463	Sequence 200463, A
496	40	35.7	526	15	US-10-424-599-283059	Sequence 283059, A
497	40	35.7	533	16	US-10-437-963-127855	Sequence 127855, A
498	40	35.7	535	14	US-10-106-698-5501	Sequence 5501, Ap
499	40	35.7	535	15	US-10-425-114-53814	Sequence 53814, A
500	40	35.7	538	15	US-10-424-599-248196	Sequence 248196, A
501	40	35.7	541	15	US-10-282-122A-77047	Sequence 77047, A
502	40	35.7	544	9	US-09-841-134-400	Sequence 400, App
503	40	35.7	544	9	US-09-759-272B-5	Sequence 5, Appl1
504	40	35.7	544	11	US-09-809-745-3	Sequence 3, Appl1
505	40	35.7	544	15	US-10-289-762-153	Sequence 153, App
506	40	35.7	544	15	US-10-282-122A-54855	Sequence 54855, A
507	40	35.7	544	16	US-10-282-122A-55161	Sequence 55161, A
508	40	35.7	549	16	US-10-470-093-5	Sequence 5, Appl1
509	40	35.7	551	15	US-10-259-194A-258	Sequence 258, App
510	40	35.7	551	15	US-10-369-493-18994	Sequence 18994, A
511	40	35.7	551	15	US-10-369-493-20184	Sequence 20184, A
512	40	35.7	553	15	US-10-425-114-37251	Sequence 37251, A
513	40	35.7	553	15	US-10-425-114-67049	Sequence 67049, A
514	40	35.7	553	15	US-10-425-114-68488	Sequence 68488, A
515	40	35.7	555	15	US-10-425-114-37250	Sequence 37250, A
516	40	35.7	555	15	US-10-425-114-49942	Sequence 49942, A
517	40	35.7	555	15	US-10-425-114-49943	Sequence 49943, A
518	40	35.7	555	15	US-10-425-114-63129	Sequence 63129, A
519	40	35.7	555	15	US-10-425-114-68181	Sequence 68181, A
520	40	35.7	564	15	US-10-425-114-67773	Sequence 67773, A
521	40	35.7	572	9	US-09-986-633-8	Sequence 8, Appl1
522	40	35.7	572	9	US-09-736-457-1815	Sequence 1815, Ap
523	40	35.7	572	9	US-09-902-941-1815	Sequence 941, Ap
524	40	35.7	572	14	US-09-849-626-1815	Sequence 1815, Ap
	40	35.7	572	14	US-10-017-754-1815	Sequence 1815, Ap



525	40	35.7	572	14	US-10-180-198-2	Sequence 2, Appl1	598	39.5	35.3	278	15	US-10-282-122A-71303	Sequence 71303, A
526	40	35.7	572	14	US-10-113-872-1815	Sequence 1815, Ap	599	39.5	35.3	221	15	US-10-369-493-154	Sequence 154, App
527	40	35.7	572	14	US-10-283-017-1815	Sequence 1815, Ap	600	39.5	35.3	307	15	US-10-156-761-11788	Sequence 11788, A
528	40	35.7	580	16	US-10-437-963-199601	Sequence 199601,	601	39.5	35.3	335	16	US-10-332-413-32	Sequence 32, Appl
529	40	35.7	584	17	US-10-472-928-1034	Sequence 1034, Ap	602	39.5	35.3	340	14	US-10-177-293-116	Sequence 116, App
530	40	35.7	600	16	US-10-437-963-104086	Sequence 104086,	603	39.5	35.3	376	9	US-09-934-060A-28	Sequence 28, Appl
531	40	35.7	609	15	US-10-108-260A-3971	Sequence 3971, Ap	604	39.5	35.3	460	17	US-10-866-527-42	Sequence 42, Appl
532	40	35.7	622	15	US-10-282-122A-60827	Sequence 60827, A	605	39.5	35.3	474	16	US-10-728-195-18	Sequence 18, Appl
533	40	35.7	627	15	US-10-425-114-59660	Sequence 59660, A	606	39.5	35.3	483	15	US-10-424-559-258507	Sequence 258507,
534	40	35.7	629	14	US-10-128-714-3099	Sequence 3099, Ap	607	39.5	35.3	506	9	US-09-934-060A-24	Sequence 24, Appl
535	40	35.7	641	16	US-10-437-963-188700	Sequence 188700,	608	39.5	35.3	506	9	US-09-934-060A-30	Sequence 30, Appl
536	40	35.7	647	15	US-10-369-493-23040	Sequence 23040, A	609	39.5	35.3	528	15	US-10-371-472-44	Sequence 44, Appl
537	40	35.7	651	16	US-10-408-765A-1578	Sequence 1578, Ap	610	39.5	35.3	554	17	US-10-855-588-18	Sequence 18, Appl
538	40	35.7	685	14	US-10-128-714-8039	Sequence 8039, Ap	611	39.5	35.3	556	9	US-09-934-060A-6	Sequence 6, Appl1
539	40	35.7	687	16	US-10-437-963-174167	Sequence 174167,	612	39.5	35.3	587	14	US-10-335-394-50	Sequence 50, Appl
540	40	35.7	703	17	US-10-480-988-2	Sequence 2, Appl1	613	39.5	35.3	580	9	US-09-934-060A-13	Sequence 13, Appl
541	40	35.7	776	15	US-10-424-599-200232	Sequence 200232,	614	39.5	35.3	585	14	US-10-335-394-56	Sequence 56, Appl
542	40	35.7	809	15	US-10-369-493-16530	Sequence 16530, A	615	39.5	35.3	601	14	US-10-335-394-52	Sequence 52, Appl
543	40	35.7	811	15	US-10-282-122A-45773	Sequence 45773, A	616	39.5	35.3	608	9	US-09-738-626-3609	Sequence 3609, Ap
544	40	35.7	822	16	US-10-645-250A-8	Sequence 8, Appl1	617	39.5	35.3	618	16	US-10-494-672-272	Sequence 272, App
545	40	35.7	829	9	US-09-925-298-602	Sequence 602, App	618	39.5	35.3	618	17	US-10-494-541-60	Sequence 60, Appl
546	40	35.7	829	14	US-10-102-806-602	Sequence 602, App	619	39.5	35.3	625	15	US-10-369-493-19782	Sequence 19782, A
547	40	35.7	839	15	US-10-424-599-200231	Sequence 200231,	620	39.5	35.3	637	9	US-09-815-242-5280	Sequence 5280, Ap
548	40	35.7	859	16	US-10-437-963-165313	Sequence 169313,	621	39.5	35.3	652	9	US-09-815-242-12140	Sequence 12140, A
549	40	35.7	1004	16	US-10-473-276-3	Sequence 3, Appl1	622	39.5	35.3	662	15	US-10-282-122A-43842	Sequence 43842, A
550	40	35.7	1024	14	US-10-211-962-41	Sequence 41, Appl	623	39.5	35.3	662	15	US-10-282-122A-71137	Sequence 71137, A
551	40	35.7	1024	14	US-10-211-962-44	Sequence 44, Appl	624	39.5	35.3	662	15	US-10-282-122A-48909	Sequence 48909, A
552	40	35.7	1036	16	US-10-322-281-160	Sequence 160, App	625	39.5	35.3	720	9	US-09-934-060A-2	Sequence 2, Appl1
553	40	35.7	1038	16	US-10-322-281-157	Sequence 157, App	626	39.5	35.3	720	9	US-09-934-060A-4	Sequence 4, Appl1
554	40	35.7	1050	15	US-10-425-114-55722	Sequence 55722, A	627	39.5	35.3	722	15	US-10-369-493-5651	Sequence 5651, Ap
555	40	35.7	1253	15	US-10-161-927-32	Sequence 32, App	628	39.5	35.3	748	15	US-10-282-122A-48709	Sequence 48709, A
556	40	35.7	1256	16	US-10-437-963-130209	Sequence 130209,	629	39.5	35.3	751	15	US-10-369-493-19004	Sequence 19004, A
557	40	35.7	1287	16	US-10-437-963-112735	Sequence 112735,	630	39.5	35.3	844	9	US-09-991-258-19	Sequence 19, Appl
558	40	35.7	1394	16	US-10-471-762-9	Sequence 9, Appl1	631	39.5	35.3	844	16	US-10-332-413-6	Sequence 6, Appl1
559	40	35.7	1444	16	US-10-609-113-11	Sequence 11, Appl	632	39.5	35.3	852	16	US-10-332-413-12	Sequence 12, Appl
560	40	35.7	1518	17	US-10-383-930-40	Sequence 40, Appl	633	39.5	35.3	858	16	US-10-332-413-145	Sequence 145, Appl
561	40	35.7	1518	17	US-10-797-821-40	Sequence 40, Appl	634	39.5	35.3	860	14	US-10-190-435-145	Sequence 145, App
562	40	35.7	1548	16	US-10-437-963-113738	Sequence 113738,	635	39.5	35.3	860	14	US-10-190-435-146	Sequence 146, App
563	40	35.7	1568	16	US-10-156-761-10037	Sequence 10037, A	636	39.5	35.3	14	9	US-09-883-825-28	Sequence 28, Appl
564	40	35.7	1987	14	US-10-132-382-6	Sequence 6, Appl1	637	39.5	35.3	14	16	US-10-697-894-28	Sequence 28, Appl
565	40	35.7	2013	14	US-10-132-382-2	Sequence 2, Appl1	638	39.5	35.3	52	9	US-09-764-887-187	Sequence 187, App
566	40	35.7	2014	15	US-10-132-382-8	Sequence 8, Appl1	639	39.5	35.3	52	14	US-10-073-961-167	Sequence 167, App
567	40	35.7	2014	15	US-10-220-955-18	Sequence 18, Appl	640	39.5	35.3	64	9	US-09-864-761-36928	Sequence 36928, A
568	40	35.7	2014	15	US-10-415-011-8	Sequence 8, Appl1	641	39.5	35.3	66	11	US-09-864-408A-8998	Sequence 8998, Ap
569	40	35.7	2040	14	US-10-132-382-4	Sequence 4, Appl1	642	39.5	35.3	74	15	US-10-424-599-144538	Sequence 144538,
570	40	35.7	2420	16	US-10-437-963-165599	Sequence 28, App	643	39.5	35.3	88	11	US-09-864-408A-7318	Sequence 7318, Ap
571	40	35.7	2477	14	US-10-360-053-28	Sequence 28, App	644	39.5	35.3	97	15	US-10-335-977-7642	Sequence 7642, Ap
572	40	35.7	2477	16	US-10-408-765A-238	Sequence 238, App	645	39.5	35.3	98	15	US-10-335-977-7641	Sequence 7641, Ap
573	40	35.7	2541	14	US-10-177-293-470	Sequence 470, App	646	39.5	35.3	100	16	US-10-658-834A-290	Sequence 290, App
574	40	35.7	2652	15	US-10-454-351-30	Sequence 30, Appl	647	39.5	35.3	100	16	US-10-658-834A-295	Sequence 295, App
575	40	35.7	2828	9	US-09-802-318-21	Sequence 21, Appl	648	39.5	35.3	100	16	US-10-658-834A-299	Sequence 299, App
576	40	35.7	2828	9	US-09-905-129-21	Sequence 21, Appl	649	39.5	35.3	101	15	US-10-424-599-246719	Sequence 246719,
577	40	35.7	2828	9	US-09-991-630-21	Sequence 21, Appl	650	39.5	35.3	119	9	US-09-764-868-637	Sequence 637, App
578	40	35.7	2828	14	US-10-176-847-54	Sequence 54, Appl	651	39.5	35.3	119	9	US-09-955-999-84	Sequence 84, Appl
579	40	35.7	2828	14	US-10-177-293-110	Sequence 110, App	652	39.5	35.3	119	11	US-09-764-878-1152	Sequence 1152, Ap
580	40	35.7	2828	14	US-10-301-822-49	Sequence 49, Appl	653	39.5	35.3	124	15	US-10-158-057-321	Sequence 321, App
581	40	35.7	2828	14	US-10-032-189-126	Sequence 126, App	654	39.5	35.3	121	15	US-10-282-122A-48956	Sequence 48956, A
582	40	35.7	2828	15	US-10-295-027-58	Sequence 58, Appl	655	39.5	35.3	122	14	US-10-194-885-21	Sequence 21, Appl
583	40	35.7	2828	15	US-10-295-027-115	Sequence 115, Ap	656	39.5	35.3	122	14	US-10-032-201B-59	Sequence 59, Appl
584	40	35.7	2828	15	US-10-072-012-607	Sequence 607, App	657	39.5	35.3	124	15	US-10-282-122A-73471	Sequence 73471, A
585	40	35.7	2828	15	US-10-072-012-608	Sequence 608, App	658	39.5	35.3	127	15	US-10-424-599-163334	Sequence 163334,
586	40	35.7	2828	15	US-10-454-351-21	Sequence 21, Appl	659	39.5	35.3	129	16	US-10-767-701-53518	Sequence 53518, A
587	40	35.7	2845	15	US-10-093-463-2	Sequence 2, Appl1	660	39.5	35.3	132	15	US-10-424-599-226031	Sequence 226031,
588	40	35.7	3442	15	US-10-282-122A-69849	Sequence 69849, A	661	39.5	35.3	135	16	US-10-437-963-16532	Sequence 16532,
589	40	35.7	5149	15	US-10-482-122A-46323	Sequence 436323, A	662	39.5	35.3	146	14	US-10-156-761-9502	Sequence 9502, A
590	40	35.7	139	16	US-10-437-963-138425	Sequence 60185, A	663	39.5	35.3	156	14	US-10-146-759-34	Sequence 34, Appl
591	40	35.7	180	16	US-10-767-701-60185	Sequence 222287,	664	39.5	35.3	158	15	US-10-424-599-192466	Sequence 192466,
592	40	35.7	196	15	US-10-424-599-22287	Sequence 122287,	665	39.5	35.3	163	16	US-10-437-963-137652	Sequence 137652,
593	40	35.7	202	15	US-10-364-397-12	Sequence 52356, A	666	39.5	35.3	166	15	US-10-425-114-56605	Sequence 56605, A
594	40	35.7	214	15	US-10-425-114-52556	Sequence 152423,	667	39.5	35.3	167	16	US-10-437-963-137652	Sequence 137652,
595	40	35.7	258	16	US-10-437-963-152423	Sequence 203722,	668	39.5	35.3	169	15	US-10-282-122A-44822	Sequence 44822, A
596	40	35.7	269	16	US-10-437-963-203722	Sequence 13506, A	669	39.5	35.3	172	15	US-10-425-114-40972	Sequence 40972, A
597	40	35.7	272	15	US-10-369-493-13506	Sequence 13506, A	670	39.5	35.3	174	15	US-10-425-114-66809	Sequence 66809, A

671	39	34.8	176	15	US-10-425-114-73069	Sequence 73069, A	744	39	34.8	448	15	US-10-282-122A-76710	Sequence 76710, A
672	39	34.8	183	15	US-10-424-599-256423	Sequence 256423, A	745	39	34.8	452	14	US-10-148-907A-15	Sequence 15, App1
673	39	34.8	184	15	US-09-873-546-15	Sequence 15, App1	746	39	34.8	455	15	US-10-369-493A-13712	Sequence 13712, A
674	39	34.8	185	16	US-10-437-963-201054	Sequence 201054, A	747	39	34.8	463	10	US-09-988-462-25	Sequence 25, App1
675	39	34.8	187	15	US-10-425-114-49529	Sequence 49529, A	748	39	34.8	464	10	US-09-988-462-25	Sequence 22, App1
676	39	34.8	187	15	US-10-425-114-57345	Sequence 57345, A	749	39	34.8	465	17	US-10-675-086-23	Sequence 23, App1
677	39	34.8	187	15	US-10-302-172-949	Sequence 949, App	750	39	34.8	468	9	US-09-815-242-10201	Sequence 10201, A
678	39	34.8	188	16	US-10-767-701-40973	Sequence 40973, A	751	39	34.8	468	9	US-09-875-573-29	Sequence 29, App1
679	39	34.8	190	14	US-10-032-585-7287	Sequence 7287, App	752	39	34.8	468	9	US-09-875-573-31	Sequence 31, App1
680	39	34.8	201	15	US-10-424-599-282990	Sequence 282990, A	753	39	34.8	468	9	US-09-875-573-37	Sequence 37, App1
681	39	34.8	214	11	US-09-764-875-870	Sequence 870, App	754	39	34.8	468	9	US-09-875-573-39	Sequence 39, App1
682	39	34.8	214	11	US-10-158-057-247	Sequence 247, App	755	39	34.8	468	9	US-09-875-573-41	Sequence 41, App1
683	39	34.8	218	15	US-10-424-599-163668	Sequence 163668, A	756	39	34.8	468	15	US-10-369-493-886	Sequence 886, App
684	39	34.8	227	15	US-10-424-599-268627	Sequence 268627, A	757	39	34.8	468	15	US-10-282-122A-56569	Sequence 56569, A
685	39	34.8	229	15	US-10-425-114-49679	Sequence 49679, A	758	39	34.8	472	15	US-10-282-122A-60359	Sequence 60359, A
686	39	34.8	230	9	US-09-984-205-6	Sequence 6, App1	759	39	34.8	473	9	US-09-815-242-5008	Sequence 5008, App
687	39	34.8	230	9	US-09-930-408-2	Sequence 2, App1	760	39	34.8	473	9	US-09-815-242-10478	Sequence 10478, A
688	39	34.8	230	16	US-10-759-277-6	Sequence 6, App1	761	39	34.8	473	15	US-10-282-122A-42521	Sequence 42521, A
689	39	34.8	235	16	US-10-437-963-165034	Sequence 165034, A	762	39	34.8	480	15	US-10-282-122A-54024	Sequence 54024, A
690	39	34.8	238	15	US-10-282-122A-43083	Sequence 43083, A	763	39	34.8	485	15	US-10-282-122A-51755	Sequence 51755, A
691	39	34.8	239	16	US-10-369-493-20567	Sequence 20567, A	764	39	34.8	486	16	US-10-437-963-120442	Sequence 120442, A
692	39	34.8	249	16	US-10-437-963-184335	Sequence 184335, A	765	39	34.8	508	15	US-10-424-599-242297	Sequence 242297, A
693	39	34.8	258	15	US-10-424-599-259680	Sequence 259680, A	766	39	34.8	510	16	US-10-437-963-143565	Sequence 143565, A
694	39	34.8	260	15	US-10-282-122A-75932	Sequence 75932, A	767	39	34.8	513	9	US-09-833-745-56	Sequence 56, App1
695	39	34.8	260	16	US-10-408-765A-408	Sequence 408, App	768	39	34.8	517	15	US-10-425-114-65871	Sequence 65871, A
696	39	34.8	260	17	US-10-791-155-1	Sequence 1, App1	769	39	34.8	520	15	US-10-369-493-11092	Sequence 11092, A
697	39	34.8	260	17	US-10-791-155-5	Sequence 5, App1	770	39	34.8	525	15	US-10-282-122A-62585	Sequence 62585, A
698	39	34.8	262	16	US-10-437-963-147300	Sequence 147300, A	771	39	34.8	525	15	US-10-282-122A-64802	Sequence 64802, A
699	39	34.8	263	16	US-10-767-701-45057	Sequence 45057, A	772	39	34.8	527	15	US-10-425-114-51766	Sequence 51766, A
700	39	34.8	265	15	US-10-425-114-45439	Sequence 45439, A	773	39	34.8	530	15	US-10-282-122A-77659	Sequence 77659, A
701	39	34.8	269	15	US-10-282-122A-77449	Sequence 77449, A	774	39	34.8	536	16	US-10-369-493-1992	Sequence 1992, App
702	39	34.8	270	16	US-10-282-122A-178643	Sequence 178643, A	775	39	34.8	545	9	US-09-995-749A-10	Sequence 10, App1
703	39	34.8	271	9	US-09-815-242-14072	Sequence 14072, A	776	39	34.8	546	11	US-09-882-227-418	Sequence 418, App1
704	39	34.8	278	15	US-10-282-122A-54649	Sequence 54649, A	777	39	34.8	546	11	US-09-921-157-6	Sequence 6, App1
705	39	34.8	283	15	US-10-282-122A-75079	Sequence 75079, A	778	39	34.8	546	15	US-10-282-122A-58603	Sequence 58603, A
706	39	34.8	303	15	US-10-424-599-208863	Sequence 208863, A	779	39	34.8	546	15	US-10-335-977-7645	Sequence 7645, App
707	39	34.8	304	9	US-09-738-626-3743	Sequence 3743, App	780	39	34.8	555	16	US-10-767-701-46075	Sequence 46075, App
708	39	34.8	305	15	US-10-424-599-208862	Sequence 208862, A	781	39	34.8	555	16	US-10-102-622-12	Sequence 12, App1
709	39	34.8	306	15	US-10-425-114-49629	Sequence 49629, A	782	39	34.8	579	15	US-10-389-566-753	Sequence 753, App
710	39	34.8	315	15	US-10-282-122A-57816	Sequence 57816, A	783	39	34.8	588	15	US-10-369-493-3206	Sequence 3206, App
711	39	34.8	316	15	US-10-369-493-13322	Sequence 13322, A	784	39	34.8	595	15	US-10-282-122A-63562	Sequence 63562, A
712	39	34.8	318	15	US-10-425-114-47355	Sequence 47355, A	785	39	34.8	595	15	US-10-282-122A-64390	Sequence 64390, A
713	39	34.8	318	15	US-10-425-114-53382	Sequence 53382, A	786	39	34.8	623	16	US-10-437-963-123925	Sequence 123925, A
714	39	34.8	318	15	US-10-425-114-53396	Sequence 53396, A	787	39	34.8	625	16	US-10-437-963-152224	Sequence 152224, A
715	39	34.8	324	15	US-10-282-122A-48373	Sequence 48373, A	788	39	34.8	635	9	US-09-833-745-38	Sequence 38, App1
716	39	34.8	343	14	US-10-223-085-12	Sequence 12, App1	789	39	34.8	647	15	US-10-282-122A-55195	Sequence 55195, A
717	39	34.8	343	14	US-10-223-084-12	Sequence 12, App1	790	39	34.8	655	15	US-10-369-493-20066	Sequence 20066, A
718	39	34.8	343	14	US-10-223-088-12	Sequence 12, App1	791	39	34.8	663	16	US-10-437-963-133909	Sequence 133909, A
719	39	34.8	343	14	US-10-223-090-12	Sequence 12, App1	792	39	34.8	670	14	US-10-106-698-6282	Sequence 6282, App
720	39	34.8	343	14	US-10-223-087-12	Sequence 12, App1	793	39	34.8	670	15	US-10-243-552-973	Sequence 973, App
721	39	34.8	343	14	US-10-223-083-12	Sequence 12, App1	794	39	34.8	689	15	US-10-369-493-135	Sequence 135, App
722	39	34.8	343	14	US-10-223-089-12	Sequence 12, App1	795	39	34.8	694	16	US-10-767-701-46291	Sequence 46291, A
723	39	34.8	343	14	US-10-223-081-12	Sequence 12, App1	796	39	34.8	700	16	US-10-408-765A-2425	Sequence 2425, App
724	39	34.8	343	14	US-10-223-082-12	Sequence 12, App1	797	39	34.8	717	15	US-10-369-493-17408	Sequence 17408, A
725	39	34.8	343	15	US-10-305-654-12	Sequence 12, App1	798	39	34.8	743	14	US-10-171-311-188	Sequence 188, App
726	39	34.8	343	15	US-10-081-055-12	Sequence 12, App1	799	39	34.8	744	16	US-10-437-963-122954	Sequence 122954, A
727	39	34.8	348	15	US-10-282-122A-46564	Sequence 46564, A	800	39	34.8	773	16	US-10-437-963-136533	Sequence 136533, A
728	39	34.8	351	15	US-10-374-780A-2118	Sequence 2118, App	801	39	34.8	790	16	US-10-437-963-199514	Sequence 199514, A
729	39	34.8	367	15	US-10-369-493-3459	Sequence 3459, App	802	39	34.8	850	9	US-09-808-602-58	Sequence 58, App1
730	39	34.8	368	9	US-09-925-300-1356	Sequence 1356, App	803	39	34.8	850	10	US-09-800-198-47	Sequence 47, App1
731	39	34.8	369	14	US-10-156-761-11423	Sequence 11423, A	804	39	34.8	851	14	US-10-259-165-260	Sequence 260, App
732	39	34.8	377	15	US-10-240-145-166	Sequence 1466, App	805	39	34.8	867	15	US-10-425-114-17669	Sequence 17669, A
733	39	34.8	382	15	US-10-424-599-149553	Sequence 149553, A	806	39	34.8	886	15	US-10-369-493-18210	Sequence 18210, A
734	39	34.8	385	14	US-10-168-274-6	Sequence 6, App1	807	39	34.8	916	15	US-10-210-130-138	Sequence 138, App
735	39	34.8	385	16	US-10-755-889-512	Sequence 512, App1	808	39	34.8	932	15	US-10-282-122A-69195	Sequence 69195, A
736	39	34.8	388	15	US-10-236-392-34	Sequence 34, App1	809	39	34.8	955	15	US-10-425-114-58617	Sequence 58617, A
737	39	34.8	393	15	US-10-282-122A-54250	Sequence 54250, A	810	39	34.8	968	15	US-10-425-114-58617	Sequence 58617, A
738	39	34.8	405	9	US-09-738-626-6717	Sequence 6717, App	811	39	34.8	972	14	US-10-231-354-2	Sequence 2, App1
739	39	34.8	408	10	US-09-988-462-21	Sequence 21, App1	812	39	34.8	983	14	US-09-808-602-73	Sequence 73, App1
740	39	34.8	420	9	US-09-946-142-2	Sequence 2, App1	813	39	34.8	983	14	US-10-013-136-2	Sequence 2, App1
741	39	34.8	420	16	US-10-781-014-136	Sequence 136, App	814	39	34.8	990	16	US-10-437-963-143591	Sequence 143591, A
742	39	34.8	446	15	US-10-282-122A-58019	Sequence 58019, A	815	39	34.8	1014	15	US-10-398-663-1	Sequence 1, App1
743	39	34.8	446	15	US-10-282-122A-63415	Sequence 63415, A	816	39	34.8	1018	14	US-10-101-464A-909	Sequence 909, App

817	39	34.8	1018	17	US-10-864-252-909	Sequence 909, App
818	39	34.8	1056	14	US-10-231-354-6	Sequence 6, Appl
819	39	34.8	1061	16	US-10-437-963-133988	Sequence 133988, Ap
820	39	34.8	1076	16	US-10-437-963-201416	Sequence 201416, Ap
821	39	34.8	1167	16	US-10-437-963-132719	Sequence 132719, A
822	39	34.8	1166	16	US-10-282-122A-68505	Sequence 68505, A
823	39	34.8	1188	16	US-10-437-963-198278	Sequence 198278, A
824	39	34.8	1250	16	US-10-437-963-151829	Sequence 151829, A
825	39	34.8	1270	14	US-10-437-963-151829	Sequence 10, Appl
826	39	34.8	1275	16	US-10-437-963-199835	Sequence 199835, A
827	39	34.8	1426	13	US-10-024-623-17	Sequence 17, Appl
828	39	34.8	1426	14	US-10-231-354-14	Sequence 14, Appl
829	39	34.8	1426	14	US-10-154-419-67	Sequence 67, Appl
830	39	34.8	1426	14	US-10-146-733-62	Sequence 62, Appl
831	39	34.8	1426	15	US-10-236-417-140	Sequence 140, App
832	39	34.8	1430	9	US-09-740-574-6	Sequence 6, Appl
833	39	34.8	1430	16	US-10-383-930-36	Sequence 36, Appl
834	39	34.8	1430	17	US-10-797-821-36	Sequence 36, Appl
835	39	34.8	1520	9	US-09-738-626-4444	Sequence 4444, Ap
836	39	34.8	1520	17	US-10-494-541-102	Sequence 102, App
837	39	34.8	1520	17	US-10-282-122A-46454	Sequence 46454, A
838	39	34.8	1783	15	US-10-188-832-86	Sequence 86, Appl
839	39	34.8	1784	16	US-10-437-963-133987	Sequence 133987, A
840	39	34.8	1803	16	US-10-343-509-3	Sequence 3, Appl
841	39	34.8	1805	16	US-10-343-509-1	Sequence 1, Appl
842	39	34.8	65	15	US-10-424-599-236158	Sequence 236158, A
843	39	34.8	103	10	US-09-764-891-3983	Sequence 3893, Ap
844	39	34.8	111	17	US-10-472-928-2534	Sequence 2534, Ap
845	39	34.8	111	17	US-10-472-928-2534	Sequence 2534, Ap
846	39	34.8	141	16	US-10-767-701-40627	Sequence 40627, A
847	39	34.8	141	16	US-10-424-599-149808	Sequence 149808, A
848	39	34.8	215	15	US-10-424-599-270242	Sequence 270242, A
849	39	34.8	220	15	US-10-424-599-270242	Sequence 270244, A
850	39	34.8	223	15	US-10-424-599-163137	Sequence 163137, A
851	39	34.8	220	16	US-10-767-701-32851	Sequence 32851, A
852	39	34.8	272	15	US-10-425-114-50274	Sequence 50274, A
853	39	34.8	312	15	US-10-425-114-50274	Sequence 50274, A
854	39	34.8	318	14	US-10-306-762-201	Sequence 63097, A
855	39	34.8	322	15	US-10-282-122A-69064	Sequence 69064, A
856	39	34.8	322	15	US-10-425-114-49665	Sequence 49665, A
857	39	34.8	325	15	US-10-425-114-43796	Sequence 43796, A
858	39	34.8	327	15	US-10-282-122A-58245	Sequence 58245, A
859	39	34.8	338	16	US-10-451-467A-44	Sequence 4, Appl
860	39	34.8	351	14	US-10-156-615-2	Sequence 2, Appl
861	39	34.8	351	17	US-10-938-016-2	Sequence 2, Appl
862	39	34.8	358	15	US-10-464-610-18	Sequence 18, Appl
863	39	34.8	365	15	US-10-464-610-4	Sequence 4, Appl
864	39	34.8	365	15	US-10-424-599-163141	Sequence 163141, A
865	39	34.8	386	17	US-10-675-086-4	Sequence 4, Appl
866	39	34.8	399	16	US-10-437-963-112378	Sequence 112378, A
867	39	34.8	413	14	US-10-156-761-15075	Sequence 15075, A
868	39	34.8	413	15	US-10-282-122A-46537	Sequence 46537, A
869	39	34.8	462	15	US-10-424-599-244189	Sequence 244189, A
870	39	34.8	469	17	US-10-866-527-40	Sequence 40, Appl
871	39	34.8	477	17	US-10-866-527-34	Sequence 34, Appl
872	39	34.8	496	17	US-10-866-527-100	Sequence 100, App
873	39	34.8	498	17	US-10-866-527-58	Sequence 58, Appl
874	39	34.8	508	16	US-10-462-040A-51	Sequence 51, Appl
875	39	34.8	509	17	US-10-866-527-36	Sequence 36, Appl
876	39	34.8	518	16	US-10-462-040A-45	Sequence 45, Appl
877	39	34.8	518	16	US-10-462-040A-46	Sequence 46, Appl
878	39	34.8	518	16	US-10-462-040A-47	Sequence 47, Appl
879	39	34.8	518	16	US-10-462-040A-48	Sequence 48, Appl
880	39	34.8	529	15	US-10-424-599-238052	Sequence 238052, A
881	39	34.8	532	15	US-10-369-493-285	Sequence 285, App
882	39	34.8	555	15	US-10-369-493-18747	Sequence 18747, A
883	39	34.8	581	15	US-10-424-599-244222	Sequence 244222, A
884	39	34.8	583	15	US-10-425-114-45048	Sequence 45048, A
885	39	34.8	640	15	US-10-369-493-19082	Sequence 19082, A
886	39	34.8	655	10	US-09-966-931-32	Sequence 32, Appl
887	39	34.8	655	16	US-10-459-121-32	Sequence 32, Appl
888	39	34.8	767	15	US-10-282-122A-44985	Sequence 44985, A
889	39	34.8	767	15	US-10-369-493-1753	Sequence 1753, Ap
					Sequence 31, Appl	
890	39	34.8	857	10	US-09-966-931-30	Sequence 30, Appl
891	39	34.8	857	16	US-10-459-121-30	Sequence 30, Appl
892	39	34.8	905	15	US-10-369-493-3573	Sequence 3573, Ap
893	39	34.8	966	15	US-10-369-493-6555	Sequence 6555, Ap
894	39	34.8	966	15	US-10-369-493-6555	Sequence 409, App
895	39	34.8	1048	9	US-09-815-242-10062	Sequence 10062, A
896	39	34.8	1048	14	US-10-301-997-85	Sequence 85, A
897	39	34.8	1048	14	US-10-282-122A-56444	Sequence 56444, A
898	39	34.8	1048	16	US-10-818-509-85	Sequence 85, Appl
899	39	34.8	1238	15	US-10-282-122A-58749	Sequence 58749, A
900	39	34.8	1480	15	US-10-359-012-22	Sequence 22, Appl
901	39	34.8	1633	15	US-10-359-012-4	Sequence 4, Appl
902	39	34.8	1795	15	US-10-170-385-37	Sequence 37, Appl
903	39	34.8	2679	14	US-10-059-271-92	Sequence 92, Appl
904	39	34.8	25	9	US-09-810-310-46	Sequence 46, Appl
905	39	34.8	37	14	US-10-044-699-68	Sequence 68, Appl
906	39	34.8	37	14	US-10-044-699-68	Sequence 68, Appl
907	39	34.8	37	15	US-10-325-810-68	Sequence 68, Appl
908	39	34.8	37	15	US-10-325-810-210	Sequence 210, App
909	39	34.8	37	16	US-10-767-701-52284	Sequence 52284, A
910	39	34.8	37	17	US-10-877-146-68	Sequence 68, Appl
911	39	34.8	37	17	US-10-877-146-210	Sequence 210, App
912	39	34.8	44	14	US-10-321-851-139	Sequence 139, App
913	39	34.8	44	14	US-10-318-675-139	Sequence 139, App
914	39	34.8	45	15	US-10-424-599-268174	Sequence 268174, A
915	39	34.8	52	9	US-09-764-891-749	Sequence 749, App
916	39	34.8	52	14	US-10-091-504-749	Sequence 749, App
917	39	34.8	52	15	US-10-227-577-749	Sequence 749, App
918	39	34.8	54	9	US-09-843-676-21	Sequence 21, Appl
919	39	34.8	54	9	US-09-843-676-21	Sequence 21, Appl
920	39	34.8	54	10	US-09-766-253-21	Sequence 21, Appl
921	39	34.8	54	14	US-09-438-486-21	Sequence 21, Appl
922	39	34.8	54	14	US-10-053-758-21	Sequence 21, Appl
923	39	34.8	54	14	US-10-054-629-21	Sequence 21, Appl
924	39	34.8	54	14	US-10-054-629-21	Sequence 21, Appl
925	39	34.8	60	16	US-10-437-963-202657	Sequence 202657, A
926	39	34.8	63	13	US-10-035-408-1	Sequence 1, Appl
927	39	34.8	68	9	US-09-756-854-22	Sequence 22, Appl
928	39	34.8	68	15	US-10-041-557-22	Sequence 22, Appl
929	39	34.8	68	16	US-10-834-966-22	Sequence 22, Appl
930	39	34.8	75	15	US-10-407-920-18	Sequence 18, Appl
931	39	34.8	77	9	US-09-887-879-17	Sequence 17, Appl
932	39	34.8	77	13	US-09-992-964-17	Sequence 17, Appl
933	39	34.8	77	14	US-10-112-793-24	Sequence 24, Appl
934	39	34.8	77	14	US-10-242-383-17	Sequence 17, Appl
935	39	34.8	79	15	US-10-282-122A-61471	Sequence 61471, A
936	39	34.8	82	15	US-10-424-599-23396	Sequence 23396, A
937	39	34.8	84	17	US-10-656-250-119	Sequence 119, App
938	39	34.8	86	9	US-09-925-299-1176	Sequence 1176, Ap
939	39	34.8	86	10	US-09-925-299-1176	Sequence 1176, Ap
940	39	34.8	95	10	US-09-877-843-27	Sequence 27, Appl
941	39	34.8	96	10	US-09-877-843-25	Sequence 25, Appl
942	39	34.8	97	10	US-09-877-843-25	Sequence 26, Appl
943	39	34.8	97	10	US-09-997-003-32	Sequence 32, Appl
944	39	34.8	97	14	US-10-304-287-3	Sequence 3, Appl
945	39	34.8	97	16	US-10-735-577-3	Sequence 3, Appl
946	39	34.8	98	15	US-10-424-599-270797	Sequence 270797, A
947	39	34.8	99	16	US-10-767-701-33384	Sequence 33384, A
948	39	34.8	100	16	US-10-658-833A-291	Sequence 291, App
949	39	34.8	103	15	US-10-424-599-156297	Sequence 156297, A
950	39	34.8	104	15	US-10-359-439-2	Sequence 2, Appl
951	39	34.8	105	9	US-09-767-215-10	Sequence 10, Appl
952	39	34.8	112	16	US-10-767-701-41099	Sequence 41099, A
953	39	34.8	113	16	US-10-437-963-122728	Sequence 122728, A
954	39	34.8	116	14	US-10-029-386-28826	Sequence 28826, A
955	39	34.8	118	16	US-09-764-891-3849	Sequence 3849, Ap
956	39	34.8	118	15	US-10-264-049-3389	Sequence 3389, Ap
957	39	34.8	121	16	US-10-437-963-121129	Sequence 121129, A
958	39	34.8	128	15	US-10-424-599-251351	Sequence 251351, A
959	39	34.8	134	10	US-09-992-600A-2	Sequence 2, Appl
960	39	34.8	134	10	US-09-924-340-2	Sequence 2, Appl
961	39	34.8	134	10	US-09-992-095B-2	Sequence 2, Appl
962	39	34.8	134	10	US-09-999-570-2	Sequence 2, Appl

```

963 38 33.9 134 14 US-10-000-489-2 Sequence 2, Appl1
964 38 33.9 134 14 US-10-000-986-2 Sequence 2, Appl1
965 38 33.9 134 14 US-10-154-678-2 Sequence 2, Appl1
966 38 33.9 134 17 US-10-838-854-2 Sequence 2, Appl1
967 38 33.9 137 9 US-09-971-309-34 Sequence 34, Appl1
968 38 33.9 144 15 US-10-424-599-161070 Sequence 161070,
969 38 33.9 147 15 US-10-424-599-176645 Sequence 176645,
970 38 33.9 147 15 US-10-425-114-61654 Sequence 61654, A
971 38 33.9 147 16 US-10-437-963-183850 Sequence 183850,
972 38 33.9 148 16 US-10-437-963-104683 Sequence 104683,
973 38 33.9 149 13 US-10-037-860-9 Sequence 9, Appl1
974 38 33.9 153 14 US-10-312-187-8 Sequence 8, Appl1
975 38 33.9 153 15 US-10-369-493-13319 Sequence 13319, A
976 38 33.9 157 15 US-10-424-599-179223 Sequence 179223,
977 38 33.9 163 16 US-10-437-963-108399 Sequence 108399,
978 38 33.9 164 9 US-09-767-041-32 Sequence 32, Appl1
979 38 33.9 164 15 US-10-282-122A-63390 Sequence 63390, A
980 38 33.9 167 15 US-10-282-122A-70573 Sequence 70573, A
981 38 33.9 169 15 US-10-424-599-212961 Sequence 212961,
982 38 33.9 170 15 US-10-424-599-285087 Sequence 285087,
983 38 33.9 172 16 US-10-437-963-123218 Sequence 123218,
984 38 33.9 182 15 US-10-236-417-62 Sequence 62, Appl1
985 38 33.9 185 15 US-10-603-260-5 Sequence 5, Appl1
986 38 33.9 185 16 US-10-767-701-39587 Sequence 39587, A
987 38 33.9 187 15 US-10-369-493-13956 Sequence 13956, A
988 38 33.9 188 15 US-10-424-599-181888 Sequence 181888,
989 38 33.9 188 16 US-10-437-963-180237 Sequence 180237,
990 38 33.9 192 14 US-10-002-631C-66 Sequence 66, Appl1
991 38 33.9 193 15 US-10-282-122A-57723 Sequence 57723, A
992 38 33.9 194 16 US-10-767-701-35943 Sequence 35943, A
993 38 33.9 198 15 US-10-425-114-46763 Sequence 46763, A
994 38 33.9 206 15 US-10-424-599-156668 Sequence 156668,
995 38 33.9 210 14 US-10-130-973A-13 Sequence 13, Appl1
996 38 33.9 214 15 US-10-425-114-62704 Sequence 62704, A
997 38 33.9 215 15 US-10-312-222-36 Sequence 36, Appl1
998 38 33.9 216 15 US-10-312-222-36 Sequence 33, Appl1
999 38 33.9 216 16 US-10-437-963-181655 Sequence 181655,
1000 38 33.9 223 15 US-10-424-599-149696 Sequence 149696,

```

## ALIGNMENTS

```

RESULT 1
; US-10-839-729-6 Application US/10839729
; Sequence 6, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 221
; TYPE: PRT
; ORGANISM: SARS Coronavirus
; US-10-839-729-6

```

```

Query Match 100.0%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MADNGTIVBELKQLEQNMNV 22
Db 1 MADNGTIVBELKQLEQNMNV 22

```

```

RESULT 2
; US-10-839-729-7 Application US/10839729
; Sequence 7, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 221
; TYPE: PRT
; ORGANISM: SARS Coronavirus
; US-10-839-729-7

```

```

Query Match 100.0%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MADNGTIVBELKQLEQNMNV 22
Db 1 MADNGTIVBELKQLEQNMNV 22

```

```

RESULT 3
; US-10-839-729-8 Application US/10839729
; Sequence 8, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 221
; TYPE: PRT
; ORGANISM: SARS Coronavirus
; US-10-839-729-8

```

```

Query Match 100.0%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MADNGTIVBELKQLEQNMNV 22
Db 1 MADNGTIVBELKQLEQNMNV 22

```

```

RESULT 4
; US-10-839-729-9 Application US/10839729
; Sequence 9, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06

```

NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 221  
TYPE: PRT  
ORGANISM: SARS Coronavirus  
US-10-839-729-9

Query Match 100.0%; Score 112; DB 16; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22  
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 5  
US-10-699-936-24  
Sequence 24, Application US/10699936  
Publication No. US20050095582A1  
GENERAL INFORMATION:  
APPLICANT: Gillim-Ross, Laura  
APPLICANT: Taylor, Jill  
APPLICANT: Scholl, David R.  
APPLICANT: Wentworth, David E.  
APPLICANT: Jollick, Joseph D.  
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory  
FILE REFERENCE: DHI-07986  
CURRENT APPLICATION NUMBER: US/10/699,936  
CURRENT FILING DATE: 2003-11-03  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 24  
LENGTH: 221  
TYPE: PRT  
ORGANISM: SARS-CoV Urbani  
US-10-699-936-24

Query Match 100.0%; Score 112; DB 17; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22  
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 6  
US-10-699-936-81  
Sequence 81, Application US/10699936  
Publication No. US20050095582A1  
GENERAL INFORMATION:  
APPLICANT: Gillim-Ross, Laura  
APPLICANT: Taylor, Jill  
APPLICANT: Scholl, David R.  
APPLICANT: Wentworth, David E.  
APPLICANT: Jollick, Joseph D.  
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory  
FILE REFERENCE: DHI-07986  
CURRENT APPLICATION NUMBER: US/10/699,936  
CURRENT FILING DATE: 2003-11-03  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 81  
LENGTH: 221  
TYPE: PRT  
ORGANISM: SARS coronavirus Tor2  
US-10-699-936-81

Query Match 100.0%; Score 112; DB 17; Length 221;

Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22  
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 7  
US-10-699-936-82  
Sequence 82, Application US/10699936  
Publication No. US20050095582A1  
GENERAL INFORMATION:  
APPLICANT: Gillim-Ross, Laura  
APPLICANT: Taylor, Jill  
APPLICANT: Scholl, David R.  
APPLICANT: Wentworth, David E.  
APPLICANT: Jollick, Joseph D.  
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory  
FILE REFERENCE: DHI-07986  
CURRENT APPLICATION NUMBER: US/10/699,936  
CURRENT FILING DATE: 2003-11-03  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 82  
LENGTH: 221  
TYPE: PRT  
ORGANISM: SARS coronavirus Shanghai QXC  
US-10-699-936-82

Query Match 100.0%; Score 112; DB 17; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22  
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 8  
US-10-699-936-83  
Sequence 83, Application US/10699936  
Publication No. US20050095582A1  
GENERAL INFORMATION:  
APPLICANT: Gillim-Ross, Laura  
APPLICANT: Taylor, Jill  
APPLICANT: Scholl, David R.  
APPLICANT: Wentworth, David E.  
APPLICANT: Jollick, Joseph D.  
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory  
FILE REFERENCE: DHI-07986  
CURRENT APPLICATION NUMBER: US/10/699,936  
CURRENT FILING DATE: 2003-11-03  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 83  
LENGTH: 221  
TYPE: PRT  
ORGANISM: SARS coronavirus Shanghai QXC  
US-10-699-936-83

Query Match 100.0%; Score 112; DB 17; Length 221;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNGTITVEELKQLLEQNMNV 22  
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 9

US-10-808-187-214  
; Sequence 214, Application US/10808187  
; Publication No. US2005009009A1  
; GENERAL INFORMATION:  
; APPLICANT: PEIRIS, JOSEPH S. M.  
; APPLICANT: YIEN, KWOK YUNG  
; APPLICANT: POON, LIT MAN  
; APPLICANT: GUAN, YI  
; APPLICANT: CHAN, KWOK HUNG  
; APPLICANT: NICHOLLS, JOHN  
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE  
; FILE REFERENCE: V9661.0078  
; CURRENT APPLICATION NUMBER: US/10/808,187  
; CURRENT FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: 60/457,031  
; PRIOR FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: 60/457,730  
; PRIOR FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: 60/459,931  
; PRIOR FILING DATE: 2003-04-02  
; PRIOR APPLICATION NUMBER: 60/460,357  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: 60/461,265  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/462,805  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: 60/468,139  
; PRIOR FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: 60/464,886  
; PRIOR FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: 60/471,200  
; PRIOR FILING DATE: 2003-05-16  
; NUMBER OF SEQ ID NOS: 2476  
; SOFTWARE: PatentIn ver. 3.2  
; SEQ ID NO 214  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Human severe acute respiratory system virus  
US-10-808-187-214  
Query Match 100.0%; Score 112; DB 17; Length 242;  
Best Local Similarity 100.0%; Pred. No. 4.1e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADNGTIVTEELKQLEOMNLV 22  
DB 22 MADNGTIVTEELKQLEOMNLV 43  
RESULT 10  
US-10-839-729-46  
; Sequence 46, Application US/10839729  
; Publication No. US2005002953A1  
; GENERAL INFORMATION:  
; APPLICANT: JENS Herold  
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES  
; FILE REFERENCE: BIOBANK 013A  
; CURRENT APPLICATION NUMBER: US/10/839,729  
; CURRENT FILING DATE: 2004-05-04  
; PRIOR APPLICATION NUMBER: 60/468703  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically prepared polypeptide sequence  
US-10-839-729-46

Query Match 65.2%; Score 73; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00083;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADNGTIVTEELKQLEOMNLV 15  
DB 1 MADNGTIVTEELKQLEOMNLV 15  
RESULT 11  
US-10-425-114-69487  
; Sequence 69487, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, JINGDONG  
; APPLICANT: ZHOU, YIHUA  
; APPLICANT: KOVALIC, DAVID K.  
; APPLICANT: SCREEN, STEVEN E.  
; APPLICANT: TABAKA, JACK B.  
; APPLICANT: CAO, YONGWEI  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 69487  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLB73003G04\_FLI.pep  
US-10-425-114-69487  
Query Match 47.8%; Score 53.5; DB 15; Length 336;  
Best Local Similarity 57.1%; Pred. No. 19;  
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;  
QY 4 NGTIVTEELKQLEOMNLV 21  
DB 196 NGTIVTEELKQLEOMNLV 216  
RESULT 12  
US-10-437-963-158994  
; Sequence 158994, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: LA ROSA, THOMAS J.  
; APPLICANT: KOVALIC, DAVID K.  
; APPLICANT: ZHOU, YIHUA  
; APPLICANT: CAO, YONGWEI  
; APPLICANT: WU, WEI  
; APPLICANT: BOKHAROV, ANDREY A.  
; APPLICANT: BARDAZUK, BRAD  
; APPLICANT: LI, PING  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 158994  
; LENGTH: 486  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_58414C.1.pep  
US-10-437-963-158994  
Query Match 47.8%; Score 53.5; DB 16; Length 486;  
Best Local Similarity 57.1%; Pred. No. 29;  
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 4 NGTITVEELKQLEQ---WNL 21  
||||:||||| | : |  
Db 346 NGTISLEELKQALAKDVPWRL 366

## RESULT 13

US-10-437-963-158996  
; Sequence 158996, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; PRIOR FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 158996  
; LENGTH: 512  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_58416C.1.pcp  
US-10-437-963-158996

Query Match 47.8%; Score 53.5; DB 16; Length 512;  
Best Local Similarity 57.1%; Pred. No. 30;  
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 4 NGTITVEELKQLEQ---WNL 21  
||||:||||| | : |  
Db 372 NGTISLEELKQALAKDVPWRL 392

## RESULT 14

US-10-425-114-57880  
; Sequence 57880, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jindong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; PRIOR FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 57880  
; LENGTH: 523  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17084F11\_FLI.pcp  
US-10-425-114-57880

Query Match 47.8%; Score 53.5; DB 15; Length 523;  
Best Local Similarity 57.1%; Pred. No. 31;  
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 4 NGTITVEELKQLEQ---WNL 21  
||||:||||| | : |

Db 383 NGTISLEELKQALAKDVPWRL 403

## RESULT 15

US-10-369-294-11  
; Sequence 11, Application US/10369294  
; Publication No. US20030162170A1  
; GENERAL INFORMATION:  
; APPLICANT: Hahn, Beatrice H.  
; APPLICANT: Gao, Feng  
; APPLICANT: Marx, Preston A.  
; APPLICANT: Shaw, George M.  
; APPLICANT: Smith, Stephen M.  
; APPLICANT: Georges-Courbot, Marie Claude  
; APPLICANT: Lu, Chang Yong  
; TITLE OF INVENTION: Complete Genome Sequences of a Simian  
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped  
; FILE REFERENCE: D6286D  
; CURRENT APPLICATION NUMBER: US/10/369,294  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 09/206,551  
; PRIOR FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 11  
; LENGTH: 855  
; TYPE: PRT  
; ORGANISM: Simian immunodeficiency virus  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of homologous region of  
; OTHER INFORMATION: A\_U455 lentiviral env protein  
US-10-369-294-11

Query Match 46.0%; Score 51.5; DB 14; Length 855;  
Best Local Similarity 43.5%; Pred. No. 1.le+02;  
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 MADNGTITVE-BLKQLEQWNLV 22  
||||:||||| | : |  
Db 401 MCPNGTITLQCRKIKIIMMQRV 423

## RESULT 16

US-10-369-294-12  
; Sequence 12, Application US/10369294  
; Publication No. US20030162170A1  
; GENERAL INFORMATION:  
; APPLICANT: Hahn, Beatrice H.  
; APPLICANT: Gao, Feng  
; APPLICANT: Marx, Preston A.  
; APPLICANT: Shaw, George M.  
; APPLICANT: Smith, Stephen M.  
; APPLICANT: Georges-Courbot, Marie Claude  
; APPLICANT: Lu, Chang Yong  
; TITLE OF INVENTION: Complete Genome Sequences of a Simian  
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped  
; FILE REFERENCE: D6286D  
; CURRENT APPLICATION NUMBER: US/10/369,294  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 09/206,551  
; PRIOR FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 12  
; LENGTH: 855  
; TYPE: PRT  
; ORGANISM: Simian immunodeficiency virus  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of homologous region of  
; OTHER INFORMATION: B\_HXB2R lentiviral env protein  
US-10-369-294-12

Query Match 46.0%; Score 51.5; DB 14; Length 855;  
Best Local Similarity 43.5%; Pred. No. 1.le+02;  
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Best Local Similarity 43.5%; Pred. No. 1.1e+02;  
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 MADNGTIVTEELKQLEQNNLV 22  
Db 401 MGPNGITTLQCRIRKQITNMQRV 423

RESULT 17  
US-09-864-761-39008  
; Sequence 39008, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 39008  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC004837.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.6  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6  
; OTHER INFORMATION: SWISSPROT HIT: P11233, EVALU 5.00e-25  
; OTHER INFORMATION: EST\_HUMAN HIT: A1344679.1, EVALU 6.00e-24  
US-09-864-761-39008

Query Match 45.5%; Score 51; DB 9; Length 54;  
Best Local Similarity 42.9%; Pred. No. 5.5;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MADNGTIVTEELKQLEQNNLV 21  
Db 23 LEDKQVSYVEAKNRARQNNV 43

RESULT 18  
US-09-873-546-10  
; Sequence 10, Application US/09873546  
; Publication No. US20030059771A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Geoff  
; APPLICANT: Ellis, Chad  
; APPLICANT: Vos, Michelle  
; TITLE OF INVENTION: Rtg. No. US20030059771A1el Ras-Related Gene  
; FILE REFERENCE: NIH-05080  
; CURRENT APPLICATION NUMBER: US/09/873,546  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-873-546-10

Query Match 45.5%; Score 51; DB 10; Length 206;  
Best Local Similarity 42.9%; Pred. No. 25;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MADNGTIVTEELKQLEQNNLV 21  
Db 131 LEDKQVSYVEAKNRARQNNV 151

RESULT 19  
US-10-153-668-214  
; Sequence 214, Application US/10153668  
; Publication No. US20030092616A1  
; GENERAL INFORMATION:  
; APPLICANT: HONDA, Goichi  
; APPLICANT: MATSUDA, Akio  
; APPLICANT: MURAMATSU, Shuji  
; APPLICANT: ISHIZAWA, Kenya  
; TITLE OF INVENTION: STAT6 Activating Gene  
; FILE REFERENCE: 1254-0207P  
; CURRENT APPLICATION NUMBER: US/10/153,668  
; CURRENT FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: US 60/293,172  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/316,031  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/328,403  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: JP 2001-157043  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: JP 2001-260681  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: JP 2001-313175  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 488  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 214  
; LENGTH: 206  
; TYPE: PRT





Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MADNGTIVTEELKQLEQNNL 21  
: ||||| |||||  
Db 131 LEDKQVSVSEAKNRRAEQNNV 151

RESULT 23  
US-10-408-765A-2022  
; Sequence 2022, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Bojn D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2022  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-2022

Query Match 45.5%; Score 51; DB 16; Length 206;  
Best Local Similarity 42.9%; Pred. No. 25;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQNNL 21  
: ||||| |||||  
Db 131 LEDKQVSVSEAKNRRAEQNNV 151

RESULT 24  
US-10-804-491-48  
; Sequence 48, Application US/10804491  
; Publication No. US20040180375A1  
; GENERAL INFORMATION:  
; APPLICANT: Cismowski, Mary  
; APPLICANT: Duzic, Emir  
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor  
; FILE REFERENCE: 60388-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/804,491  
; CURRENT FILING DATE: 2004-03-19  
; PRIOR APPLICATION NUMBER: US/03/709,103  
; PRIOR FILING DATE: 2000-11-08  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-804-491-48

Query Match 45.5%; Score 51; DB 16; Length 206;  
Best Local Similarity 42.9%; Pred. No. 25;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQNNL 21  
: ||||| |||||  
Db 131 LEDKQVSVSEAKNRRAEQNNV 151

RESULT 25  
US-10-231-913-66

; Sequence 66, Application US/10231913  
; Publication No. US20040005576A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Xiaojia S.  
; APPLICANT: Li, Li  
; APPLICANT: Baturajan, Meera  
; APPLICANT: Shinkets, Richard A.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Malyanar, Uriel M.  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vernet, Corine A.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Alsdbrook II, John P.  
; APPLICANT: Edinger, Schlomit  
; APPLICANT: Peyman, John A.  
; APPLICANT: Stone, David J.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Gangolli, Bsha A.  
; APPLICANT: Boldog, Ference L.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Eissen, Andrew J.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Radigaru, Muralidhara  
; APPLICANT: Spaderna, Steven K.  
; APPLICANT: Zerhusen, Bryan D.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-216  
; CURRENT APPLICATION NUMBER: US/10/231,913  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: 60/251,660  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: 60/255,029  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/260,326  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/263,800  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/269,942  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/286,183  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: 60/313,627  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/318,712  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 292  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-231-913-66

Query Match 45.5%; Score 51; DB 15; Length 209;  
Best Local Similarity 42.9%; Pred. No. 26;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVTEELKQLEQNNL 21  
: ||||| |||||  
Db 134 LEDKQVSVSEAKNRRAEQNNV 154

RESULT 26  
US-10-282-122A-51593  
; Sequence 51593, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl

APPLICANT: Zykkind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Foreyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITPA.03A  
CURRENT APPLICATION NUMBER: US/10/282.122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 51593  
LENGTH: 351  
TYPE: PRT  
ORGANISM: Clostridium acetobutylicum  
US-10-282-122A-51593

Query Match 45.5%; Score 51; DB 15; Length 351;  
Best Local Similarity 42.1%; Pred. No. 46;  
Matches 8; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 4 NGTIVBELKQLEQWNLV 22

DB 132 NGELSTBELKQWMDASIV 150

RESULT 27  
US-10-424-599-219887  
Sequence 219887, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO: 219887  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_40586C.1.pep  
US-10-424-599-219887

Query Match 44.6%; Score 50; DB 15; Length 92;

Best Local Similarity 47.4%; Pred. No. 14;  
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 DNGITVEBELKQLEQWNL 21

DB 25 NSGFTTVEBELQALREYRM 43

RESULT 28  
US-10-437-963-186189  
Sequence 186189, Application US/10437963  
Publication No. US2004012343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO: 186189  
LENGTH: 174  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_83010C.1.pep  
US-10-437-963-186189

Query Match 44.6%; Score 50; DB 16; Length 174;  
Best Local Similarity 55.6%; Pred. No. 29;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 NGTIVBELKQLEQWNL 21

DB 119 NGVITAEELRLRLRLNL 136

RESULT 29  
US-10-417-700A-49  
Sequence 49, Application US/10417700A  
Publication No. US2004003581A1  
GENERAL INFORMATION:  
APPLICANT: ECOPIA BIOSCIENCES INC.  
APPLICANT: ZAZOROUTOS, Emmanuel  
APPLICANT: STAFPA, Alfredo  
APPLICANT: FARNET, Chris  
TITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribosome  
TITLE OF INVENTION: Peptide synthetase systems  
FILE REFERENCE: 3002-14US  
CURRENT APPLICATION NUMBER: US/10/417,700A  
CURRENT FILING DATE: 2003-04-17  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 49  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Pseudomonas syringae pv. syringae strain B301D  
US-10-417-700A-49

Query Match 44.6%; Score 50; DB 15; Length 469;  
Best Local Similarity 64.3%; Pred. No. 89;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 ITVEELKQLEQWNL 20

DB 432 LPLNERKQLEQWNL 445

```
RESULT 30
US-10-424-599-203557
; Sequence 203557, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 203557
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25838C.1.pep
US-10-424-599-203557

Query Match          44.6%; Score 50; DB 15; Length 546;
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLEQWNL 21
Db 477 NSGFITTELEQLAREYNM 495

RESULT 31
US-10-425-114-54704
; Sequence 54704, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54704
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-GWFL02220063C09_FLI.pep
US-10-425-114-54704

Query Match          44.6%; Score 50; DB 15; Length 549;
Best Local Similarity 47.4%; Pred. No. 1.1e+02;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 DNGTIVEELKQLEQWNL 21
Db 480 NSGFITTELEQLAREYNM 498

RESULT 32
US-10-282-122A-76721
; Sequence 76721, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76721
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Ureaplasma urealyticum
US-10-282-122A-76721

Query Match          44.6%; Score 50; DB 15; Length 673;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 VEELKQLEQWNL 20
Db 8 IDELKQKLDQWNL 19

RESULT 33
US-09-953-348-132
; Sequence 132, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingqiang
; APPLICANT: Varoglu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.5300S1
; CURRENT APPLICATION NUMBER: US/09/953,348
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/06394
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/266965
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 153
```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 123
; TYPE: PRF
; ORGANISM: Streptomyces lavendulae
; US-09-953-348-132

```

```

Query Match      43.8%; Score 49; DB 10; Length 123;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      4 NGTIVTEELKQLE 17
      |||:||||:|
Db      86 NGTVPEELREWE 99

```

```

RESULT 34
US-10-267-255-132
; Sequence 132, Application US/10267255
; Publication No. US20030124689A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600,456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/624,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 132
; LENGTH: 123
; TYPE: PRF
; ORGANISM: Streptomyces lavendulae
; US-10-267-255-132

```

```

Query Match      43.8%; Score 49; DB 14; Length 123;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      4 NGTIVTEELKQLE 17
      |||:||||:|
Db      86 NGTVPEELREWE 99

```

```

RESULT 35
US-10-231-913-63
; Sequence 63, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patnurajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Sheno, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.

```

```

; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangoli, Baha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eissen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Zernusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 206
; TYPE: PRF
; ORGANISM: Mus musculus
; US-10-231-913-63

```

```

Query Match      42.9%; Score 48; DB 15; Length 206;
Best Local Similarity 38.1%; Pred. No. 69;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      1 MADNGTIVTEELKQLEQNNL 21
      :|||:||||:|
Db      131 LEDKQVSYEAKNRADQNNV 151

```

```

RESULT 36
US-10-231-913-65
; Sequence 65, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patnurajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Sheno, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangoli, Baha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eissen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara

```

APPLICANT: Spaderma, Steven K.  
APPLICANT: Zehrusen, Bryan D.  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-216  
CURRENT APPLICATION NUMBER: US/10/231,913  
CURRENT FILING DATE: 2002-08-30  
PRIOR APPLICATION NUMBER: 60/251,660  
PRIOR FILING DATE: 2000-12-06  
PRIOR APPLICATION NUMBER: 60/255,029  
PRIOR FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/260,326  
PRIOR FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: 60/263,800  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/269,942  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/286,183  
PRIOR FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: 60/313,627  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: 60/318,712  
PRIOR FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 292  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 65  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-231-913-65

Query Match 42.9%; Score 48; DB 15; Length 206;  
Best Local Similarity 38.1%; Pred. No. 69;  
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQNL 21  
DB 131 LEDKQVSYEAKSRADQNV 151

RESULT 37  
US-10-231-913-67  
Sequence 67, Application US/10231913  
Publication No. US20040005576A1  
GENERAL INFORMATION:  
APPLICANT: Guo, Xiaojia S.  
APPLICANT: Li, Li  
APPLICANT: Patuturajan, Meera  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Malyanekar, Uriel M.  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Vernet, Corine A.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Alsobrook II, John P.  
APPLICANT: Edinger, Schlomilt  
APPLICANT: Peyman, John A.  
APPLICANT: Stone, David J.  
APPLICANT: Ellertman, Karen  
APPLICANT: Ganggoli, Esha A.  
APPLICANT: Boldog, Ference L.  
APPLICANT: Colman, Steven D.  
APPLICANT: Bisen, Andrew J.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Spaderma, Steven K.  
APPLICANT: Zehrusen, Bryan D.  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-216  
CURRENT APPLICATION NUMBER: US/10/231,913  
CURRENT FILING DATE: 2002-08-30  
PRIOR APPLICATION NUMBER: 60/251,660  
PRIOR FILING DATE: 2000-12-06

PRIOR APPLICATION NUMBER: 60/255,029  
PRIOR FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/260,326  
PRIOR FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: 60/263,800  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/269,942  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/286,183  
PRIOR FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: 60/313,627  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: 60/318,712  
PRIOR FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 292  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 67  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Xenopus laevis  
US-10-231-913-67

Query Match 42.9%; Score 48; DB 15; Length 206;  
Best Local Similarity 38.1%; Pred. No. 69;  
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADNGTIVBELKQLEQNL 21  
DB 131 LEDKQVSYEAKSRADQNV 151

RESULT 38  
US-10-437-963-124248  
Sequence 124248, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharirov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 36-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 124248  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_27005C.1.pap  
US-10-437-963-124248

Query Match 42.9%; Score 48; DB 16; Length 299;  
Best Local Similarity 58.8%; Pred. No. 16+02;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 DNGTIVBELKQLEQNL 19  
DB 281 DSGTIVBELKQLEQNL 297

RESULT 39  
US-10-369-493-10440  
Sequence 10440, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei

```

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10440
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10440
```

```

Query Match          42.9%; Score 48; DB 15; Length 401;
Best Local Similarity 46.7%; Pred. No. 1.5e+02;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 GTTVEELKQLLEQW 19
DB      184 GNVTLQVKKLSKRW 198
```

```

RESULT 40
US-10-314-657-45
; Sequence 45; Application US/10314657
; Publication No. US20030175888A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, Ben
; APPLICANT: CHENG, Yi-Qiang
; APPLICANT: TANG, Gong-Li
; TITLE OF INVENTION: Discrete Acyltransferases Associated with Type I Polyketide
; FILE REFERENCE: 054030-0021
; CURRENT APPLICATION NUMBER: US/10/314,657
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: PCT/US02/08937
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/278,935
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 4437
; TYPE: PRT
; ORGANISM: Streptomyces atroolivaceus
US-10-314-657-45
```

```

Query Match          42.9%; Score 48; DB 14; Length 4437;
Best Local Similarity 42.1%; Pred. No. 2.2e+03;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      2 ADNGTIVBELKQLLEQW 20
DB      949 ADDEVRGAEHLKILHEWN 967
```

```

RESULT 41
US-10-473-193-45
; Sequence 45; Application US/10473193
; Publication No. US20050080247A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; APPLICANT: TANG, Gong-Li
; APPLICANT: CHENG, Yi-Qiang
; APPLICANT: TANG, Gong-Li
; TITLE OF INVENTION: LEIHAMCIN BIOSYNTHESIS GENE CLUSTER AND ITS COMPONENTS AND THEIR
; FILE REFERENCE: 309T-000110US
; CURRENT APPLICATION NUMBER: US/10/473,193
```

```

; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/278,935
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/US02/08937
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 4437
; TYPE: PRT
; ORGANISM: Streptomyces atroolivaceus
US-10-473-193-45
```

```

Query Match          42.9%; Score 48; DB 17; Length 4437;
Best Local Similarity 42.1%; Pred. No. 2.2e+03;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      2 ADNGTIVBELKQLLEQW 20
DB      949 ADDEVRGAEHLKILHEWN 967
```

```

RESULT 42
US-10-429-812-4
; Sequence 4; Application US/10429812
; Publication No. US20040003432A1
; GENERAL INFORMATION:
; APPLICANT: Obukowicz, Mark
; TITLE OF INVENTION: THE PRODUCTION OF HEXOSAMINES AND USES THEREFORE
; FILE REFERENCE: 18438/09004
; CURRENT APPLICATION NUMBER: US/10/429,812
; CURRENT FILING DATE: 2003-05-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-429-812-4
```

```

Query Match          42.0%; Score 47; DB 15; Length 159;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      5 GTTVEELKQLLEQW 20
DB      31 GTTPESFSLIKIKYWN 46
```

```

RESULT 43
US-10-612-779-30
; Sequence 30; Application US/10612779
; Publication No. US20040091976A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Ming-De
; APPLICANT: Angerer, J. David
; APPLICANT: Cyron, Don
; APPLICANT: Grund, Alan
; APPLICANT: Jerrell Jr., Thomas
; APPLICANT: Leanna, Candice
; APPLICANT: Mathre, Owen
; APPLICANT: Rosson, Reinhardt
; APPLICANT: Running, Jeff
; APPLICANT: Severson, Dave
; APPLICANT: Song, Linsheng
; APPLICANT: Wassink, Sarah
; TITLE OF INVENTION: Process and Materials for Production of Glucosamine and N-Acetylte
; FILE REFERENCE: 3161-18-2
; CURRENT APPLICATION NUMBER: US/10/612,779
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 60/393,348
; PRIOR FILING DATE: 2002-07-01
```

NUMBER OF SEQ ID NOS: 137  
 SOFTWARE: Patent version 3.1  
 SEQ ID NO 30  
 LENGTH: 159  
 TYPE: PRT  
 ORGANISM: Saccharomyces cerevisiae  
 US-10-612-779-30

Query Match 42.0%; Score 47; DB 15; Length 159;  
 Best Local Similarity 50.0%; Pred. No. 71;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTTVEELKQLLEQWN 20  
 Db 31 GTTPESFSKLIRKWN 46

RESULT 44  
 US-10-823-397-33

Sequence 33, Application US/10823397  
 Publication No. US20050042735A1  
 GENERAL INFORMATION:

APPLICANT: McMullin, Thomas  
 APPLICANT: Ding, Ming-De  
 APPLICANT: Grund, Alan

TITLE OF INVENTION: Metabolic Engineering for Enhanced Production of Chitin and  
 TITLE OF INVENTION: Chitosan in Microorganisms

FILE REFERENCE: 3161-18-3  
 CURRENT APPLICATION NUMBER: US/10/823,397

CURRENT FILING DATE: 2004-04-12  
 PRIOR APPLICATION NUMBER: 60/462,087

PRIOR FILING DATE: 2003-04-11  
 NUMBER OF SEQ ID NOS: 59

SOFTWARE: Patent version 3.2  
 SEQ ID NO 33

LENGTH: 159  
 TYPE: PRT

ORGANISM: Saccharomyces cerevisiae  
 US-10-823-397-33

Query Match 42.0%; Score 47; DB 17; Length 159;  
 Best Local Similarity 50.0%; Pred. No. 71;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTTVEELKQLLEQWN 20  
 Db 31 GTTPESFSKLIRKWN 46

RESULT 45  
 US-10-686-947-238

Sequence 238, Application US/10686947  
 Publication No. US20040162420A1  
 GENERAL INFORMATION:

APPLICANT: Profigen Inc.  
 APPLICANT: Profigen Inc.

TITLE OF INVENTION: Cloning of Cytochrome P450 Genes from Tobacco  
 FILE REFERENCE: 79601

CURRENT APPLICATION NUMBER: US/10/686,947  
 CURRENT FILING DATE: 2003-10-16

PRIOR APPLICATION NUMBER: US 10/387346  
 PRIOR FILING DATE: 2003-03-12

NUMBER OF SEQ ID NOS: 298  
 SOFTWARE: Patent version 3.2

SEQ ID NO 238  
 LENGTH: 508

TYPE: PRT  
 ORGANISM: NICOTIANATABACUM

US-10-686-947-238

Query Match 42.0%; Score 47; DB 16; Length 508;  
 Best Local Similarity 47.1%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 6 TTTVEELKQLLEQWNLY 22  
 Db 196 TVRVEDLYLVDMQWFL 212

RESULT 46  
 US-10-686-947-266

Sequence 266, Application US/10686947  
 Publication No. US20040162420A1  
 GENERAL INFORMATION:

APPLICANT: Profigen Inc.  
 APPLICANT: Profigen Inc.

TITLE OF INVENTION: Cloning of Cytochrome P450 Genes from Tobacco  
 FILE REFERENCE: 79601

CURRENT APPLICATION NUMBER: US/10/686,947  
 CURRENT FILING DATE: 2003-10-16

PRIOR APPLICATION NUMBER: US 10/387346  
 PRIOR FILING DATE: 2003-03-12

NUMBER OF SEQ ID NOS: 298  
 SOFTWARE: Patent version 3.2

SEQ ID NO 266  
 LENGTH: 508

TYPE: PRT  
 ORGANISM: NICOTIANATABACUM

US-10-686-947-266

Query Match 42.0%; Score 47; DB 16; Length 508;  
 Best Local Similarity 47.1%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 6 TTTVEELKQLLEQWNLY 22  
 Db 196 TVRVEDLYLVDMQWFL 212

RESULT 47  
 US-10-686-947-240

Sequence 240, Application US/10686947  
 Publication No. US20040162420A1  
 GENERAL INFORMATION:

APPLICANT: Profigen Inc.  
 APPLICANT: Profigen Inc.

TITLE OF INVENTION: Cloning of Cytochrome P450 Genes from Tobacco  
 FILE REFERENCE: 79601

CURRENT APPLICATION NUMBER: US/10/686,947  
 CURRENT FILING DATE: 2003-10-16

PRIOR APPLICATION NUMBER: US 10/387346  
 PRIOR FILING DATE: 2003-03-12

NUMBER OF SEQ ID NOS: 298  
 SOFTWARE: Patent version 3.2

SEQ ID NO 240  
 LENGTH: 509

TYPE: PRT  
 ORGANISM: NICOTIANATABACUM

US-10-686-947-240

Query Match 42.0%; Score 47; DB 16; Length 509;  
 Best Local Similarity 47.1%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 6 TTTVEELKQLLEQWNLY 22  
 Db 197 TVRVEDLYLVDMQWFL 213

RESULT 48  
 US-10-369-493-2600

Sequence 2600, Application US/10369493  
 Publication No. US2003023675A1  
 GENERAL INFORMATION:

APPLICANT: Cao, Yongwei  
 APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.  
 APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng



```

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2600
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Synechocystis sp.
US-10-369-493-2600

Query Match      42.0%; Score 47; DB 15; Length 659;
Best Local Similarity 56.2%; Pred. NO. 3.6e+02;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      4 NGTTVEELKQLEOW 19
DB      633 NGQITLESRRLLDGY 648

RESULT 49
US-10-156-761-14515
; Sequence 14515, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14515
; LENGTH: 987
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14515

Query Match      42.0%; Score 47; DB 14; Length 987;
Best Local Similarity 50.0%; Pred. NO. 5.6e+02;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 ADNGTIVBELKQLEOW 19
DB      652 ADGDEIDVEDLRKRIEY 669

RESULT 50
US-10-282-122A-77230
; Sequence 77230, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```

```

; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77230
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77230

```

```

Query Match      41.5%; Score 46.5; DB 15; Length 428;
Best Local Similarity 42.9%; Pred. NO. 2.6e+02;
Matches 9; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY      1 MADNGTIVBELKQLEOW 20
DB      107 LADSGVAVEVSLKMLQYWH 127

```

Search completed: May 11, 2005, 21:43:28  
Job time : 100.66 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using bw model

Run on: May 11, 2005, 21:05:14 ; Search time 133.511 Seconds

(without alignments)  
72.421 Million cell updates/sec

Title: US-10-712-812-6

Perfect score: 127  
Sequence: 1 KKKMADNGRTVEELKLEQNNLV 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : A.Geneseq\_16Dec04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	112	88.2	221	8	AD195325
2	55	43.3	54	4	AD195325
3	55	43.3	54	4	AD195325
4	55	43.3	54	4	AD195325
5	55	43.3	54	4	AD195325
6	55	43.3	54	4	AD195325
7	55	43.3	54	4	AD195325
8	55	43.3	54	4	AD195325
9	55	43.3	54	4	AD195325
10	55	43.3	54	4	AD195325
11	55	43.3	54	4	AD195325
12	55	43.3	54	4	AD195325
13	55	43.3	54	4	AD195325
14	55	43.3	54	4	AD195325
15	55	43.3	54	4	AD195325
16	55	43.3	54	4	AD195325
17	55	43.3	54	4	AD195325
18	55	43.3	54	4	AD195325
19	55	43.3	54	4	AD195325
20	55	43.3	54	4	AD195325
21	55	43.3	54	4	AD195325
22	55	43.3	54	4	AD195325
23	55	43.3	54	4	AD195325
24	55	43.3	54	4	AD195325
25	55	43.3	54	4	AD195325

26	51	40.2	217	6	AAE34443	AAE34443 Human lip
27	51	40.2	224	4	AAE62621	AAE62621 Human SNR
28	51	40.2	224	6	ABU00236	ABU00236 Human nov
29	51	40.2	572	2	AAW68488	AAW68488 Mouse Utl
30	51	40.2	626	5	ABR49107	ABR49107 Listeria
31	51	40.2	626	6	ABU32651	ABU32651 Protein e
32	50	39.4	100	3	AAE02044	AAE02044 Human sec
33	50	39.4	300	6	ADA12194	ADA12194 Actinocoba
34	50	39.4	300	7	AAE39415	AAE39415 Actinocoba
35	50	39.4	469	7	ADG33790	ADG33790 Actinomyc
36	50	39.4	516	4	AAE35470	AAE35470 Human cyc
37	50	39.4	534	8	ABM83406	ABM83406 Human dia
38	50	39.4	536	2	AAW95110	AAW95110 Human RPM
39	50	39.4	536	8	ADAE8253	ADAE8253 Human pro
40	50	39.4	536	8	ADAE8253	ADAE8253 Human pro
41	50	39.4	536	8	ADAE8253	ADAE8253 Human pro
42	50	39.4	537	8	ADAE8253	ADAE8253 Human pro
43	50	39.4	545	3	AAE19080	AAE19080 Amino ac
44	50	39.4	554	6	ABM83407	ABM83407 Human dia
45	50	39.4	673	6	ABU48797	ABU48797 Protein e
46	50	39.4	808	7	ADAE4170	ADAE4170 Human pro
47	50	39.4	867	7	ADAE1288	ADAE1288 Novel hum
48	50	39.4	1803	5	ABE77072	ABE77072 Euglena g
49	50	39.4	1805	5	ABE77072	ABE77072 Euglena g
50	50	39.4	2000	8	ADAE4333	ADAE4333 Anticpso
51	50	39.4	2472	7	ADAE5535	ADAE5535 Rat prote
52	50	39.4	2472	7	ADAE5535	ADAE5535 Rat prote
53	50	39.4	2472	7	ADAE5535	ADAE5535 Rat prote
54	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
55	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
56	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
57	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
58	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
59	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
60	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
61	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
62	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
63	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
64	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
65	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
66	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
67	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
68	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
69	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
70	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
71	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
72	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
73	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
74	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
75	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
76	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
77	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
78	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
79	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
80	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
81	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
82	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
83	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
84	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
85	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
86	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
87	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
88	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
89	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
90	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
91	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
92	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
93	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
94	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
95	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
96	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
97	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
98	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
99	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote
100	50	39.4	2477	7	ADAE5535	ADAE5535 Rat prote

99	48	37.8	1297	2	AY08403	May08403 C. elegan	172	46	36.2	974	6	ABU41895	Abu41895 Protein e
100	48	37.8	1297	7	ADB85337	Abd85337 C. elegan	173	46	36.2	998	7	ABO70704	AbO70704 Pseudomon
101	48	37.8	1297	6	ABU11384	Abu11384 Protein e	174	46	36.2	1052	3	AA063355	AA063355 Rat subti
102	47.5	37.4	114	4	ABM70970	Abm70970 Drosophil	175	46	36.2	1062	8	ADP25429	ADP25429 Plasmodiu
103	47	37.0	215	7	ADM25823	Adm25823 Hyperther	176	45.5	35.8	422	6	ABU50276	ABU50276 Protein e
104	47	37.0	608	2	AA106783	AA106783 M. grisea	177	45.5	35.8	759	6	ABM70917	ABM70917 StraphyLoc
105	47	37.0	659	8	ADN19947	Adn19947 Bacterial	178	45	35.4	106	5	ABP30657	ABP30657 Streptoco
106	47	37.0	955	3	AA030852	AA030852 Arabidops	179	45	35.4	106	5	ABP30640	ABP30640 Streptoco
107	47	37.0	1058	3	AA030851	AA030851 Arabidops	180	45	35.4	114	7	ADC69973	ADC69973 E. faeciu
108	47	37.0	1198	3	AA030850	AA030850 Arabidops	181	45	35.4	119	8	ADL04570	ADL04570 M. catarr
109	46.5	36.6	403	4	AAU54649	AAU54649 Propionib	182	45	35.4	150	5	ABR92496	ABR92496 Helicoba
110	46.5	36.6	403	6	ABM51168	ABM51168 Propionib	183	45	35.4	151	5	ABU52093	ABU52093 Helicoba
111	46.5	36.6	428	6	ABU9306	ABU9306 Protein e	184	45	35.4	205	5	ABU50891	ABU50891 Helicoba
112	46.5	36.6	849	3	AA096945	AA096945 HIV synth	185	45	35.4	210	4	AAE07899	AAE07899 Diphtheri
113	46	36.2	189	5	ABG59978	ABG59978 Human DIT	186	45	35.4	210	6	AAE35688	AAE35688 Corynebact
114	46	36.2	210	5	ABU51679	ABU51679 Helicoba	187	45	35.4	215	5	AAU12143	AAU12143 Brassaica
115	46	36.2	216	4	AA082765	AA082765 S. epider	188	45	35.4	216	5	AAU12142	AAU12142 Brassaica
116	46	36.2	216	6	ABJ19037	Abj19037 Pathogen	189	45	35.4	216	5	ABU51709	ABU51709 Helicoba
117	46	36.2	253	8	ADQ37007	Adq37007 Cell prol	190	45	35.4	241	5	ABU52152	ABU52152 Helicoba
118	46	36.2	253	8	ADQ15677	Adq15677 Rice stre	191	45	35.4	242	8	ABM83829	ABM83829 Human dta
119	46	36.2	258	2	AA047099	AA047099 Amino aci	192	45	35.4	255	6	ABP97859	ABP97859 Amino aci
120	46	36.2	274	5	ABP40434	ABP40434 Staphyloc	193	45	35.4	255	6	ABP97806	ABP97806 Carrier p
121	46	36.2	274	8	ADSO5966	ADSO5966 Staphyloc	194	45	35.4	260	5	AAE16385	AAE16385 Human deo
122	46	36.2	296	4	AA082555	AA082555 Human pro	195	45	35.4	260	6	AAO26448	AAO26448 Deoxycyti
123	46	36.2	385	3	AA034981	AA034981 Arabidops	196	45	35.4	260	6	AAO26449	AAO26449 Deoxycyti
124	46	36.2	394	5	ABG93276	ABG93276 C. albica	197	45	35.4	260	6	AAO26446	AAO26446 Deoxycyti
125	46	36.2	398	3	AA023096	AA023096 Arabidops	198	45	35.4	260	6	AAO26447	AAO26447 Deoxycyti
126	46	36.2	401	5	ABU51322	ABU51322 Helicoba	199	45	35.4	260	7	ADJ68602	ADJ68602 Human hea
127	46	36.2	415	5	ABU52179	ABU52179 Helicoba	200	45	35.4	260	7	ADN95414	ADN95414 Human BEC
128	46	36.2	420	3	AA034980	AA034980 Arabidops	201	45	35.4	260	8	ADR73958	ADR73958 Human deo
129	46	36.2	433	3	AA023095	AA023095 Arabidops	202	45	35.4	260	8	ADR73962	ADR73962 Human deo
130	46	36.2	460	4	AAE05398	AAE05398 Human int	203	45	35.4	273	8	ADR04184	ADR04184 E. faecium
131	46	36.2	460	4	AAE05403	AAE05403 Human IRA	204	45	35.4	276	2	AAW89994	AAW89994 Expressed
132	46	36.2	460	5	AAE05404	AAE05404 Human IRA	205	45	35.4	277	6	ABU29809	ABU29809 Protein e
133	46	36.2	460	5	AAE24859	AAE24859 Human IRA	206	45	35.4	317	8	ADK28295	ADK28295 Human KXP
134	46	36.2	460	5	AAE24865	AAE24865 Human IRA	207	45	35.4	317	8	ABM83828	ABM83828 Human dta
135	46	36.2	460	5	AAE38908	AAE38908 Human IRA	208	45	35.4	325	6	ABP97865	ABP97865 RSV G pro
136	46	36.2	460	5	AAE38902	AAE38902 Human IL-	209	45	35.4	325	6	ABP97809	ABP97809 G protein
137	46	36.2	460	6	ABR44401	ABR44401 Human IL-	210	45	35.4	329	8	ABO58567	ABO58567 Human gen
138	46	36.2	460	8	AD044001	AD044001 Amino aci	211	45	35.4	360	5	ABP26080	ABP26080 Streptoco
139	46	36.2	477	2	AA040993	AA040993 H. pylori	212	45	35.4	361	6	ABP97862	ABP97862 RSV G pro
140	46	36.2	480	5	ABP66120	ABP66120 Bifidobac	213	45	35.4	376	6	ADA34683	ADA34683 Acinetoba
141	46	36.2	512	6	AAE38226	AAE38226 Human enz	214	45	35.4	377	3	AA020649	AA020649 Arabidops
142	46	36.2	514	2	AAE33337	AAE33337 HyPB prot	215	45	35.4	377	3	AA045918	AA045918 Arabidops
143	46	36.2	544	2	AAE73383	AAE73383 C. psittaci	216	45	35.4	384	5	ABU51926	ABU51926 Helicoba
144	46	36.2	544	2	AAW10975	AAW10975 Chlamydia	217	45	35.4	386	6	ABP97868	ABP97868 Amino aci
145	46	36.2	544	2	AAW11863	AAW11863 Polypepti	218	45	35.4	387	7	ADJ81609	ADJ81609 Chimeric
146	46	36.2	544	2	AAW11735	AAW11735 Amino aci	219	45	35.4	387	7	ADG32242	ADG32242 Mutant B_
147	46	36.2	544	2	AAE11757	AAE11757 Chlamydia	220	45	35.4	398	5	ABU51209	ABU51209 Helicoba
148	46	36.2	544	5	AB094272	AB094272 Chlamydia	221	45	35.4	399	3	AA020648	AA020648 Arabidops
149	46	36.2	544	5	ABG31261	ABG31261 Chlamydia	222	45	35.4	399	3	AA045917	AA045917 Arabidops
150	46	36.2	544	5	ADL97984	ADL97984 C. psittaci	223	45	35.4	401	2	AAW16339	AAW16339 DAB389-SP
151	46	36.2	544	5	ADL97987	ADL97987 C. trachit	224	45	35.4	404	3	AA020647	AA020647 Arabidops
152	46	36.2	544	6	ABU26931	ABU26931 Protein e	225	45	35.4	404	3	AA045916	AA045916 Arabidops
153	46	36.2	544	6	ABU27237	ABU27237 Protein e	226	45	35.4	410	5	ABP30521	ABP30521 Streptoco
154	46	36.2	551	8	ADK29961	ADK29961 Bacterial	227	45	35.4	429	5	ABP26315	ABP26315 Streptoco
155	46	36.2	551	8	ADK41754	ADK41754 Bacterial	228	45	35.4	429	5	ABP29714	ABP29714 Streptoco
156	46	36.2	553	3	AAW68489	AAW68489 Human par	229	45	35.4	440	6	ABP97860	ABP97860 Amino aci
157	46	36.2	572	5	ABG32231	ABG32231 Human Uti	230	45	35.4	440	6	ABP97807	ABP97807 Carrier p
158	46	36.2	572	7	ADP65307	ADP65307 Human dth	231	45	35.4	448	4	AAE07896	AAE07896 Modified
159	46	36.2	572	8	AAQ18668	AAQ18668 Human sof	232	45	35.4	452	2	AAW80217	AAW80217 48 Kda mo
160	46	36.2	577	2	AA032922	AA032922 Amino aci	233	45	35.4	455	2	AAW34055	AAW34055 Modified
161	46	36.2	597	4	ABH58247	ABH58247 Drosophil	234	45	35.4	462	6	AAU25173	AAU25173 Protein e
162	46	36.2	605	8	ADN20888	ADN20888 Bacterial	235	45	35.4	468	1	AA090626	AA090626 51 KD mod
163	46	36.2	605	8	ADN20888	ADN20888 Bacterial	236	45	35.4	469	2	AAW34056	AAW34056 Modified
164	46	36.2	643	6	ABU93109	ABU93109 Protein e	237	45	35.4	472	2	AAW86327	AAW86327 Kidney in
165	46	36.2	704	2	AAW10976	AAW10976 Dihydrofo	238	45	35.4	480	2	AAW80218	AAW80218 51 Kda mo
166	46	36.2	704	2	AAW11864	AAW11864 DHFR/Poly	239	45	35.4	494	4	ABW68783	ABW68783 Drosophil
167	46	36.2	792	6	ABP55389	ABP55389 Human col	240	45	35.4	496	2	AAE35058	AAE35058 Gal4-DT-I
168	46	36.2	959	6	ABU40118	ABU40118 Protein e	241	45	35.4	497	7	ADB64193	ADB64193 Human pro
169	46	36.2	963	4	AAU36226	AAU36226 Pseudomon	242	45	35.4	508	8	ADN10589	ADN10589 Nicotiana
170	46	36.2	963	6	ABU58329	ABU58329 Protein e	243	45	35.4	510	6	ABP97866	ABP97866 RSV G pro
171	46	36.2	964	8	ADK24725	ADK24725 Bacterial	244	45	35.4	510	6	ABP97810	ABP97810 G protein

245	45	35.4	518	2	AA040208	Sequence	318	45	35.4	677	6	AAE35690	AAE35690	TENT-Hc-D
246	45	35.4	528	2	AA044892	AA044892	319	45	35.4	677	6	AAE35691	AAE35691	TENT-Hc-D
247	45	35.4	532	2	AA044890	AA044890	320	45	35.4	685	6	ABJ26041	ABJ26041	Abj26041
248	45	35.4	533	2	AA044891	AA044891	321	45	35.4	778	7	AA039122	AA039122	AA039122
249	45	35.4	533	2	AA044889	AA044889	322	45	35.4	778	7	ADD71161	ADD71161	ADD71161
250	45	35.4	533	2	AA044894	AA044894	323	45	35.4	795	8	ADL98340	ADL98340	ADL98340
251	45	35.4	533	2	AA044899	AA044899	324	45	35.4	799	4	ABG17242	ABG17242	Novel hum
252	45	35.4	533	2	AA044898	AA044898	325	45	35.4	805	4	AA040908	AA040908	Human pol
253	45	35.4	533	2	AA044902	AA044902	326	45	35.4	810	6	AAE35714	AAE35714	TENT-Hc-D
254	45	35.4	533	2	AA044901	AA044901	327	45	35.4	810	6	AAE35715	AAE35715	TENT-Hc-D
255	45	35.4	533	2	AA044900	AA044900	328	45	35.4	862	4	AAE07890	AAE07890	Modified
256	45	35.4	533	2	AA044897	AA044897	329	45	35.4	869	1	AA093171	AA093171	AA093171
257	45	35.4	533	2	AA044893	AA044893	330	45	35.4	869	1	AA090705	AA090705	AA090705
258	45	35.4	533	2	AA044895	AA044895	331	45	35.4	869	4	AA075525	AA075525	AA075525
259	45	35.4	533	2	AA044896	AA044896	332	45	35.4	872	4	AA090753	AA090753	Human she
260	45	35.4	534	2	AA080216	AA080216	333	45	35.4	872	6	ABO07233	ABO07233	ABO07233
261	45	35.4	535	1	AA090181	AA090181	334	45	35.4	872	6	ABO52930	ABO52930	Human sp1
262	45	35.4	535	2	AA042201	AA042201	335	45	35.4	872	8	ABM81277	ABM81277	ABM81277
263	45	35.4	535	2	AA044888	AA044888	336	45	35.4	882	8	ADP54088	ADP54088	ADP54088
264	45	35.4	535	2	AA086825	AA086825	337	45	35.4	882	4	AAE07889	AAE07889	Modified
265	45	35.4	535	2	AA086826	AA086826	338	45	35.4	887	4	AAE07892	AAE07892	Modified
266	45	35.4	535	2	AA024876	AA024876	339	45	35.4	895	5	AA075369	AA075369	AA075369
267	45	35.4	535	2	AA046448	AA046448	340	45	35.4	895	5	AA075368	AA075368	AA075368
268	45	35.4	535	2	AA068090	AA068090	341	45	35.4	896	5	AA075367	AA075367	AA075367
269	45	35.4	535	3	AA096456	AA096456	342	45	35.4	896	5	AA075366	AA075366	AA075366
270	45	35.4	535	3	AA097280	AA097280	343	45	35.4	896	6	AA029672	AA029672	AA029672
271	45	35.4	535	6	AB097867	AB097867	344	45	35.4	896	6	AA029671	AA029671	AA029671
272	45	35.4	545	2	AA074339	AA074339	345	45	35.4	907	4	AAE07891	AAE07891	Modified
273	45	35.4	545	2	AA067374	AA067374	346	45	35.4	907	4	AAE35713	AAE35713	AAE35713
274	45	35.4	545	2	AA066732	AA066732	347	45	35.4	999	6	AAE35712	AAE35712	AAE35712
275	45	35.4	546	2	AA041200	AA041200	348	45	35.4	1052	3	AA066336	AA066336	AA066336
276	45	35.4	546	2	AA041661	AA041661	349	45	35.4	1052	3	AA066334	AA066334	AA066334
277	45	35.4	546	2	AA098776	AA098776	350	45	35.4	1052	3	AA054619	AA054619	AA054619
278	45	35.4	546	6	ABU03679	ABU03679	351	45	35.4	1052	3	AA066982	AA066982	AA066982
279	45	35.4	546	7	ADD55415	ADD55415	352	45	35.4	1052	3	AA084227	AA084227	AA084227
280	45	35.4	546	7	ADD55417	ADD55417	353	45	35.4	1052	3	AA084228	AA084228	AA084228
281	45	35.4	548	6	ABP97863	ABP97863	354	45	35.4	1052	3	AA085820	AA085820	AA085820
282	45	35.4	548	6	ABP97863	ABP97863	355	45	35.4	1052	5	AA014527	AA014527	AA014527
283	45	35.4	560	1	AA060516	AA060516	356	45	35.4	1052	5	AA014528	AA014528	AA014528
284	45	35.4	560	1	AA070597	AA070597	357	45	35.4	1052	5	ABG31096	ABG31096	ABG31096
285	45	35.4	560	6	ABP96305	ABP96305	358	45	35.4	1192	6	AAE35711	AAE35711	AAE35711
286	45	35.4	560	8	ADP44536	ADP44536	359	45	35.4	1192	6	AAE35710	AAE35710	AAE35710
287	45	35.4	560	8	ADP44538	ADP44538	360	45	35.4	1212	6	AAE35709	AAE35709	AAE35709
288	45	35.4	567	2	AA066607	AA066607	361	45	35.4	1212	6	AAE35708	AAE35708	AAE35708
289	45	35.4	567	4	AA000220	AA000220	362	45	35.4	1256	4	AB064133	AB064133	AB064133
290	45	35.4	568	2	AA023924	AA023924	363	45	35.4	1537	4	AA083971	AA083971	AA083971
291	45	35.4	605	4	AA073924	AA073924	364	45	35.4	1537	4	ADN23049	ADN23049	ADN23049
292	45	35.4	615	2	AA095056	AA095056	365	45	35.4	1577	4	ABG10016	ABG10016	ABG10016
293	45	35.4	617	2	AA095057	AA095057	366	45	35.4	1596	7	ADJ69016	ADJ69016	ADJ69016
294	45	35.4	629	2	AA026486	AA026486	367	45	35.4	1720	6	AA078886	AA078886	AA078886
295	45	35.4	629	6	ABJ25441	ABJ25441	368	45	35.4	1720	6	AB007715	AB007715	AB007715
296	45	35.4	637	5	AA075365	AA075365	369	45	35.4	1721	4	AA079870	AA079870	AA079870
297	45	35.4	638	5	AA075370	AA075370	370	45	35.4	3432	6	ABU41925	ABU41925	ABU41925
298	45	35.4	641	2	AA099383	AA099383	371	44.5	35.0	280	5	AB055405	AB055405	AB055405
299	45	35.4	642	5	AA075382	AA075382	372	44.5	35.0	368	2	AA084128	AA084128	AA084128
300	45	35.4	642	5	AA029675	AA029675	373	44.5	35.0	368	2	AA097885	AA097885	AA097885
301	45	35.4	643	5	AA075390	AA075390	374	44.5	35.0	368	8	ADK39716	ADK39716	ADK39716
302	45	35.4	643	6	AA029670	AA029670	375	44.5	35.0	417	8	AD042706	AD042706	AD042706
303	45	35.4	645	4	AA070894	AA070894	376	44.5	35.0	424	6	ABM67843	ABM67843	ABM67843
304	45	35.4	645	6	AA025692	AA025692	377	44.5	35.0	499	8	AD026143	AD026143	AD026143
305	45	35.4	645	6	AA075383	AA075383	378	44.5	35.0	549	8	ADP04793	ADP04793	ADP04793
306	45	35.4	645	6	AA075389	AA075389	379	44.5	35.0	549	5	AA052842	AA052842	AA052842
307	45	35.4	657	5	AA075389	AA075389	380	44.5	35.0	549	5	AA052842	AA052842	AA052842
308	45	35.4	657	6	AA075389	AA075389	381	44.5	35.0	549	5	AA052842	AA052842	AA052842
309	45	35.4	660	4	AA070898	AA070898	382	44.5	35.0	619	5	AA075316	AA075316	AA075316
310	45	35.4	665	4	AA070895	AA070895	383	44.5	35.0	619	5	AA075315	AA075315	AA075315
311	45	35.4	665	6	AA025689	AA025689	384	44.5	35.0	619	5	AA075315	AA075315	AA075315
312	45	35.4	666	5	AA025689	AA025689	385	44.5	35.0	619	5	AA075315	AA075315	AA075315
313	45	35.4	666	6	AA025689	AA025689	386	44.5	35.0	619	5	AA075315	AA075315	AA075315
314	45	35.4	671	2	AA075389	AA075389	387	44.5	35.0	619	5	AA075315	AA075315	AA075315
315	45	35.4	676	1	AA093172	AA093172	388	44.5	35.0	842	8	AD073868	AD073868	AD073868
316	45	35.4	676	3	AA090706	AA090706	389	44.5	35.0	847	8	AD005103	AD005103	AD005103
317	45	35.4	676	4	AA075266	AA075266	390	44	34.6	151	5	AB055486	AB055486	AB055486

391	44	34.6	157	8	ADN17554	Adn17554	Bacterial	464	43.5	34.3	495	5	AAM48000	Aam48000	Arabidops
392	44	34.6	172	4	ABG09791	Abg09791	Novel hum	465	43.5	34.3	501	3	AAG35776	Aag35776	Arabidops
393	44	34.6	176	3	AAG54430	Aag54430	Zea mays	466	43.5	34.3	501	5	AAM48001	Aam48001	Arabidops
394	44	34.6	215	5	AAG54429	Aag54429	Zea mays	467	43.5	34.3	523	3	AAG10101	Aag10101	Arabidops
395	44	34.6	282	3	ABP27289	Abp27289	Streptoco	468	43.5	34.3	523	8	ADN73153	Adn73153	Thale cre
396	44	34.6	302	3	AAG54428	Aag54428	Zea mays	469	43.5	34.3	540	7	ADP05702	Adp05702	Bacterial
397	44	34.6	308	8	ADS44636	Ads44636	Bacterial	470	43.5	34.3	555	2	AAR43340	Aar43340	Alpha-glu
398	44	34.6	322	6	ABU79113	Abu79113	Staphyloc	471	43.5	34.3	619	8	ADS30170	Ads30170	Bacterial
399	44	34.6	322	7	ADP43360	Adp43360	Bacterial	472	43.5	34.3	1551	4	AAG85026	Aag85026	Shrimp wh
400	44	34.6	378	3	AAG46567	Aag46567	Arabidops	473	43.5	34.3	2402	4	AAU07131	Aau07131	Porcine r
401	44	34.6	404	3	AAG46566	Aag46566	Arabidops	474	43.5	34.3	42	8	ABO58010	AbO58010	Human gen
402	44	34.6	420	3	AAG20726	Aag20726	Arabidops	475	43.5	34.3	71	6	ABU01950	Abu01950	S. pneumo
403	44	34.6	429	6	ABM15850	Abm15850	Mycobacte	476	43.5	34.3	126	4	ABH62908	Abh62908	Drosophi
404	44	34.6	443	3	AAB96153	Aab96153	Putative	477	43.5	34.3	148	5	ABU51032	Abu51032	Helicobac
405	44	34.6	463	3	AAG46565	Aag46565	Arabidops	478	43.5	34.3	162	7	ADP06342	Adp06342	Bacterial
406	44	34.6	480	6	ADA48242	Ada48242	Rice prot	479	43.5	34.3	172	6	ABU40649	Abu40649	Protein e
407	44	34.6	484	6	ABU24912	Abu24912	Protein e	480	43.5	34.3	172	8	ADS42775	Ads42775	Bacterial
408	44	34.6	491	4	ANU34175	Anu34175	Staphyloc	481	43.5	34.3	184	6	ABU62866	Abu62866	Ras-fam1
409	44	34.6	504	4	AAU37099	Aau37099	Staphyloc	482	43.5	34.3	184	7	ADH59010	Adh59010	Rat Prote
410	44	34.6	504	6	ABM72813	Abm72813	Staphyloc	483	43.5	34.3	184	7	ADH59012	Adh59012	Human pro
411	44	34.6	511	6	ABU16504	Abu16504	Protein e	484	43.5	34.3	184	7	ADG31704	Adg31704	Human pro
412	44	34.6	523	3	AAG20725	Aag20725	Arabidops	485	43.5	34.3	184	8	ADOS5215	Ado55215	Human Ras
413	44	34.6	530	6	ABU49735	Abu49735	Protein e	486	43.5	34.3	184	8	ABM80954	Abm80954	Tumour-as
414	44	34.6	534	4	ABH6941	Abh6941	Drosophi	487	43.5	34.3	184	8	ADP23197	Adp23197	PRO polyP
415	44	34.6	540	3	AAV75735	Aay75735	Neisseria	488	43.5	34.3	186	6	ABM72361	Abm72361	Staphyloc
416	44	34.6	547	3	AAG92001	Aag92001	C. glutam	489	43.5	34.3	196	4	ABB03883	Abb03883	Human mus
417	44	34.6	547	7	ADD13276	Add13276	C. glutam	490	43.5	34.3	196	6	ABU13177	Abu13177	Novel hum
418	44	34.6	553	8	ADS28434	Ads28434	Bacterial	491	43.5	34.3	196	8	ADJ29203	Adj29203	Human mus
419	44	34.6	555	2	AAW49098	Aaw49098	Amino aci	492	43.5	34.3	256	3	AAW82452	Aaw82452	Spinach c
420	44	34.6	555	8	ADG46834	Adg46834	Bacterial	493	43.5	34.3	276	7	ADH86761	Adh86761	Enterococ
421	44	34.6	555	8	ADG46831	Adg46831	Bacterial	494	43.5	34.3	311	6	ADH96401	Adh96401	Prochloro
422	44	34.6	555	8	ADG46816	Adg46816	Bacterial	495	43.5	34.3	332	8	ADH56074	Adh56074	Debaromy
423	44	34.6	555	8	ADG46832	Adg46832	Bacterial	496	43.5	34.3	352	4	AAU23088	Aau23088	Novel hum
424	44	34.6	555	8	ADG46833	Adg46833	Bacterial	497	43.5	34.3	389	5	ABH53959	Abh53959	Lactococc
425	44	34.6	555	8	ADG46835	Adg46835	Bacterial	498	43.5	34.3	399	7	ADH88134	Adh88134	Enterococ
426	44	34.6	556	5	AAE27868	Aae27868	Mutant Tn	499	43.5	34.3	407	7	ADM05407	Adm05407	Human pro
427	44	34.6	556	5	AAE27867	Aae27867	Mutant Tn	500	43.5	34.3	436	8	ADQ26344	Adq26344	Chromobac
428	44	34.6	556	5	AAE27863	Aae27863	Wild-type	501	43.5	34.3	455	8	ADS29127	Ads29127	Bacterial
429	44	34.6	556	5	AAE27866	Aae27866	Mutant Tn	502	43.5	34.3	467	3	AAW99855	Aaw99855	Escherich
430	44	34.6	556	5	AAE27870	Aae27870	Mutant Tn	503	43.5	34.3	467	3	AAW99854	Aaw99854	Escherich
431	44	34.6	556	5	AAE27869	Aae27869	Mutant Tn	504	43.5	34.3	467	3	AAW99853	Aaw99853	Escherich
432	44	34.6	560	6	ABM68550	Abm68550	Phototrab	505	43.5	34.3	467	7	ADG33780	Adg33780	Actinomyc
433	44	34.6	571	8	ADN17386	Adn17386	Bacterial	506	43.5	34.3	468	3	AAW99857	Aaw99857	Escherich
434	44	34.6	580	4	ABG20724	Abg20724	Arabidops	507	43.5	34.3	468	3	AAW99856	Aaw99856	Escherich
435	44	34.6	584	4	ABG26094	Abg26094	Novel hum	508	43.5	34.3	468	3	AAW99858	Aaw99858	Escherich
436	44	34.6	586	4	ABH58288	Abh58288	Drosophi	509	43.5	34.3	469	8	ADN20290	Adn20290	Bacterial
437	44	34.6	726	6	ABP96033	Abp96033	Human sur	510	43.5	34.3	477	6	ABO07142	AbO07142	Novel hum
438	44	34.6	748	6	ABU20785	Abu20785	Protein e	511	43.5	34.3	481	8	ADN01952	Adn01952	Staphyloc
439	44	34.6	765	7	ADF74168	Adf74168	Human nov	512	43.5	34.3	481	8	ADN01939	Adn01939	Staphyloc
440	44	34.6	814	6	ABU24538	Abu24538	Protein e	513	43.5	34.3	481	8	ADN01953	Adn01953	Staphyloc
441	44	34.6	904	8	ADG67715	Adg67715	Novel hum	514	43.5	34.3	481	8	ADN01955	Adn01955	Staphyloc
442	44	34.6	952	7	ABO68769	AbO68769	Pseudomon	515	43.5	34.3	486	6	ABM71573	Abm71573	Staphyloc
443	44	34.6	1577	2	AAAR1047	Aaar1047	Alpha-D-g	516	43.5	34.3	486	6	ABW71573	Abw71573	Staphyloc
444	44	34.6	2349	6	AAOI6359	Aaoi6359	Human tra	517	43.5	34.3	486	7	ABO70890	AbO70890	Pseudomon
445	44	34.6	2415	4	ABG20278	Abg20278	Novel hum	518	43.5	34.3	490	2	AAW89764	Aaw89764	Staphyloc
446	44	34.6	2415	4	ABG20279	Abg20279	Novel hum	519	43.5	34.3	490	2	ADN01954	Adn01954	Staphyloc
447	44	34.6	3196	6	ABU41611	Abu41611	Protein e	520	43.5	34.3	495	7	ABO74573	AbO74573	Staphyloc
448	44	34.6	113	3	AAG04528	Aag04528	Arabidops	521	43.5	34.3	510	8	ADN17403	Adn17403	Bacterial
449	44	34.6	113	3	AAG25612	Aag25612	Arabidops	522	43.5	34.3	521	7	ABO23592	AbO23592	Rickettsi
450	44	34.6	169	3	AAG25611	Aag25611	Arabidops	523	43.5	34.3	539	2	AAW33906	Aaw33906	Amino aci
451	44	34.6	189	8	ADG45845	Adg45845	Staphyloc	524	43.5	34.3	539	8	ADY13178	Ady13178	Stress re
452	44	34.6	208	7	ADL57018	Adl57018	Chicken b	525	43.5	34.3	540	6	ABU20002	Abu20002	Protein e
453	44	34.6	215	3	AAG04527	Aag04527	Arabidops	526	43.5	34.3	542	4	AAG64458	Aag64458	S. putref
454	44	34.6	224	3	AAG04526	Aag04526	Arabidops	527	43.5	34.3	543	2	AAR42456	Aar42456	Enzyme in
455	44	34.6	384	3	AAG10103	Aag10103	Arabidops	528	43.5	34.3	543	2	AAW99465	Aaw99465	Bioynthe
456	44	34.6	399	3	AAG35778	Aag35778	Arabidops	529	43.5	34.3	543	2	AAW37053	Aaw37053	S. putref
457	44	34.6	425	3	AAG35777	Aag35777	Arabidops	530	43.5	34.3	543	2	AAW89403	Aaw89403	S. putref
458	44	34.6	426	3	AAG10102	Aag10102	Arabidops	531	43.5	34.3	543	3	AAW10470	Aaw10470	Shewanell
459	44	34.6	429	6	ABU47911	Abu47911	Protein e	532	43.5	34.3	549	3	ABU24163	Abu24163	Protein e
460	44	34.6	467	3	AAV51615	Aay51615	A. thalia	533	43.5	34.3	549	6	AAW99642	Aaw99642	B. pseudo
461	44	34.6	467	5	ABH81597	Abh81597	Herbicida	534	43.5	34.3	550	6	ABU22093	Abu22093	Protein e
462	44	34.6	477	5	ABU83398	Abu83398	Salmonell	535	43.5	34.3	552	2	ADY23918	Ady23918	Amino aci
463	44	34.6	490	8	ADW72386	Adw72386	A. thalia	536	43.5	34.3	552	8	ADN20146	Adn20146	Bacterial

537	43	33.9	555	6	ABU9997	Abu9997 Protein e	610	42.5	33.5	278	6	ADA87267	Ada87267 Novel hum
538	43	33.9	555	8	ADM57219	Adm57219 A thalian	611	42.5	33.5	278	6	ADA816469	Ada816469 Human PRO
539	43	33.9	575	4	AA979220	Aag79220 Amino aci	612	42.5	33.5	278	6	ADA91561	Ada91561 Novel hum
540	43	33.9	579	8	ADJ48749	Adj48749 Oll-aseoc	613	42.5	33.5	278	6	ADBI4624	Adbi4624 Human PRO
541	43	33.9	580	6	ABM69228	Abm69228 Phototrab	614	42.5	33.5	278	6	ADBI8585	Adbi8585 Novel hum
542	43	33.9	587	6	ABU29807	Abu29807 Protein e	615	42.5	33.5	278	6	ADA93800	Ada93800 Human PRO
543	43	33.9	594	8	ADN20584	Adn20584 Bacterial	616	42.5	33.5	278	6	ADBI1696	Adbi1696 Novel hum
544	43	33.9	597	8	ADC97426	E. faeciu	617	42.5	33.5	278	6	ADBI3008	Adbi3008 Human PRO
545	43	33.9	608	6	ABU43518	Abu43518 Protein e	618	42.5	33.5	278	6	ABO43216	Aboc43216 Novel hum
546	43	33.9	684	6	ABU19991	Abu19991 Protein e	619	42.5	33.5	278	6	ADA74262	Ada74262 Human PRO
547	43	33.9	774	8	ABM63465	Abm63465 Human dia	620	42.5	33.5	278	6	ADB24495	Adb24495 Human PRO
548	43	33.9	786	4	AAV70243	Aay70243 Human RNA	621	42.5	33.5	278	6	ADA82019	Ada82019 Human PRO
549	43	33.9	798	4	ABBB61410	Abbb61410 Drosophil	622	42.5	33.5	278	6	ADA74982	Ada74982 Human PRO
550	43	33.9	815	7	ADBE2881	Rat Prote	623	42.5	33.5	278	6	ADA85060	Ada85060 Novel hum
551	43	33.9	821	8	ADN20138	Adn20138 Bacterial	624	42.5	33.5	278	6	ADA84508	Ada84508 Human PRO
552	43	33.9	887	4	AAU37586	Aau37586 Streptoco	625	42.5	33.5	278	6	ADB29764	Adb29764 Human PRO
553	43	33.9	890	6	ABP81476	Abp81476 Streptoco	626	42.5	33.5	278	6	ADA80292	Ada80292 Human PRO
554	43	33.9	890	6	ABU46263	Abu46263 Protein e	627	42.5	33.5	278	6	ADA75534	Ada75534 Human PRO
555	43	33.9	890	8	ADK48224	Adk48224 Streptoco	628	42.5	33.5	278	6	ADA676759	Ada676759 Human PRO
556	43	33.9	1086	7	ADFO7411	Adfo7411 Bacterial	629	42.5	33.5	278	6	ADB25055	Adb25055 Human PRO
557	43	33.9	1133	3	AAAG38914	Aag38914 Arabidops	630	42.5	33.5	278	6	ADA93231	Ada93231 Human PRO
558	43	33.9	1136	3	AAAB1528	Aab1528 Human ORF	631	42.5	33.5	278	6	ADB26581	Adb26581 Human PRO
559	43	33.9	1188	8	ADOB0423	Adob0423 Zebrafish	632	42.5	33.5	278	6	ADB30868	Adb30868 Human PRO
560	43	33.9	1192	7	ADBE2883	Adbe2883 Human PRO	633	42.5	33.5	278	6	ADA60796	Ada60796 Homo sapi
561	43	33.9	1193	3	AAAG38913	Aag38913 Arabidops	634	42.5	33.5	278	6	ADB23943	Adb23943 Human PRO
562	43	33.9	1214	4	ABG22123	Abg22123 Novel hum	635	42.5	33.5	278	6	ADA96272	Ada96272 Human PRO
563	43	33.9	1363	6	ABU08100	Abu08100 Human kin	636	42.5	33.5	278	6	ADA80844	Ada80844 Human PRO
564	43	33.9	1467	5	ABB97605	Abb97605 Novel hum	637	42.5	33.5	278	6	ADA95720	Ada95720 Human PRO
565	43	33.9	1673	5	ABP69698	Abp69698 Human pol	638	42.5	33.5	278	6	ADB26029	Adb26029 Human PRO
566	43	33.9	1683	3	AAV71160	Aay71160 Rat phosph	639	42.5	33.5	278	6	ADB21514	Adb21514 Novel hum
567	43	33.9	1690	5	ABP69699	Abp69699 Human pol	640	42.5	33.5	278	7	ADA77293	Ada77293 Human PRO
568	43	33.9	1893	5	AAU84593	Aau84593 HIV Casse	641	42.5	33.5	278	7	ADBI8033	Adbi8033 Human PRO
569	43	33.9	1896	5	AAU84590	Aau84590 HIV Casse	642	42.5	33.5	278	7	ADA86716	Ada86716 Novel hum
570	43	33.9	2188	6	ADA36476	Ada36476 Actinocoba	643	42.5	33.5	278	7	ADA87819	Ada87819 Novel hum
571	43	33.9	3290	6	ADA34199	Ada34199 Actinocoba	644	42.5	33.5	278	7	ADA6207	Ada6207 Novel hum
572	43	33.9	5245	7	AD123931	Adi23931 Streptomy	645	42.5	33.5	278	7	ADB28237	Adb28237 Human PRO
573	43	33.9	5245	7	AD123931	Adi23931 Streptomy	646	42.5	33.5	278	7	ADB28789	Adb28789 Human PRO
574	43	33.9	5746	8	AAU84596	Aau84596 HIV compl	647	42.5	33.5	278	7	ADA76741	Ada76741 Human PRO
575	43	33.5	147	8	ADRA9441	Adra9441 Mouse sma	648	42.5	33.5	278	7	ADA88371	Ada88371 Novel hum
576	42.5	33.5	210	3	AAAB07846	Aab07846 Amino aci	649	42.5	33.5	278	7	ADA73736	Ada73736 Human PRO
577	42.5	33.5	226	5	ABP40649	Abp40649 Staphyloc	650	42.5	33.5	278	7	ADB27133	Adb27133 Human PRO
578	42.5	33.5	226	8	ADSO7889	Adso7889 Staphyloc	651	42.5	33.5	278	7	ADB22066	Adb22066 Novel hum
579	42.5	33.5	227	6	ABM72833	Abm72833 Staphyloc	652	42.5	33.5	278	7	ADA66757	Ada66757 Human PRO
580	42.5	33.5	240	6	ABU57647	Abu57647 Different	653	42.5	33.5	278	7	ADB22618	Adb22618 Human PRO
581	42.5	33.5	256	7	ADC25187	Adg25187 A. altern	654	42.5	33.5	278	7	ADB23391	Adb23391 Human PRO
582	42.5	33.5	276	4	AAU02498	Aau02498 Murine tr	655	42.5	33.5	278	7	ADB22113	Adb22113 Novel hum
583	42.5	33.5	276	8	ADRA9483	Adra9483 Mouse sma	656	42.5	33.5	278	7	ADB15176	Adb15176 Human PRO
584	42.5	33.5	277	2	AAW78312	Aaw78312 Fragment	657	42.5	33.5	278	7	ADB38428	Adb38428 Novel hum
585	42.5	33.5	277	2	AAW78312	Aaw78312 Fragment	658	42.5	33.5	278	7	ADB37876	Adb37876 Novel hum
586	42.5	33.5	278	4	AAU02499	Aau02499 Human PRO	659	42.5	33.5	278	7	ADB66348	Adb66348 Novel hum
587	42.5	33.5	278	4	AAU02499	Aau02499 Human PRO	660	42.5	33.5	278	7	ADB69428	Adb69428 Human PRO
588	42.5	33.5	278	6	ABU69616	Abu69616 Human NF-	661	42.5	33.5	278	7	ADB80160	Adb80160 Human PRO
589	42.5	33.5	278	6	ABOI7683	Aboi7683 Novel hum	662	42.5	33.5	278	7	ADB39261	Adb39261 Novel hum
590	42.5	33.5	278	6	ABU08037	Abu08037 Human PRO	663	42.5	33.5	278	7	ADB46884	Adb46884 Novel hum
591	42.5	33.5	278	6	ABU66637	Abu66637 Human PRO	664	42.5	33.5	278	7	ADB86491	Adb86491 Novel hum
592	42.5	33.5	278	6	ABU59718	Abu59718 Novel sec	665	42.5	33.5	278	7	ADB77096	Adb77096 Human PRO
593	42.5	33.5	278	6	ABO24908	Aboc24908 Human sec	666	42.5	33.5	278	7	ADB34253	Adb34253 Human PRO
594	42.5	33.5	278	6	ABU6913	Abu6913 Human sec	667	42.5	33.5	278	7	ADB35357	Adb35357 Human PRO
595	42.5	33.5	278	6	ABU58397	Abu58397 Human NOV	668	42.5	33.5	278	7	ADB33701	Adb33701 Human PRO
596	42.5	33.5	278	6	ADA45655	Ada45655 Novel hum	669	42.5	33.5	278	7	ADB34805	Adb34805 Human PRO
597	42.5	33.5	278	6	ADA76086	Ada76086 Human PRO	670	42.5	33.5	278	7	ADB35909	Adb35909 Human PRO
598	42.5	33.5	278	6	ADA18736	Ada18736 Human PRO	671	42.5	33.5	278	7	ADB46304	Adb46304 Novel hum
599	42.5	33.5	278	6	ADA61359	Ada61359 Homo sapi	672	42.5	33.5	278	7	ADC50177	Adc50177 Novel hum
600	42.5	33.5	278	6	ADB19144	Adb19144 Novel hum	673	42.5	33.5	278	7	ADC71724	Adc71724 Novel hum
601	42.5	33.5	278	6	ADB27685	Adb27685 Human PRO	674	42.5	33.5	278	7	ADC59703	Adc59703 Novel hum
602	42.5	33.5	278	6	ADA86164	Ada86164 Novel hum	675	42.5	33.5	278	7	ADC52710	Adc52710 Novel hum
603	42.5	33.5	278	6	ADBI5728	Adbi5728 Human PRO	676	42.5	33.5	278	7	ADC57064	Adc57064 Novel hum
604	42.5	33.5	278	6	ADA47514	Ada47514 Human PRO	677	42.5	33.5	278	7	ADC60255	Adc60255 Novel hum
605	42.5	33.5	278	6	ADA67309	Ada67309 Human PRO	678	42.5	33.5	278	7	ADC50730	Adc50730 Novel hum
606	42.5	33.5	278	6	ADB30316	Adb30316 Human PRO	679	42.5	33.5	278	7	ADC55257	Adc55257 Human PRO
607	42.5	33.5	278	6	ADA85612	Ada85612 Novel hum	680	42.5	33.5	278	7	ADC43355	Adc43355 Novel hum
608	42.5	33.5	278	6	ADA96824	Ada96824 Human PRO	681	42.5	33.5	278	7	ADC53316	Adc53316 Novel hum
609	42.5	33.5	278	6	ADA79128	Ada79128 Human PRO	682	42.5	33.5	278	7	ADC58839	Adc58839 Novel hum

683	42.5	33.5	278	7	ADCS5717	Novel	hum	756	42.5	33.5	278	8	ADBE8999	Human	PRO	Adbe8999	Human	PRO
684	42.5	33.5	278	7	ADCS8287	Novel	hum	757	42.5	33.5	278	8	ADBE1818	Human	PRO	Adbe1818	Human	PRO
685	42.5	33.5	278	7	ADDO2961	Novel	hum	758	42.5	33.5	278	8	ADBE8847	Human	PRO	Adbe8847	Human	PRO
686	42.5	33.5	278	7	ADCB9953	Novel	hum	759	42.5	33.5	278	8	ADBE3467	Human	PRO	Adbe3467	Human	PRO
687	42.5	33.5	278	7	ADCB9372	Novel	hum	760	42.5	33.5	278	8	ADBE9087	Human	PRO	Adbe9087	Human	PRO
688	42.5	33.5	278	7	ADCA8261	Human	PRO	761	42.5	33.5	278	8	ADBE5019	Human	PRO	Adbe5019	Human	PRO
689	42.5	33.5	278	7	ADDO9790	Human	PRO	762	42.5	33.5	278	8	ADBE3129	Human	PRO	Adbe3129	Human	PRO
690	42.5	33.5	278	7	ADDO4365	Novel	hum	763	42.5	33.5	278	8	ADFB3470	Human	PRO	Adfb3470	Human	PRO
691	42.5	33.5	278	7	ADCB0321	Novel	hum	764	42.5	33.5	278	8	ADBE2025	Novel	hum	Adbe2025	Novel	hum
692	42.5	33.5	278	7	ADDO10828	Human	PRO	765	42.5	33.5	278	8	ADBE90326	Human	PRO	Adbe90326	Human	PRO
693	42.5	33.5	278	7	ADCA7709	Human	PRO	766	42.5	33.5	278	8	ADBE1473	Novel	hum	Adbe1473	Novel	hum
694	42.5	33.5	278	7	ADCB9769	Novel	hum	767	42.5	33.5	278	8	ADGO2052	Human	PRO	Adgo2052	Human	PRO
695	42.5	33.5	278	7	ADDO9238	Human	PRO	768	42.5	33.5	278	8	ADG21838	Novel	hum	Adg21838	Novel	hum
696	42.5	33.5	278	7	ADDO40951	Novel	hum	769	42.5	33.5	278	8	ADG11908	Human	PRO	Adg11908	Human	PRO
697	42.5	33.5	278	7	ADDO52090	Human	PRO	770	42.5	33.5	278	8	ADFB97814	Human	PRO	Adfb97814	Human	PRO
698	42.5	33.5	278	7	ADDO52830	Human	PRO	771	42.5	33.5	278	8	ADG24031	Novel	hum	Adg24031	Novel	hum
699	42.5	33.5	278	7	ADDO53382	Novel	hum	772	42.5	33.5	278	8	ADFB98385	Human	PRO	Adfb98385	Human	PRO
700	42.5	33.5	278	7	ADDO51538	Human	PRO	773	42.5	33.5	278	8	ADGO3216	Human	PRO	Adgo3216	Human	PRO
701	42.5	33.5	278	7	ADDO2337	Human	PRO	774	42.5	33.5	278	8	ADFB98937	Human	PRO	Adfb98937	Human	PRO
702	42.5	33.5	278	7	ADDO1771	Human	PRO	775	42.5	33.5	278	8	ADG16522	Human	PRO	Adg16522	Human	PRO
703	42.5	33.5	278	7	ADDO53953	Novel	hum	776	42.5	33.5	278	8	ADGO4981	Human	PRO	Adgo4981	Human	PRO
704	42.5	33.5	278	7	ADDO92270	Human	PRO	777	42.5	33.5	278	8	ADG119248	Human	PRO	Adg119248	Human	PRO
705	42.5	33.5	278	7	ADDO91166	Human	PRO	778	42.5	33.5	278	8	ADG13085	Human	PRO	Adg13085	Human	PRO
706	42.5	33.5	278	7	ADBO3780	Human	PRO	779	42.5	33.5	278	8	ADGO8142	Novel	hum	Adgo8142	Novel	hum
707	42.5	33.5	278	7	ADBE32077	Novel	hum	780	42.5	33.5	278	8	ADG15312	Human	PRO	Adg15312	Human	PRO
708	42.5	33.5	278	7	ADBE22009	Human	PRO	781	42.5	33.5	278	8	ADFB96710	Human	PRO	Adfb96710	Human	PRO
709	42.5	33.5	278	7	ADDO79233	Human	PRO	782	42.5	33.5	278	8	ADGO5895	Human	PRO	Adgo5895	Human	PRO
710	42.5	33.5	278	7	ADBE1769	Human	PRO	783	42.5	33.5	278	8	ADG23479	Human	PRO	Adg23479	Human	PRO
711	42.5	33.5	278	7	ADBE17586	Human	PRO	784	42.5	33.5	278	8	ADGO3768	Human	PRO	Adgo3768	Human	PRO
712	42.5	33.5	278	7	ADDO91738	Novel	hum	785	42.5	33.5	278	8	ADG24669	Novel	hum	Adg24669	Novel	hum
713	42.5	33.5	278	7	ADBE33181	Novel	hum	786	42.5	33.5	278	8	ADGO6966	Novel	hum	Adgo6966	Novel	hum
714	42.5	33.5	278	7	ADBE33733	Novel	hum	787	42.5	33.5	278	8	ADGO7518	Novel	hum	Adgo7518	Novel	hum
715	42.5	33.5	278	7	ADDO79785	Human	PRO	788	42.5	33.5	278	8	ADGO5013	Novel	hum	Adgo5013	Novel	hum
716	42.5	33.5	278	7	ADDO92822	Human	PRO	789	42.5	33.5	278	8	ADGO60677	Novel	hum	Adgo60677	Novel	hum
717	42.5	33.5	278	7	ADBE19242	Human	PRO	790	42.5	33.5	278	8	ADG61781	Novel	hum	Adg61781	Novel	hum
718	42.5	33.5	278	7	ADBE18690	Human	PRO	791	42.5	33.5	278	8	ADG81982	Novel	hum	Adg81982	Novel	hum
719	42.5	33.5	278	7	ADBE12886	Human	PRO	792	42.5	33.5	278	8	ADG57221	Novel	hum	Adg57221	Novel	hum
720	42.5	33.5	278	7	ADDO95675	Human	PRO	793	42.5	33.5	278	8	ADG56669	Novel	hum	Adg56669	Novel	hum
721	42.5	33.5	278	7	ADBE22561	Human	PRO	794	42.5	33.5	278	8	ADG55565	Novel	hum	Adg55565	Novel	hum
722	42.5	33.5	278	7	ADDO78679	Human	PRO	795	42.5	33.5	278	8	ADG58325	Novel	hum	Adg58325	Novel	hum
723	42.5	33.5	278	7	ADBE32629	Novel	hum	796	42.5	33.5	278	8	ADG70691	Novel	hum	Adg70691	Novel	hum
724	42.5	33.5	278	7	ADBE42321	Human	PRO	797	42.5	33.5	278	8	ADG57773	Novel	hum	Adg57773	Novel	hum
725	42.5	33.5	278	7	ADDO80337	Human	PRO	798	42.5	33.5	278	8	ADG53357	Novel	hum	Adg53357	Novel	hum
726	42.5	33.5	278	7	ADDO89365	Human	PRO	799	42.5	33.5	278	8	ADG71243	Novel	hum	Adg71243	Novel	hum
727	42.5	33.5	278	7	ADBE40649	Human	PRO	800	42.5	33.5	278	8	ADG81430	Novel	hum	Adg81430	Novel	hum
728	42.5	33.5	278	7	ADBE04448	Human	PRO	801	42.5	33.5	278	8	ADH30392	Human	PRO	Adh30392	Human	PRO
729	42.5	33.5	278	7	ADBE92577	Human	PRO	802	42.5	33.5	278	8	ADH11759	Novel	hum	Adh11759	Novel	hum
730	42.5	33.5	278	7	ADG21286	Novel	hum	803	42.5	33.5	278	8	ADG52181	Novel	hum	Adg52181	Novel	hum
731	42.5	33.5	278	7	ADG22927	Novel	hum	804	42.5	33.5	278	8	ADG53909	Novel	hum	Adg53909	Novel	hum
732	42.5	33.5	278	7	ADFP97262	Human	PRO	805	42.5	33.5	278	8	ADG80878	Human	PRO	Adg80878	Human	PRO
733	42.5	33.5	278	7	ADG80326	Human	PRO	806	42.5	33.5	278	8	ADG56117	Novel	hum	Adg56117	Novel	hum
734	42.5	33.5	278	7	ADG79774	Human	PRO	807	42.5	33.5	278	8	ADH12383	Novel	hum	Adh12383	Novel	hum
735	42.5	33.5	278	7	ADH55066	Novel	hum	808	42.5	33.5	278	8	ADG61229	Novel	hum	Adg61229	Novel	hum
736	42.5	33.5	278	7	ADH55618	Novel	hum	809	42.5	33.5	278	8	ADH28316	Human	PRO	Adh28316	Human	PRO
737	42.5	33.5	278	7	ADH63837	Novel	hum	810	42.5	33.5	278	8	ADG54461	Novel	hum	Adg54461	Novel	hum
738	42.5	33.5	278	7	ADH64786	Novel	hum	811	42.5	33.5	278	8	ADG59501	Novel	hum	Adg59501	Novel	hum
739	42.5	33.5	278	7	ADH81699	Novel	hum	812	42.5	33.5	278	8	ADH80925	Human	PRO	Adh80925	Human	PRO
740	42.5	33.5	278	7	ADH81147	Novel	hum	813	42.5	33.5	278	8	ADGO9668	Novel	hum	Adgo9668	Novel	hum
741	42.5	33.5	278	7	ADH82316	Novel	hum	814	42.5	33.5	278	8	ADH15139	Novel	hum	Adh15139	Novel	hum
742	42.5	33.5	278	7	ADH15715	Novel	hum	815	42.5	33.5	278	8	ADGO9016	Novel	hum	Adgo9016	Novel	hum
743	42.5	33.5	278	7	ADH16344	Novel	hum	816	42.5	33.5	278	8	ADH14471	Novel	hum	Adh14471	Novel	hum
744	42.5	33.5	278	7	ADH15163	Novel	hum	817	42.5	33.5	278	8	ADH18066	Novel	hum	Adh18066	Novel	hum
745	42.5	33.5	278	7	ADH14611	Novel	hum	818	42.5	33.5	278	8	ADH63347	Novel	hum	Adh63347	Novel	hum
746	42.5	33.5	278	7	ADH63285	Novel	hum	819	42.5	33.5	278	8	ADH77242	Novel	hum	Adh77242	Novel	hum
747	42.5	33.5	278	8	ADCB0873	Novel	hum	820	42.5	33.5	278	8	ADH65364	Novel	hum	Adh65364	Novel	hum
748	42.5	33.5	278	8	ADDF6321	Human	PRO	821	42.5	33.5	278	8	ADH27500	Human	PRO	Adh27500	Human	PRO
749	42.5	33.5	278	8	ADDB7685	Human	PRO	822	42.5	33.5	278	8	ADH42224	Human	PRO	Adh42224	Human	PRO
750	42.5	33.5	278	8	ADDB6089	Human	PRO	823	42.5	33.5	278	8	ADH28086	Human	PRO	Adh28086	Human	PRO
751	42.5	33.5	278	8	ADDF5537	Human	PRO	824	42.5	33.5	278	8	ADH17575	Human	PRO	Adh17575	Human	PRO
752	42.5	33.5	278	8	ADBE23113	Human	PRO	825	42.5	33.5	278	8	ADH95568	Human	PRO	Adh95568	Human	PRO
753	42.5	33.5	278	8	ADBE23665	Human	PRO	826	42.5	33.5	278	8	ADH96120	Novel	hum	Adh96120	Novel	hum
754	42.5	33.5	278	8	ADBE24308	Human	PRO	827	42.5	33.5	278	8	ADH49444	Human	PRO	Adh49444	Human	PRO
755	42.5	33.5	278	8	ADDB7133	Human	PRO	828	42.5	33.5	278	4	AAU02500	Expressio		Aau02500	Expressio	



829	42.5	33.5	291	7	ADG96763	E. faeciu	902	42	33.1	278	8	ADG04614	Ado04614 Human lys
830	42.5	33.5	351	6	ABB82606	Abb82606 Maize X-r	903	42	33.1	278	8	ADQ19763	Adq19763 Human sof
831	42.5	33.5	353	5	ABP41913	Abp41913 Human ova	904	42	33.1	278	8	ABM81103	Abm81103 Tumour-as
832	42.5	33.5	424	8	ADN17579	Adn17579 Bacterial	905	42	33.1	282	6	ABU36887	Abu36887 Protein e
833	42.5	33.5	429	1	AAp91958	AAp91958 Peptide e	906	42	33.1	282	6	ABU34865	Abu34865 Protein e
834	42.5	33.5	429	2	AAp51887	AAp51887 DAPA Synt	907	42	33.1	284	8	ADN22257	Adn22257 Bacterial
835	42.5	33.5	429	1	AAU34505	AAU34505 E. coli c	908	42	33.1	292	5	ADG64666	Adg64666 Saccharom
836	42.5	33.5	429	6	ABU28561	ABU28561 Protein e	909	42	33.1	302	5	ABG70074	Abg70074 Human pre
837	42.5	33.5	429	6	ADP04948	ADP04948 Bacterial	910	42	33.1	306	6	ABM69568	Abm69568 Photocarb
838	42.5	33.5	429	8	ADN18117	Adn18117 Bacterial	911	42	33.1	307	2	AAW93255	AAw93255 Tobacco C
839	42.5	33.5	421	2	AAW73903	AAw73903 E. coli D	912	42	33.1	311	7	ADP59532	Adp59532 Human pol
840	42.5	33.5	435	6	ABU31641	ABU31641 Protein e	913	42	33.1	321	8	ADN18479	Adn18479 Bacterial
841	42.5	33.5	447	7	ABO67770	ABO67770 K1ebsiell	914	42	33.1	324	6	ABU29166	ABU29166 Protein e
842	42.5	33.5	513	7	ADG63833	ADG63833 Rat Prote	915	42	33.1	324	7	ADM25910	Adm25910 Hyperther
843	42.5	33.5	546	4	AAU23561	AAU23561 Novel hum	916	42	33.1	326	2	AAV20119	AAv20119 B. burgdo
844	42.5	33.5	546	4	AAU87604	AAU87604 Novel cen	917	42	33.1	328	7	ADH86358	ADh86358 Enterococ
845	42.5	33.5	546	8	AD154919	AD154919 Novel hum	918	42	33.1	328	7	ADH86358	ADh86358 Enterococ
846	42.5	33.5	568	8	ADU87314	ADU87314 Novel cen	919	42	33.1	331	8	ADN47212	ADn47212 Thermococ
847	42.5	33.5	568	8	AD154629	AD154629 Novel hum	920	42	33.1	341	8	ADN47212	ADn47212 Thermococ
848	42.5	33.5	586	2	AAp49855	AAp49855 Sequence	921	42	33.1	349	5	ABP73534	ABp73534 Candida a
849	42.5	33.5	624	4	AAU22925	AAU22925 Novel hum	922	42	33.1	357	6	ABU24898	ABU24898 Protein e
850	42.5	33.5	846	3	AAAB69345	AAb69345 HIV-1 non	923	42	33.1	358	8	ADP30357	ADp30357 Human sec
851	42.5	33.5	883	4	AAAB82761	AAb82761 Anticentr	924	42	33.1	359	2	AAI20118	AAi20118 B. burgdo
852	42.5	33.5	1300	7	ADG63060	ADG63060 Rat Prote	925	42	33.1	366	5	ABP29871	ABp29871 Streptoco
853	42.5	33.5	1809	7	ADG55015	ADG55015 Rat Prote	926	42	33.1	370	7	ADG31201	ADg31201 Human dia
854	42.5	33.5	1809	7	ADG55009	ADG55009 Rat Prote	927	42	33.1	372	8	ADG81063	ADg81063 HIV prote
855	42.5	33.5	1809	7	ADG55006	ADG55006 Rat Prote	928	42	33.1	374	8	AD142450	AD142450 Plant tra
856	42.5	33.5	1809	7	ADG55012	ADG55012 Rat Prote	929	42	33.1	376	8	AD142449	AD142449 Plant tra
857	42	33.1	55	8	AAV91084	AAv91084 Human LPA	930	42	33.1	395	4	AAU03633	AAU03633 Group B S
858	42	33.1	60	4	AAAB30625	AAb30625 Fragment	931	42	33.1	395	5	ABP28295	ABp28295 Streptoco
859	42	33.1	60	5	AAAB15301	AAe15301 Human pro	932	42	33.1	396	4	ABG04922	ABG04922 Novel hum
860	42	33.1	60	6	ABG74257	ABg74257 Human LPA	933	42	33.1	410	4	ABG04922	ABG04922 Novel hum
861	42	33.1	60	6	ABG74257	ABg74257 Human LPA	934	42	33.1	415	4	AAAB63528	AAb63528 Antino aci
862	42	33.1	60	8	ADU93807	ADu93807 Human Lys	935	42	33.1	420	4	AAAB62035	AAb62035 P. furios
863	42	33.1	60	8	ADN49491	ADn49491 Human Lys	936	42	33.1	431	8	ADG44487	ADg44487 Bacterial
864	42	33.1	70	8	ADG04630	ADG04630 Human Lys	937	42	33.1	435	3	AAAY83780	AAy83780 Human ATI
865	42	33.1	70	3	AAAG12432	AAg12432 Zee maye	938	42	33.1	435	4	AAAG63540	AAg63540 Antino aci
866	42	33.1	78	8	ADG41591	ADg41591 Bacterial	939	42	33.1	436	5	AAU74345	AAU74345 Human cye
867	42	33.1	82	7	ADG00634	ADG00634 Enterococ	940	42	33.1	436	7	ADG39836	ADg39836 Protein e
868	42	33.1	95	8	ADN46185	ADn46185 Thermococ	941	42	33.1	436	8	ADG66697	ADG66697 Human pro
869	42	33.1	115	6	ADG434222	ADg434222 Actinocob	942	42	33.1	436	8	ADG66355	ADG66355 Human pro
870	42	33.1	117	3	AAAG12617	AAg12617 Zee maye	943	42	33.1	440	3	AAAY83777	AAy83777 Mouse ATI
871	42	33.1	120	8	ADG065051	ADG065051 Novel hum	944	42	33.1	450	6	ABU41584	ABU41584 Protein e
872	42	33.1	127	3	AAAG12616	AAg12616 Zee maye	945	42	33.1	451	6	ABU39727	ABU39727 Protein e
873	42	33.1	129	7	ADH86956	ADh86956 Enterococ	946	42	33.1	451	8	ADN46347	ADN46347 Thermococ
874	42	33.1	156	3	AAAG12615	AAg12615 Zee maye	947	42	33.1	459	3	AAAG29591	AAg29591 Arabidops
875	42	33.1	178	6	ABM71384	ABm71384 Staphyloc	948	42	33.1	459	5	ABBS3427	ABb3427 Lactococ
876	42	33.1	185	8	ADH72789	ADh72789 B. subcili	949	42	33.1	474	4	AAU46847	AAU46847 Propionib
877	42	33.1	206	5	ABP51289	ABp51289 Human MDD	950	42	33.1	460	7	ADG33874	ADg33874 Actinomyc
878	42	33.1	211	4	ABM67384	ABm67384 Photocarb	951	42	33.1	462	6	ABU25489	ABu25489 Protein e
879	42	33.1	218	4	AAAM25257	AAm25257 Human pro	952	42	33.1	464	8	ADN24352	ADn24352 Bacterial
880	42	33.1	222	5	ABP39419	ABp39419 Staphyloc	953	42	33.1	470	5	ABR52410	ABr52410 Protein e
881	42	33.1	222	8	ADG04520	ADG04520 Staphyloc	954	42	33.1	474	4	AAU46847	AAU46847 Propionib
882	42	33.1	225	6	ABU50105	ABU50105 Protein e	955	42	33.1	474	6	ABM43366	ABm43366 Propionib
883	42	33.1	240	4	AAAB95831	AAb95831 Human pro	956	42	33.1	485	4	AAAG63531	AAg63531 Antino aci
884	42	33.1	240	7	ADG39837	ADg39837 Protein e	957	42	33.1	490	8	ADG57426	ADG57426 Bacterial
885	42	33.1	244	7	ADG10006	ADG10006 Human NOV	958	42	33.1	509	5	ABAB95866	ABa95866 Listeria
886	42	33.1	244	8	ADN20298	ADn20298 Bacterial	959	42	33.1	517	8	ADG65825	ADG65825 Novel hum
887	42	33.1	247	5	ABP28843	ABp28843 Streptoco	960	42	33.1	518	4	ABG16535	ABg16535 Novel hum
888	42	33.1	250	4	ABB60023	ABb60023 Drosophil	961	42	33.1	529	3	AAAG29590	AAg29590 Arabidops
889	42	33.1	262	7	ADG64936	ADG64936 Human pro	962	42	33.1	541	6	ABU29251	ABU29251 Protein e
890	42	33.1	268	6	ADG36831	ADg36831 Actinocob	963	42	33.1	541	6	ABU29521	ABU29521 Protein e
891	42	33.1	274	2	AAAB88117	AAb88117 Human Lys	964	42	33.1	542	3	AAAG29589	AAg29589 Arabidops
892	42	33.1	275	8	ADN25015	ADN25015 Bacterial	965	42	33.1	545	7	ADH86674	ADh86674 Enterococ
893	42	33.1	278	2	AAAG29875	AAg29875 Lyophosp	966	42	33.1	546	6	ABU22008	ABU22008 Protein e
894	42	33.1	278	2	AAAG29875	AAg29875 Lyophosp	967	42	33.1	550	6	AAAG29875	AAg29875 Lyophosp
895	42	33.1	278	3	AAAY96589	AAy96589 Human Lys	968	42	33.1	559	5	ADJ33778	ADj33778 Protein o
896	42	33.1	278	3	AAAY91082	AAy91082 Human Lys	969	42	33.1	560	4	AAU31067	AAU31067 Novel hum
897	42	33.1	278	4	AAAB30623	AAb30623 Antino aci	970	42	33.1	564	8	ABAB66319	ABa66319 Drosophil
898	42	33.1	278	5	AAE15289	AAe15289 Human LPA	971	42	33.1	564	4	ADG089714	ADg089714 Antagonis
899	42	33.1	278	6	ABG74252	ABG74252 Human LPA	972	42	33.1	574	8	ADK70709	ADk70709 Coliapsin
900	42	33.1	278	8	ADJ93791	ADj93791 Human Lys	973	42	33.1	576	2	AAAB66929	AAb66929 AMWL chro
901	42	33.1	278	8	ADN49475	ADn49475 Human Lys	974	42	33.1	585	4	AAAG3530	AAg3530 Antino aci

975	42	33.1	585	6	ABU43406	Abu43406	Protein e
976	42	33.1	596	4	AU33748	Au33748	Staphyloc
977	42	33.1	603	6	AAE37962	Aae37962	Human kin
978	42	33.1	604	4	AU36932	Au36932	Staphyloc
979	42	33.1	604	6	ABU6053	Abu6053	Protein e
980	42	33.1	604	6	ABW73224	Abw73224	Staphyloc
981	42	33.1	611	8	ADN22551	Adn22551	Bacterial
982	42	33.1	618	5	ABP38324	Abp38324	Staphyloc
983	42	33.1	618	8	ADSO4832	Adso4832	Staphyloc
984	42	33.1	621	7	ADF30481	Adf30481	Rat angio
985	42	33.1	650	8	ADK70696	Adk70696	Chicken C
986	42	33.1	659	5	ABB93561	Abb93561	Herbicide
987	42	33.1	658	8	ADS24539	Ads24539	Bacterial
988	42	33.1	698	8	ADS29165	Ads29165	Bacterial
989	42	33.1	747	6	ADR86215	Adr86215	Aspergill
990	42	33.1	769	6	ABU20332	Abu20332	Protein e
991	42	33.1	816	2	AAR66931	Aar66931	AMWL chro
992	42	33.1	835	3	AA801470	Aa801470	Human CAR
993	42	33.1	835	4	AA856674	Aab56674	Novel pro
994	42	33.1	835	6	ABR41886	Ab41886	Human car
995	42	33.1	835	8	AD129282	Ad129282	Human MAR
996	42	33.1	835	8	AD057048	Ado57048	Human car
997	42	33.1	885	2	AAR66930	Aar66930	AMWL chro
998	42	33.1	889	4	AAU33860	Aau33860	Staphyloc
999	42	33.1	902	7	ABR62799	Ab62799	VISA Scap
1000	42	33.1	910	7	ABR62791	Ab62791	MESA 2-ke

## ALIGNMENTS

RESULT 1  
AD195325 standard; protein; 221 AA.

AD195325;  
04-NOV-2004 (first entry)

OSPF-related SARS coronavirus matrix protein.

immuno response; overlapping synthetic peptide formulation; OSPF;  
immunostimulant; virucide; antibacterial; antiparasitic; cytostatic;  
vaccine; viral; bacterial; parasitic infection; prion disease;  
neoplastic; toxin; matrix.

SARS coronavirus.

MO2004002415-A2.

08-JAN-2004.

27-JUN-2003; 2003WO-US020322.

27-JUN-2002; 2002US-0392718P.

(DAND ) DANA FARBER CANCER INST INC.

Ruprecht RM, Jiang S;  
WPI, 2004-082868/08.

Modulating an immune response, useful for treating immune disorders, e.g.  
viral, bacterial and parasitic infections, prion diseases, or neoplastic  
diseases, administering to a subject an overlapping synthetic peptide  
formulation.

Claim 13; SEQ ID NO 233; 175bp; English.

The invention relates to a novel method for modulating an immune response  
comprising administering to a subject an overlapping synthetic peptide  
formulation (OSPF) which comprises a combination of single chain peptides  
corresponding to the amino acid sequence of a protein of interest. The

CC method of the invention has immunostimulant, virucide, antibacterial,  
CC antiparasitic and cytostatic applications and may be useful during  
CC vaccine production and for treating immune disorders including viral,  
CC bacterial and parasitic infections, prion diseases, neoplastic diseases,  
CC as well as providing protection against toxins. The current sequence is  
CC that of the OSPF-related SARS coronavirus matrix protein of the  
CC invention.

XX  
SQ Sequence 221 AA;

Query Match 88.2%; Score 112; DB 8; Length 221;  
Best Local Similarity 100.0%; Pred. No. 5.8e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTITVEELKQLLEQNNLV 25  
Db 1 MADNGTITVEELKQLLEQNNLV 22

RESULT 2  
AAM19303 standard; protein; 54 AA.

AAM19303;  
12-OCT-2001 (first entry)

Peptide #5737 encoded by probe for measuring cervical gene expression.

XX  
XX Probe; human; microarray; gene expression; cervical epithelial cell;  
XX cervical cancer.

XX Homo sapiens.

XX MO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000670.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn Sq, Hanzel DK, Chen W, Rank DR;  
XX WPI, 2001-488901/53.

XX 27-JUN-2003; 2003WO-US020322.

XX 27-JUN-2002; 2002US-0392718P.

XX (DAND ) DANA FARBER CANCER INST INC.

XX Ruprecht RM, Jiang S;  
XX WPI, 2004-082868/08.

XX The Present invention relates to human single exon nucleic acid probes  
XX (SENP: see A1110068-A1128459). The present sequence is a peptide encoded  
XX by one such probe. The SENPs are derived from human HeLa cells. The SENPs  
XX can be used to produce a single exon microarray, which can be used for  
XX measuring human gene expression in a sample derived from human cervical  
XX epithelial cells. By measuring gene expression, the probes are therefore  
XX useful in grading and/or staging of diseases of the cervix, notably  
XX cervical cancer. Note: The sequence data for this patent did not form  
XX part of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 54 AA;

Query Match 43.3%; Score 55; DB 4; Length 54;

Best Local Similarity 41.7%; Pred. No. 6.1;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGTITVEELKQLLEQWNL 24  
DB 20 KSDLEDKQVSVVEAKNRAEQWNV 43

## RESULT 3

ABB38595  
ID ABB38595 standard; peptide; 54 AA.

AC ABB38595;

DT 04-FEB-2002 (first entry)

DE Peptide #6101 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX PI WPI; 2001-483447/52.

XX DR Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human fetal liver.

XX PS Claim 27; SEQ ID NO 31230; 639pp + Sequence Listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring

XX CC human gene expression in a sample derived from human foetal liver. The

XX CC single exon nucleic acid probes may be used for predicting, measuring and

XX CC displaying gene expression in samples derived from human fetal liver. The

XX CC present sequence is a peptide encoded by a single exon nucleic acid probe

XX CC of the invention. Note: The sequence data for this patent did not form

XX CC part of the printed specification, but was obtained in electronic format

XX CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 54 AA;

XX Query Match 43.3%; Score 55; DB 4; Length 54;

XX Best Local Similarity 41.7%; Pred. No. 6.1;

XX Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

DT 17-OCT-2001 (first entry)

DE Peptide #6086 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;

OS genetic disorder.

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX PI WPI; 2001-488897/53.

XX DR Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human placenta.

XX PS Claim 27; SEQ ID NO 32318; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP:

XX CC see A131315-A157546). The present sequence is a peptide encoded by one

XX CC such probe. The probes are useful for producing a microarray for

XX CC predicting, measuring and displaying gene expression in samples derived

XX CC from human placenta. The probes are useful for antenatal diagnosis of

XX CC human genetic disorders

XX SQ Sequence 54 AA;

XX Query Match 43.3%; Score 55; DB 4; Length 54;

XX Best Local Similarity 41.7%; Pred. No. 6.1;

XX Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

XX QY 1 KKKMADNGTITVEELKQLLEQWNL 24

XX DB 20 KSDLEDKQVSVVEAKNRAEQWNV 43

XX RESULT 5

XX ABB23710

XX ID ABB23710 standard; protein; 54 AA.

XX AC ABB23710;

XX DT 23-JAN-2002 (first entry)

XX DE Protein #5709 encoded by probe for measuring heart cell gene expression.

XX KW Human; gene expression; heart; microarray; vascular system;

XX KW cardiovascular disease; hypertension; cardiac arrhythmia;

XX KW congenital heart disease.

XX OS Homo sapiens.

XX PN WO200157274-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000666.

```

XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207455P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 15; SEQ ID NO 25480; 530bp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC AB82155-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 54 AA;
XX
Query Match 43.3%; Score 55; DB 4; Length 54;
Beat Local Similarity 41.7%; Pred. NO. 6.1;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0.
QY 1 KKKMADNGTIVVEIKQLLEQWNL 24
| : | : | : | : | : | : | :
Db 20 KSDLEDKRQVSEAEKNAEIQWNV 43
XX
RESULT 6
AA71757
XX ID AAM71757 standard; protein; 54 AA.
XX
AC AAM71757;
XX
DT 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 32063.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukemia; lymphoma; myeloma.
XX
XX Homo sapiens.
XX OS
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX

```

PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488900/53.  
DR  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human bone marrow.  
PS Example 4; SEQ ID NO 32063; 658bp + Sequence Listing; English.  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention  
XX  
SQ Sequence 54 AA;

Query Match 43.3%; Score 55; DB 4; Length 54;  
Best Local Similarity 41.7%; Pred. No. 6.1;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Oy 1 KKKMADNGTITVEELKQLLEGQNL 24  
      ::|||::|||:  
Db 20 KSDLEDKROVSVSEAKRAEQMVN 43

RESULT 7  
AAMS9222  
ID AAMS9222 standard; protein; 54 AA.  
AC AAMS9222;  
XX  
DT 05-NOV-2001 (first entry)  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31327.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
OS Homo sapiens.  
FN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000667.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483446/52.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
XX brains.  
PS Example 4; SEQ ID NO 31327; 650pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system













CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
 CC hypersensitivity, urticaria, an immunologic disease of the lung,  
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
 CC pneumonitis, a transplantation associated disease, graft rejection or  
 CC graft-versus-host disease. The present sequence represents a PRO protein  
 CC of the invention.  
 XX  
 SQ Sequence 209 AA;  
 Query Match 43.3%; Score 55; DB 8; Length 209;  
 Best Local Similarity 41.7%; Pred. No. 26;  
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 KKKMADNGITTYEELKQLEQNL 24  
 DB 131 KSDLEDKQVSEAKNRAEQNV 154  
 RESULT 18  
 ADS34490 standard; protein; 209 AA.  
 XX  
 AC ADS34490;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE POSH protein associated protein #54.  
 XX  
 KW cytosolic; neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;  
 KW antiviral; neurotropic; central nervous system; POSH polypeptide;  
 KW POSH-associated protein; POSH-AP; HERPUDI; Ubiquitin ligase;  
 KW antiviral agent; anti-apoptotic agent; anti-cancer agent;  
 KW secretory pathway trafficking inhibitor;  
 KW neurological disorder progression disorder; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; schizophrenia;  
 KW Niemann-Pick's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 XX  
 PF 02-MAR-2004; 2004WO-US006308.  
 XX  
 PR 03-MAR-2003; 2003US-0451437P.  
 PR 05-MAR-2003; 2003US-0452284P.  
 PR 19-MAR-2003; 2003US-0455760P.  
 PR 20-MAR-2003; 2003US-0456640P.  
 PR 03-APR-2003; 2003US-0460526P.  
 PR 04-APR-2003; 2003US-0460792P.  
 PR 21-APR-2003; 2003US-0464285P.  
 PR 09-MAY-2003; 2003US-0469462P.  
 PR 15-MAY-2003; 2003US-0471378P.  
 PR 20-MAY-2003; 2003US-0472327P.  
 PR 30-MAY-2003; 2003US-0474706P.  
 PR 03-JUN-2003; 2003US-0475825P.  
 PR 17-JUN-2003; 2003US-0479317P.  
 PR 19-JUN-2003; 2003US-0480215P.  
 PR 19-JUN-2003; 2003US-0480376P.  
 PR 08-AUG-2003; 2003US-0493860P.  
 PR 28-AUG-2003; 2003US-049834P.  
 PR 16-SEP-2003; 2003US-0503931P.  
 PR 10-NOV-2003; 2003US-05035712.  
 PR 05-FEB-2004; 2004WO-US003600.  
 PR 02-MAR-2004; 2004US-0549896P.  
 XX  
 PA (PROT-) PROTEOLOGICS INC.  
 XX

PI Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;  
 PI Greener T;  
 XX  
 DR WPI; 2004-662346/64.  
 XX  
 PT Isolated, purified or recombinant complex, useful for identifying an  
 PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and  
 PT POSH-associated protein (POSH-AP).  
 PS  
 XS Disclosure; SEQ ID NO 254; 374pp; English.  
 XX  
 CC The invention relates to an isolated, purified or recombinant complex (I)  
 CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)  
 CC or HERPUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are  
 CC useful for identifying an agent that modulates an activity of a POSH  
 CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-  
 CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking  
 CC of a protein through the secretory pathway, an agent that inhibits the  
 CC progression of a neurological disorder, an agent that modulates a POSH  
 CC function, an agent that modulates a HERPUDI function. The methods can be  
 CC used for treating a viral infection, for inhibiting an activity of a POSH  
 CC -AP in a cell, for treating a POSH-associated disease in a subject. The  
 CC POSH-associated disease is viral infection, POSH-associated cancer or  
 CC POSH-associated neurological disorder. The methods are useful for  
 CC treating or preventing POSH-associated neurological disorder in a subject  
 CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,  
 CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a  
 CC protein of the invention.  
 XX  
 SQ Sequence 209 AA;  
 Query Match 43.3%; Score 55; DB 8; Length 209;  
 Best Local Similarity 41.7%; Pred. No. 26;  
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 KKKMADNGITTYEELKQLEQNL 24  
 DB 131 KSDLEDKQVSEAKNRAEQNV 154  
 RESULT 19  
 AAU31548  
 ID AAU31548 standard; protein; 246 AA.  
 XX  
 AC AAU31548;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Novel human secreted protein #2039.  
 XX  
 KW Human; vaccination; gene therapy; nutritional supplement;  
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200179449-A2.  
 PD 25-OCT-2001.  
 XX  
 PF 16-APR-2001; 2001WO-US008656.  
 XX  
 PR 18-APR-2000; 2000US-00552929.  
 PR 26-JAN-2001; 2001US-00770160.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-611725/70.  
 XX  
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
 PT vaccination, testing and therapy.

XX Claim 20; Page 457; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising the

CC nucleic acids encoding the polypeptides and cells genetically engineered

CC to express them are also useful for producing the proteins. The proteins

CC are useful in genetic vaccination, testing and therapy, and can be used

CC as nutritional supplements. They may be used to increase stem cell

CC proliferation; to regulate hematopoiesis; and in bone, cartilage, tendon

CC and/or nerve tissue growth or regeneration; immune suppression and/or

CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

CC AAU29510-AAU3304 represent the amino acid sequences of novel human

CC secreted proteins of the invention

XX

XX Sequence 246 AA:

SO

Query Match 43.3%; Score 55; DB 4; Length 246;

Best Local Similarity 41.7%; Pred. No. 31;

Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVEELKQLEQNL 24

DB 133 KSDLEDKQGVSEAKQRAEQMV 156

RESULT 20

ADP07641

XX ADF07641 standard; protein; 300 AA.

XX

AC ADF07641;

XX

DT 12-FEB-2004 (first entry)

XX

DE Bacterial polypeptide #3754.

XX

KM Proteus mirabilis infection; bacterial infection; antibacterial;

XX Immunostimulant.

XX

OS Proteus mirabilis.

XX

PN US6605709-B1.

XX

PD 12-AUG-2003.

XX

PF 05-APR-2000; 2000US-00543681.

XX

PR 09-APR-1999; 99US-0128706P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Breton GL;

XX

DR WPI; 2003-895291/82.

XX

DR N-PADB; ADF03469.

XX

PT New Proteus mirabilis polypeptides and polymnucleotides, useful as

XX reagents for diagnosis of bacterial disease, as components of

XX antibacterial vaccines, as targets for antibacterial drugs, or as

XX biocontrol agents for plants.

XX

PS Disclosure; SEQ ID NO 7926; 870pp; English.

XX

CC The invention relates to new Proteus mirabilis polypeptides and

CC polymnucleotides. The invention also relates to antibodies against the

CC polypeptides, methods for producing the polypeptides, a method of

CC generating vaccines for immunising an individual against P. mirabilis, a

CC method for evaluating a compound for the ability to bind a P. mirabilis

CC polypeptide and a method for screening test compounds for anti-bacterial

CC activity. The polypeptides and polymnucleotides are useful as molecular

CC targets for diagnosing, preventing and treating pathological conditions

CC resulting from bacterial infection, as reagents for diagnosis of

CC bacterial diseases, as components of antibacterial vaccines, as targets

CC for antibacterial drugs or as bio-control agents for plants. This

CC sequence represents a Proteus mirabilis polypeptide of the invention.

XX

XX Sequence 300 AA:

SO

Query Match 41.7%; Score 53; DB 7; Length 300;

Best Local Similarity 47.6%; Pred. No. 72;

Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KXMDNGITVEELKQLEQNL 23

DB 59 KLTDDAIIYEHAKQILAQFN 79

RESULT 21

ABU23669

XX ABU23669 standard; protein; 351 AA.

XX

AC ABU23669;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by prokaryotic essential gene #9196.

XX

KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Clostridium acetobutylicum.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

XX

PR 06-SEP-2001; 2001US-00948993.

XX

PR 25-OCT-2001; 2001US-0342923P.

XX

PR 08-FEB-2002; 2002US-00072851.

XX

PR 06-MAR-2002; 2002US-0362599P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

XX

DR N-PADB; ACA27539.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening

XX for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 51593; 1766pp; English.

XX

XX The invention relates to an isolated nucleic acid comprising any one of

XX the 6213 antisense sequences given in the specification where expression

XX of the nucleic acid inhibits proliferation of a cell. Also included are:

XX (1) a vector comprising a promoter operably linked to the nucleic acid

XX encoding a polypeptide whose expression is inhibited by the antisense

XX nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX polypeptide or its fragment whose expression is inhibited by the

XX antisense nucleic acid; (4) an antibody capable of specifically binding

XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX proliferation or the activity of a gene in an operon required for

XX proliferation; (7) identifying a compound that influences the activity of

XX the gene product or that has an activity against a biological pathway

XX required for proliferation, or that inhibits cellular proliferation; (8)



PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
 useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
 XX  
 PS Claim 2; SEQ ID NO 266; 1205bp; French.  
 CC The invention relates to the isolation of genes and their encoded  
 CC proteins from Photorhabdus luminescens. The isolated sequences are  
 CC sources of probes and primers for detecting the genome of P. luminescens  
 CC and related species; to study polymorphisms; for gene analysis and for  
 CC detection/amplification of the genes. Antibodies (Ab) raised against the  
 CC polypeptides encoded by the genes are used for detection/identification  
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
 CC carry a gene-containing vector are used to select compounds that  
 CC modulate, regulate, induce or inhibit expression of the genes in plants,  
 CC animals or microorganisms other than P. luminescens and are able to alter  
 CC response or sensitivity to toxins and antibiotics produced by P.  
 CC luminescens. Cells transformed to express the genes are useful for  
 CC recombinant production of the proteins, particularly toxins and  
 CC antibacterials useful as insecticides, bactericides and fungicides. The  
 CC genes, proteins, vectors containing the genes and Ab are also useful  
 CC therapeutically (to treat microbial infection by bacteria or fungi that  
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
 CC biopesticides. Other uses of the genes and the proteins are as virulence  
 CC factors and for identifying targets of human diseases for which P.  
 CC luminescens is a model (particularly plague and whooping cough). This  
 CC sequence represents one of the isolated P. luminescens proteins  
 XX  
 SQ Sequence 16368 AA;  
 Query Match 40.9%; Score 52; DB 6; Length 16368;  
 Best Local Similarity 71.4%; Pred. No. 7.1e+03;  
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 10 ITVEELKQLLEQWN 23  
 :|||:|||||  
 Db 14404 LTVEERKLLLESWN 14417  
 RESULT 24  
 AAB43377  
 ID AAB43377 standard; protein; 162 AA.  
 XX  
 AC AAB43377;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human ORFX ORF3141 polypeptide sequence SEQ ID NO:6282.  
 XX  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnerary; antiparasitic; antiparkinsonian; nootropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antirheumatic; antihypertoid;  
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive.  
 OS  
 OS Homo sapiens.  
 XX  
 PN WO200058473-A2.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 31-MAR-2000; 2000WO-US008621.  
 XX  
 PR 31-MAR-1999; 99US-0127607P.  
 PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.  
 PR 30-MAR-2000; 2000US-00540763.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimketa RA, Leach W;  
 DR WPI; 2000-602362/57.  
 DR N-PSDB; AAC7586.  
 XX  
 PT Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease.  
 XX  
 PS Claim 11; Page 5469; 5507bp; English.  
 XX  
 CC AAC74446 to AAC7586 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;  
 CC antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic;  
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;  
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;  
 CC dermatological; immunosuppressive; antirheumatic; antibacterial;  
 CC antiviral; antifungal; antirheumatic; antihypertoid; and antianemic. The  
 CC sequences can be used for determining the presence of or predisposition  
 CC to, or preventing or treating pathological conditions associated with an  
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX  
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be  
 CC used to treat cancers, proliferative disorders, neurodegenerative  
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,  
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester  
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency  
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune  
 CC disorders, asthma, allergy, aplastic anaemia, burns, wounds, bone and  
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to  
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive  
 XX  
 SQ Sequence 162 AA;  
 Query Match 40.2%; Score 51; DB 3; Length 162;  
 Best Local Similarity 50.0%; Pred. No. 69;  
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 KKKMADNGTITVEELKQLLEQWN 24  
 :|||:|||||:|||||:|  
 Db 34 KKKQVANVEKQLEAKELQMDL 57  
 RESULT 25  
 ABG99957  
 ID ABG99957 standard; protein; 162 AA.  
 XX  
 AC ABG99957;  
 XX  
 DT 17-JAN-2003 (first entry)  
 XX  
 DE Human novel polypeptide #70.  
 XX  
 KW Human; genetic disorder; gene mapping; medical imaging; cancer;  
 KW neurodegenerative disorder; lymphoid cell disorder; osteoporosis;  
 KW Parkinson's disease; Alzheimer's disease; bone degenerative disorder;  
 KW osteoarthritis; periodontal disease; liver fibrosis; viral infection;  
 KW fungal infection; bacterial infection; autoimmune disease; diabetes;  
 KW atopic dermatitis.  
 OS  
 OS Homo sapiens.  
 XX  
 PN WO200274961-A1.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PR 14-MAR-2002; 2002WO-US005109.

PR 15-MAR-2001; 2001US-00810173.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Dimaac RT;  
 XX  
 DR MPI; 2003-040556/03.  
 DR N-PSDB; ABX05055.  
 XX  
 PT New isolated polypeptides and polynucleotides, useful for preventing,  
 PT treating or ameliorating medical conditions, such as cancer,  
 PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative  
 PT disorders, and infections.  
 XX  
 PS Claim 9; SEQ ID NO 596; 235pp; English.  
 XX  
 CC The invention relates to human polynucleotides and the polypeptides they  
 CC encode. The polynucleotides and polypeptides are useful in diagnostics,  
 CC forensics, gene mapping, medical imaging, identification of mutations,  
 CC responsible for genetic disorders or other traits, assessing biodiversity  
 CC and producing many other types of data and products dependent on DNA and  
 CC amino acid sequences. They are also useful for preventing, treating or  
 CC ameliorating medical conditions, such as cancer, neurodegenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell  
 CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,  
 CC periodontal diseases, liver fibrosis, infections (e.g. viral, fungal or  
 CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).  
 CC Sequences ABG9888-ABG9989 and ABU0010-ABU0043 represent human  
 CC polypeptides of the invention. Note: The sequence data for this patent is  
 CC not represented in the printed specification but is based on sequence  
 CC information supplied by the European Patent Office  
 XX  
 SQ Sequence 162 AA;  
 Query Match 40.2%; Score 51; DB 6; Length 162;  
 Best Local Similarity 50.0%; Pred. No. 69;  
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 KKKMADNGITVEELKQLEQNL 24  
 Db 34 KKKMADVKEQLEAKELQMDL 57  
 RESULT 26  
 AAE34443  
 ID AAE34443 standard; protein; 217 AA.  
 AC AAE34443;  
 XX  
 DT 14-MAY-2003 (first entry)  
 XX  
 DE Human lipid-associated molecule (LIPAM)-4 protein.  
 XX  
 KW Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke;  
 KW arteriovenous fistula; atherosclerosis; hypertension; Raynaud's disease;  
 KW aneurysm; congestive heart failure; thrombophlebitis; angina pectoris;  
 KW ischaemic heart disease; rheumatic heart disease; peptic oesophagitis;  
 KW gastrointestinal disorder; lipid metabolism disorder; Crohn's disease;  
 KW nausea; peptic ulcer; fatty liver; Fabry's disease; Gaucher's disease;  
 KW diabetes mellitus; hyperlipidaemia; hypercholesterolaemia; epilepsy;  
 KW autoimmune disorder; inflammatory disorder; neurological disorder; kuru;  
 KW acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; asthma;  
 KW dementia; prion disease; Creutzfeldt-Jakob disease; leukaemia; cancer;  
 KW adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy;  
 KW protein replacement therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 185..213  
 FT /note="Transmembrane domain"

XX  
 PN WO200294988-A2.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 17-MAY-2002; 2002MO-US015688.  
 XX  
 XX 18-MAY-2001; 2001US-0292242P.  
 XX 25-MAY-2001; 2001US-0293726P.  
 PR 01-JUN-2001; 2001US-0295346P.  
 PR 06-JUL-2001; 2001US-0303404P.  
 PR 24-AUG-2001; 2001US-0314754P.  
 PR 22-JUN-2002; 2002US-0351262P.  
 PR 29-MAR-2002; 2002US-0368799P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Tang YT, Yue H, Azimzai Y, Baughn MR, Burford N, Reddy R;  
 PI Walla NK, Das D, Nguyen DB, Yao WG, Arvizu CS, Lu Y, Gandhi AR;  
 PI Griffin JA, Elliott VS, Ramkumar J, Lal PG, Lu DM, Lee EA, Lee SY;  
 PI Yue H, Yang J, Tribouley CM, Kable AE, Swarnakar A;  
 XX  
 DR MPI; 2003-120797/11.  
 DR N-PSDB; AAD52629.  
 XX  
 PT New human lipid-associated molecule (LIPAM) proteins and polynucleotides,  
 PT useful for diagnosing, treating or preventing cardiovascular disorders  
 PT (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or  
 PT cancers.  
 XX  
 PS Claim 59; Page 144-145; 171pp; English.  
 XX  
 CC The present invention relates to novel human lipid-associated molecules  
 CC (LIPAM) and polynucleotides encoding such proteins. Sequences of the  
 CC invention are useful for treating diseases or conditions associated with  
 CC decreased expression of functional LIPAM. The antagonist is useful for  
 CC treating a disease or condition associated with the overexpression of  
 CC functional LIPAM. They are useful for diagnosing, treating or preventing  
 CC cardiovascular disorders (e.g. arteriovenous fistula, atherosclerosis,  
 CC hypertension, Raynaud's disease, aneurysms, varicose veins, congestive  
 CC heart failure, thrombophlebitis, angina pectoris, ischaemic heart disease  
 CC or rheumatic heart disease), gastrointestinal disorders (e.g. peptic  
 CC oesophagitis, nausea, peptic ulcer or Crohn's disease), lipid metabolism  
 CC disorders (e.g. fatty liver, Fabry's disease, Gaucher's disease, diabetes  
 CC mellitus, hyperlipidaemia, hypercholesterolaemia), autoimmune disorders  
 CC or inflammatory disorders (e.g. acquired immunodeficiency syndrome,  
 CC anaemia, asthma or Crohn's disease), neurological disorders (e.g. stroke,  
 CC epilepsy, dementia, Alzheimer's disease, or prion diseases such as kuru  
 CC or Creutzfeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia,  
 CC lymphoma, melanoma, myeloma or sarcoma). They are also used in gene  
 CC therapy and protein replacement therapy. The present sequence is human  
 CC LIPAM-4 protein  
 XX  
 SQ Sequence 217 AA;  
 Query Match 40.2%; Score 51; DB 6; Length 217;  
 Best Local Similarity 50.0%; Pred. No. 94;  
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 KKKMADNGITVEELKQLEQNL 24  
 Db 34 KKKMADVKEQLEAKELQMDL 57  
 RESULT 27  
 AAG62621  
 ID AAG62621 standard; protein; 224 AA.  
 AC AAG62621;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Human SNARE protein 25.

XX Human; SNARE protein 25; cancer; blood disease; HIV infection;  
 KW Immunological disease; inflammation; gene therapy.  
 XX Homo sapiens.  
 OS  
 PN WO200138390-A1.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 20-NOV-2000; 2000WO-CN000477.  
 XX  
 PR 26-NOV-1999; 99CN-00124120.  
 XX  
 PA (BIO-R) BIOROAD GENE DEV LTD SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2001-355907/37.  
 XX  
 DR N-PSDB; AAA45791.  
 XX  
 PT Human SNARE protein 25 and encoded polynucleotide, used in diagnosis and  
 PT treatment of malignant tumors, hemopathy, human immunodeficiency virus  
 XX infection, immunological diseases and inflammation.  
 PS Claim 1; Page 23-24; 33pp; Chinese.  
 XX  
 CC The present invention provides the protein and coding sequences of the  
 CC human SNARE protein 25. The sequences can be used in the treatment of  
 CC blood diseases, cancer, HIV infection, immunological diseases and  
 CC inflammation. The present sequence is the protein of the invention  
 XX  
 SQ Sequence 224 AA;  
 XX  
 Query Match 40.2%; Score 51; DB 4; Length 224;  
 Best Local Similarity 50.0%; Pred. No. 97;  
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 KKKQADNGTITVEELKQLLEQMNLL 24  
 Db 34 KKKQVANVEKQLEAKELLEQMDL 57  
 XX  
 RESULT 28  
 ABU00236  
 ID ABU00236 standard; protein; 224 AA.  
 XX  
 AC ABU00236;  
 XX  
 DT 17-JAN-2003 (first entry)  
 XX  
 DE Human novel polypeptide #329.  
 XX  
 KW Human; genetic disorder; gene mapping; medical imaging; cancer;  
 KW neurodegenerative disorder; lymphoid cell disorder; osteoporosis;  
 KW Parkinson's disease; Alzheimer's disease; bone degenerative disorder;  
 KW osteoarthritis; periodontal disease; liver fibrosis; viral infection;  
 KW fungal infection; bacterial infection; autoimmune disease; diabetes;  
 KW atopic dermatitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200274961-A1.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 14-MAR-2002; 2002WO-US005109.  
 XX  
 PR 15-MAR-2001; 2001US-00810173.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PT Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Dirmanac RT;  
 XX  
 DR WPI; 2003-040556/03.  
 XX  
 DR N-PSDB; ABX05314.  
 XX  
 PT New isolated polypeptides and polynucleotides, useful for preventing,  
 PT treating or ameliorating medical conditions, such as cancer,  
 PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative  
 PT disorders, and infections.  
 XX  
 PS Claim 9; SEQ ID NO 855; 235pp; English.  
 XX  
 CC The invention relates to human polynucleotides and the polypeptides they  
 CC encode. The polynucleotides and polypeptides are useful in diagnostics,  
 CC forensics, gene mapping, medical imaging, identification of mutations,  
 CC responsible for genetic disorders or other traits, assessing biodiversity  
 CC and producing many other types of data and products dependent on DNA and  
 CC amino acid sequences. They are also useful for preventing, treating or  
 CC ameliorating medical conditions, such as cancer, neurodegenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell  
 CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,  
 CC periodontal disease, liver fibrosis, infections (e.g. viral, fungal or  
 CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).  
 CC Sequences ABG93888-ABG93989 and ABU00010-ABU00433 represent human  
 CC polypeptides of the invention. Note: The sequence data for this patent is  
 CC not represented in the printed specification but is based on sequence  
 CC information supplied by the European Patent Office  
 XX  
 SQ Sequence 224 AA;  
 XX  
 Query Match 40.2%; Score 51; DB 6; Length 224;  
 Best Local Similarity 50.0%; Pred. No. 97;  
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 KKKQADNGTITVEELKQLLEQMNLL 24  
 Db 34 KKKQVANVEKQLEAKELLEQMDL 57  
 XX  
 RESULT 29  
 AAM68488  
 ID AAM68488 standard; protein; 572 AA.  
 XX  
 AC AAM68488;  
 XX  
 DT 08-DEC-1998 (first entry)  
 XX  
 DE Mouse ULIP-4 protein.  
 XX  
 KW Mouse; Unc-33-like phospho-protein; ULIP; rat; neoplasia; tumorigenesis;  
 KW neurodegenerative disorder; diagnosis.  
 XX  
 OS Mus musculus.  
 XX  
 PN FR2759701-A1.  
 XX  
 PD 21-AUG-1998.  
 XX  
 PF 19-FEB-1997; 97FR-00001961.  
 XX  
 PR 19-FEB-1997; 97FR-00001961.  
 XX  
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX  
 PI Aguera M, Belin MF, Hommorat J, Kolatukudy P, Quach TT, Byk T;  
 PI Sobel A;  
 XX  
 DR WPI; 1998-449610/39.  
 XX  
 DR N-PSDB; AAV60817.  
 XX  
 PT Mouse and human ULIP polypeptide(s) - useful in detection of para-  
 PT neoplastic neurological syndromes.

XX Claim 1; Fig 11; 90pp; French.  
PS  
XX  
CC This sequence represents the mouse Unc-33-like phospho-protein (ULIP)-4.  
CC The coding sequence was isolated based on similarity to the rat ULIP  
CC sequence. Proteins of the ULIP family or their corresponding nucleic  
CC acids can be used in compositions for treating neurodegenerative  
CC disorders and neoplasms, especially for para-neoplastic neurological  
CC syndromes and/or for the early diagnosis of tumorigenesis  
XX  
SQ Sequence 572 AA;  
Query Match 40.2%; Score 51; DB 2; Length 572;  
Best Local Similarity 64.7%; Pred. No. 2.7e+02;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 5 ADNGTIVELKQLLEQ 21  
DB 199 AENGDIVBQRRLLEQ 215  
RESULT 30  
ID ABB49107 standard; protein; 626 AA.  
XX ABB49107;  
AC  
XX  
XX  
DT 05-FEB-2002 (first entry)  
XX  
XX  
DE Listeria monocytogenes protein #1811.  
XX  
XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;  
KW vitamin B12; bacterial infection; disease.  
XX  
XX Listeria monocytogenes.  
OS  
XX WO200177335-A2.  
XX  
XX  
PD 18-OCT-2001.  
XX  
XX  
PF 11-APR-2001; 2001MO-FR001118.  
XX  
XX 11-APR-2000; 2000FR-00004629.  
XX  
XX (INSP) INST PASTEUR.  
XX  
XX Buchrieser C, Frangoul L, Couve E, Rusanick C, Feibi H, Dehoux P;  
PI Duesurget O, Chetouani F, Nedjati H, Glaeser P, Kunat F, Cosrart P;  
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;  
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;  
PI Chakraborty T, Demann E, Hain T, Berche P, Charbit A, Durant L;  
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;  
PI Madueno E, De Pablos B, Weiland J, Kaerst U, Entian K, Hauf J;  
PI Rose M, Voss H;  
XX  
XX WPI; 2002-010914/01.  
XX  
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment  
PT and prevention of Listeria and related bacterial infections, and related  
PT polypeptides.  
XX  
XX Claim 6; SEQ ID NO 1812; 192pp; French.  
XX  
XX The present invention relates to the genome sequence of Listeria  
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of  
CC it are useful for selecting probes and primers for detecting genes in L.  
CC monocytogenes and related organisms, and for studying genetic  
CC polymorphisms and other genomes. The present sequence is a protein  
CC encoded by the genome sequence of the present invention. Proteins  
CC expressed from the genome sequence are useful for raising specific  
CC antibodies, identification of L. monocytogenes and related organisms, and  
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin  
CC B12. The genome sequence and proteins encoded by it are also useful for

CC selecting compounds that regulate gene expression and cell replication  
CC and modulate L. monocytogenes-related diseases. In addition, the genome  
CC sequence and proteins encoded by it are useful in pharmaceutical and  
CC vaccines compositions for the treatment or prevention of infections by L.  
CC monocytogenes and related organisms. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 626 AA;  
Query Match 40.2%; Score 51; DB 5; Length 626;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 2 KKMADNGTIVELKQLLEQ 21  
DB 417 KQLADEFLITIELKQLLQ 436  
RESULT 31  
ID ABU32651 standard; protein; 626 AA.  
XX ABU32651;  
AC  
XX  
XX  
DT 19-JUN-2003 (first entry)  
XX  
XX  
DE Protein encoded by prokaryotic essential gene #18176.  
XX  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
XX Listeria monocytogenes.  
OS  
XX WO200277183-A2.  
XX  
XX  
PD 03-OCT-2002.  
XX  
XX  
PF 21-MAR-2002; 2002MO-US009107.  
XX  
XX  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyckind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
XX WPI; 2003-029926/02.  
XX  
XX N-PSDB; ACA36521.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 60575; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 623 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)



CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-regulated gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SO Sequence 626 AA;

Query Match 40.2%; Score 51; DB 6; Length 626;  
 Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 2 KXWADNGTIVBELKOLLEQ 21

Db 417 KOLADEPELITLTKOOLQ 436

RESULT 32

AAAG02044

ID AAAG02044 standard; protein; 100 AA.

XX AAAG02044;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 6125.

KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX gene therapy; chromosome mapping.

OS Homo sapiens.

PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000BP-00200610.

PR 26-FEB-1999; 99US-0122487P.

(GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

DR N-PSDB; AAC02050.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 13; SEQ ID NO 6125; 71bp + Sequence Listing; English.

CC The present sequence is a polypeptide encoded by one of a large number of  
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
 CC sequences derived from the 5' ends of mRNAs and even in those cases where

CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
 CC are also used in diagnostic, forensic, gene therapy and chromosome  
 CC mapping procedures. They are used to obtain upstream regulatory sequences  
 CC and to design expression and secretion vectors

SO Sequence 100 AA;

Query Match 39.4%; Score 50; DB 3; Length 100;  
 Best Local Similarity 55.6%; Pred. No. 56;  
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 KXWADNGTIVBELKOLLE 20

Db 44 KOLENSEINIBELKNLE 61

RESULT 33

ADA12194

ID ADA12194 standard; protein; 300 AA.

XX ADA12194;

DT 06-NOV-2003 (first entry)

DE Acinetobacter sp. hydrolase.

KM adipic acid synthetase; cyclohexanone monooxygenase;

KW 6-aldehyde hexanoic dehydrogenase; cyclohexanol dehydrogenase;

XX cyclohexanol; adipic acid; hydrolase; enzyme.

OS Acinetobacter sp.

PN US6498242-B1.

PD 24-DEC-2002.

PF 14-UTL-1999; 99US-00648004.

PR 19-FEB-1999; 99US-00252553.

(DUPO) DU PONT DE NEMOURS & CO E. I.

PI Cheng Q, Nagarajan V, Thomas SM;

DR WPI; 2003-605313/57.

DR N-PSDB; ADA12193.

PT New nucleic acid fragment isolated from Acinetobacter for converting  
 PT cyclohexanol to adipic acid, encodes adipic acid synthesizing enzymes  
 PT e.g. cyclohexanone monooxygenase and caprolactone hydrolase.

PS Example 2; Col 57-58; 43bp; English.

CC The invention relates to an isolated nucleic acid fragment from  
 CC Acinetobacter sp. encoding adipic acid synthesizing enzymes where the  
 CC nucleic acid comprises open reading frames encoding e.g. cyclohexanone  
 CC monooxygenase, 6-aldehyde hexanoic dehydrogenase and cyclohexanol  
 CC dehydrogenase. The nucleic acid fragment is useful for isolating cDNAs  
 CC and genes encoding homologous enzymes from the same or other bacterial  
 CC species, and for the conversion of cyclohexanol to adipic acid. The  
 CC nucleic acid fragment is also useful in immunological screening cDNA  
 CC expression libraries, and as probes for genetically and physically  
 CC mapping the genes that they are a part of, and as markers for traits  
 CC linked to expression of the enzymes. The nucleic acid fragment is useful  
 CC to design and produce primer pairs for use in the amplification reaction  
 CC or in primer extension reactions, and for the creation of recombinant  
 CC organisms that have the ability to produce adipic acid while growing on  
 CC cyclohexanol. The present sequence represents the amino acid sequence of  
 CC the Acinetobacter sp. hydrolase.

SO Sequence 300 AA;

Query Match 39.4%; Score 50; DB 6; Length 300;  
Best Local Similarity 22.7%; Pred. No. 1.8e+02;  
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKMADNGITVEELKQLLEQWN 23  
DB 20 RRMQENPNMTIEDFRSMFDEWH 41

RESULT 34  
AAE39415  
ID AAE39415 standard; protein; 300 AA.  
AC AAE39415;  
DT 18-DEC-2003 (first entry)  
DE Acinetobacter sp. caprolactone hydrolase.  
KW Adipic acid; nylon-6,6; lubricant; plasticiser; food acidulant; enzyme;  
KM caprolactone hydrolase.  
XX Acinetobacter sp.  
OS  
XX US2003087403-A1.  
PN 08-MAY-2003.  
PD  
XX 16-OCT-2002; 2002US-00272419.  
PF  
XX 19-FEB-1999; 99US-00252553.  
PR 14-JUL-1999; 99US-00648004.  
XX  
XX (CHEN/) CHENG Q.  
PA (NAGA/) NAGARAJAN V.  
PA (THOM/) THOMAS S M.  
XX  
XX Cheng Q, Nagarajan V, Thomas SM;  
PI  
XX WPI; 2003-755145/71.  
DR N-PSDB; AADS9830.  
XX  
XX New nucleic acid fragment encoding an adipic acid synthesizing enzyme,  
PT useful for producing nylon-6,6, lubricants and plasticizers, or as food  
PT acidulant.  
XX  
XX Claim 4; Page 31-32; 45pp; English.  
XX  
XX The present invention provides novel nucleic acid molecules derived from  
CC Acinetobacter sp. encoding adipic acid synthesizing enzymes, useful for  
CC producing nylon-6,6, lubricants and plasticizers. The invention is also  
CC useful as food acidulant. The present sequence is Acinetobacter sp.  
CC caprolactone hydrolase enzyme. This enzyme is involved in the synthesis  
CC of adipic acid  
XX  
XX Sequence 300 AA;

Query Match 39.4%; Score 50; DB 7; Length 300;  
Best Local Similarity 22.7%; Pred. No. 1.8e+02;  
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KKMADNGITVEELKQLLEQWN 23  
DB 20 RRMQENPNMTIEDFRSMFDEWH 41

RESULT 35  
ADG33790  
ID ADG33790 standard; protein; 469 AA.  
AC ADG33790;  
XX

DT 26-FEB-2004 (first entry)  
XX  
XX Actinomycetes dual condensation/epimerisation NRPS domain protein ID 49.  
DE  
XX non-ribosomal peptide synthetase; NRPS; dual condensation; epimerisation;  
KM ramoplanin; complestatin; actinomycetes taxon.  
XX  
XX Pseudomonas syringae pv. syringae.  
XX  
XX WO2003089641-A2.  
PN  
XX 30-OCT-2003.  
PD  
XX 17-APR-2003; 2003WO-CA000575.  
PF  
XX 17-APR-2002; 2002US-0372790P.  
PR  
XX (ECOP-) ECOPIA BIOSCIENCES INC.  
PA  
XX Farnet CM, Staiffa A;  
PI  
XX WPI; 2003-854123/79.  
DR N-PSDB; ADG33791.  
XX  
XX New dual condensation/epimerization non-ribosomal peptide synthetase  
PT domain and encoding polynucleotide, useful for modifying the  
PT stereochemistry of synthesized peptides (e.g. ramoplanin or complestatin)  
PT in vitro or in vivo.  
XX  
XX Claim 9; SEQ ID NO 49; 245pp; English.  
PS  
XX This invention relates to novel domains of non-ribosomal peptide  
CC synthetases (NRPSs) that exhibit dual condensation and epimerisation  
CC activities. Specifically, these domains allow incorporation of non-  
CC proteinogenic substrates (e.g. D-amino acids) into peptide products.  
CC Furthermore, they can be used in vivo to modify the stereochemistry of  
CC synthesised peptides (e.g. ramoplanin or complestatin) at selected amino  
CC acid sites by the addition of non-chiral residues. The present invention  
CC describes the identification of isolated polynucleotide NRPS domains in  
CC various organisms from the actinomycetes taxon, and the encoded  
CC polypeptides thereof, as well as suitable expression vectors. This  
CC polypeptide sequence is a dual condensation/epimerisation NRPS domain  
CC protein of the invention.  
XX  
XX Sequence 469 AA;

Query Match 39.4%; Score 50; DB 7; Length 469;  
Best Local Similarity 64.3%; Pred. No. 2.9e+02;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 ITVEELKQLLEQWN 23  
DB 432 LPLNERKQLLEQWN 445

RESULT 36  
AAB35470  
ID AAB35470 standard; protein; 516 AA.  
XX  
XX AAB35470;  
AC  
XX 06-JUN-2001 (first entry)  
DT  
XX Human cyclic nucleic acid phosphodiesterase PDE1B2.  
DE  
XX Human; cyclic nucleic acid phosphodiesterase; PDE1B2; spleen;  
KW cardiovascular disease; gastrointestinal disorder; sexual dysfunction.  
XX  
XX Homo sapiens.  
OS  
XX EP1085092-A1.  
PN  
XX 21-MAR-2001.  
PD

XX 14-SEP-2000; 2000EP-00307982.  
PF 17-SEP-1999; 99GB-00022125.  
PR (PFI2 ) PFIZER LTD.  
PA (PFI2 ) PFIZER INC.  
XX  
PI Fldock MD;  
XX  
XX WPI; 2001-246901/26.  
DR N-PSDB; AAF62301.  
XX  
PT Human cyclic nucleotide phosphodiesterase 1B2 and its nucleotide sequence  
PT useful for treating cardiovascular, gastrointestinal and spleen disorders  
PT and screening for drugs to treat associated disorders.  
PS  
XX Claim 1; Page 42-45; 58pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC human cyclic nucleic acid phosphodiesterase PDE1B2. This is thought to be  
CC a splice variant of PDE1, and capable of catalysing the degradation of  
CC cAMP and/or cGMP. The sequences are useful in the treatment of  
CC cardiovascular, gastrointestinal and spleen disorders, and in the  
CC enhancement of the male erectile response and treatment of female sexual  
CC dysfunction. The present sequence is the PDE1B2 protein  
XX  
SQ Sequence 516 AA;  
XX  
Query Match 39.4%; Score 50; DB 4; Length 516;  
Best Local Similarity 55.6%; Pred. No. 3.2e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 3 KXADNGTIVVEIKKOLE 20  
DB | : | | : | | : | |  
24 KOLENGEINIEELKKNLE 41  
XX  
RESULT 37  
ABM83406  
ID ABM83406 standard; protein; 534 AA.  
XX  
AC ABM83406;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human diagnostic and therapeutic protein SEQ ID NO:3655.  
XX  
KM gene therapy; human diagnostic and therapeutic polynucleotide; dltbp.  
XX  
OS Homo sapiens.  
XX  
PN WO2004023973-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 12-SEP-2003; 2003WO-US028227.  
XX  
PR 12-SEP-2002; 2002US-0410259P.  
PR 12-SEP-2002; 2002US-0410260P.  
XX  
PA (INCY-) INCYTE CORP.  
XX  
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic NM, Shen F;  
PI Hartshorne TA, Suchanowski MT, Altus CM, Pites SJ, Elder LV;  
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;  
PI Beralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES,  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzen D;  
PI Fatury S, Shi X, Suarez CJ;  
XX  
XX WPI; 2004-329368/30.

DR N-PSDB; ACN42058.  
XX  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
PS Claim 27; Page; 190pp; English.  
XX  
CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dltbp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dltbp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dltbp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
SQ Sequence 534 AA;  
XX  
Query Match 39.4%; Score 50; DB 8; Length 534;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 3 KXADNGTIVVEIKKOLE 20  
DB | : | | : | | : | |  
24 KOLENGEINIEELKKNLE 41  
XX  
RESULT 38  
AAW95110  
ID AAW95110 standard; protein; 536 AA.  
XX  
AC AAW95110;  
XX  
DT 26-MAY-1999 (first entry)  
XX  
DE Human RPW1 8392 cell phosphodiesterase, PDE1B1.  
XX  
KM Antisense oligodeoxynucleotide; phosphodiesterase; PDE1B1; enzyme; PDE;  
KM cell death; apoptosis; cancer; Ca2+-calmodulin; lymphoblastoid; RNase H;  
KM RPW1 8392; RNA degradation; cAMP; immunoproliferative disorder; breast;  
KM immune dysfunction; acute lympholytic leukemia; prostate; human.  
XX  
OS Homo sapiens.  
XX  
PN US5885834-A.  
XX  
PD 23-MAR-1999.  
XX  
PF 30-SEP-1997; 97US-00940332.  
XX  
PR 30-SEP-1996; 96US-0027207P.  
XX  
PA (EPST/) EPSTEIN P M.  
XX  
PI Epstein PM;  
XX  
XX WPI; 1999-228548/19.  
DR N-PSDB; AAX26288.  
XX  
PT Antisense oligodeoxynucleotides specific for mRNA encoding  
PT phosphodiesterase PDE1B1 enzymes and method for using them to induce  
PT apoptosis of cells - useful in the treatment of immunoproliferative  
PT disorders and immune dysfunctions.

XX Disclosure; Fig 8A-D; 35pp; English.  
PS  
XX  
CC The invention relates to antisense oligodeoxynucleotides (AS-ODN) which  
CC will bind to mRNA encoding phosphodiesterase PDE1B1 enzymes and their use  
CC in inducing programmed cell death (apoptosis) in cancer cells. PDE1 is a  
CC Ca2+-calmodulin dependent phosphodiesterase found in cytosolic extracts  
CC of human lymphoblastoid cell line, RPMI 8392. The method in which  
CC programmed cell death is induced in cancer cells comprises: (1)  
CC identifying the phosphodiesterase enzyme PDE1B1 in a cell line containing  
CC the cancer cells; (2) synthesizing an AS-ODN inhibitor which will bind to  
CC mRNA encoding PDE1B1; and (3) applying the AS-ODN to the cell line to  
CC inhibit the enzymatic activity of the PDE1B1 and induce apoptosis in the  
CC cells. The AS-ODNs inhibit the expression of a protein by two mechanisms:  
CC (i) by degradation of RNA by the ubiquitous enzyme RNase H, which  
CC selectively cleaves the RNA of DNA-RNA heteroduplexes; and (ii) the  
CC arrest of translation initiation caused by AS-ODN hybridization to the 5'  
CC un-translated region or the translation initiation site on the mRNA.  
CC Inhibition of phosphodiesterase (PDE) enzyme expression results in  
CC elevated levels of cAMP in the cells due to PDE1B1 being involved in the  
CC metabolism of cAMP. The elevated cAMP levels result in apoptosis by  
CC inhibition of DNA synthesis. The method and AS-ODN are useful in inducing  
CC cAMP stimulated apoptosis and in the treatment of immunoproliferative  
CC disorders and immune dysfunction such as acute lympholytic leukemia,  
CC breast and prostate cancer. The present sequence represents a human RPMI  
CC 8392 cell PDE1B1  
CC  
SQ Sequence 536 AA;  
Query Match 39.4%; Score 50; DB 2; Length 536;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
Qy 3 KXADNGTIVTELKQLE 20  
| : | | : | | | : | |  
Db 44 KOLENGEINIEELKNLE 61  
RESULT 39  
ADES8253  
ID ADE58253 standard; protein; 536 AA.  
AC ADE58253;  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Human Protein Q01064, SEQ ID NO 4124.  
DE  
XX  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003016475-A2.  
PN  
XX  
XX 27-FEB-2003.  
PD  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-033347P.  
XX  
XX (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
XX DR GENBANK: Q01064.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
SQ Sequence 536 AA;  
Query Match 39.4%; Score 50; DB 7; Length 536;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
Qy 3 KXADNGTIVTELKQLE 20  
| : | | : | | | : | |  
Db 44 KOLENGEINIEELKNLE 61  
RESULT 40  
ADO40394  
ID ADO40394 standard; protein; 536 AA.  
AC ADO40394;  
XX  
XX 18-NOV-2004 (first entry)  
DT  
XX  
XX Human phosphodiesterase 1B protein.  
DE  
XX  
XX Phosphodiesterase 1B; PDE1B; calmodulin-dependent phosphodiesterase 1B;  
KW hyperproliferative disorder; gene therapy; human; enzyme.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2004092461-A1.  
PN  
XX  
XX 13-MAY-2004.  
PD  
XX  
XX 11-NOV-2002; 2002US-00292312.  
PF  
XX  
XX 11-NOV-2002; 2002US-00292312.  
PR  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX  
XX Bennett CF, Dobie KW;  
XX  
XX WPI: 2004-374979/35.  
XX DR N-PSDB; ADO40339.  
XX  
XX

PT New compound that modulates phosphodiesterase 1B expression, useful in  
PT treating an animal having a disease or condition, i.e. hyperproliferative  
PT disorder.  
XX  
XX Disclosure; Page 21-23; 34pp; English.  
XX  
CC The present invention is directed to antisense oligonucleotides which are  
CC targeted to nucleic acid molecule encoding phosphodiesterase 1B (also  
CC known as PDE1B and calmodulin-dependent phosphodiesterase 1B) and which  
CC modulate the expression of phosphodiesterase 1B. The invention is  
CC useful in treating an animal having a disease or condition such as  
CC hyperproliferative disorder. The invention is also useful in gene  
CC therapy. The present sequence is human phosphodiesterase 1B protein.  
XX  
XX Sequence 536 AA;  
SQ  
Query Match 39.4%; Score 50; DB 8; Length 536;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 3 KMANGTITVEELKQLE 20  
DB 44 KQLENGEINIEELKKNLE 61  
| : | | | : | | | : | |  
RESULT 41  
ADS75985  
ID ADS75985 standard; protein; 536 AA.  
XX  
XX ADS75985;  
AC  
XX  
XX 16-DEC-2004 (first entry)  
DT  
XX  
XX Human phosphodiesterase 1B protein.  
DE  
XX  
XX cardiant; neuroprotective; nephrotoxic; cytostatic; gastrointestinal;  
XX respiratory; gene therapy; cancer; hematological disease;  
XX metabolic disease; cardiovascular disease; gastrointestinal disease;  
XX hepatic disease; neurological disease; urological disease;  
XX respiratory disease; phosphodiesterase 1B; PDE1B; human.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004080270-A2.  
PN  
XX  
XX 23-SEP-2004.  
PD  
XX  
XX 27-FEB-2004; 2004WO-EP002065.  
PF  
XX  
XX 13-MAR-2003; 2003EP-00005386.  
PR  
XX  
XX (FARB) BAYER HEALTHCARE AG.  
PA  
XX  
XX Golz S, Brueggemeier U, Geerts A;  
PI  
XX  
XX WPI; 2004-690439/67.  
DR  
XX  
XX N-PSDB; ADS75984.  
PT  
XX  
XX Screening for therapeutic agents for treating e.g., cardiovascular or  
PT neurological diseases by contacting a test compound with a  
PT phosphodiesterase 1B (PDE1B) polypeptide or polynucleotide and detecting  
PT binding of the test compound.  
XX  
XX Disclosure; SEQ ID NO 2; 131pp; English.  
XX  
XX The invention relates to a method of screening for therapeutic agents for  
XX treating a disease consisting of cancer or hematological, metabolic,  
XX cardiovascular, gastrointestinal, hepatic, neurological, urological or  
XX respiratory diseases in a mammal by: (a) contacting a test compound or  
XX a phosphodiesterase 1B (PDE1B) polypeptide or polynucleotide; and (b)  
XX detecting binding of the test compound to the PDE1B polypeptide or  
XX polynucleotide. Screening for therapeutic agents for treating a disease  
XX consisting of cancer or hematological, metabolic, cardiovascular,

CC gastrointestinal, hepatic, neurological, urological or respiratory  
CC diseases in a mammal. The regulators of PDE1B are useful in regulating  
CC PDE1B activity in a mammal having a disease comprising cancer or  
CC hematological, metabolic, cardiovascular, gastrointestinal, hepatic,  
CC neurological, urological or respiratory diseases. This sequence  
CC represents the human phosphodiesterase 1B protein.  
XX  
XX Sequence 536 AA;  
SQ  
Query Match 39.4%; Score 50; DB 8; Length 536;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 3 KMANGTITVEELKQLE 20  
DB 44 KQLENGEINIEELKKNLE 61  
| : | | | : | | | : | |  
RESULT 42  
ADF04444  
ID ADF04444 standard; protein; 537 AA.  
XX  
XX ADF04444;  
AC  
XX  
XX 12-FEB-2004 (first entry)  
DT  
XX  
XX Bacterial polypeptide #557.  
DE  
XX  
XX Proteus mirabilis infection; bacterial infection; antibacterial;  
XX immunostimulant.  
XX  
XX Proteus mirabilis.  
OS  
XX  
XX US6605709-B1.  
PN  
XX  
XX 12-AUG-2003.  
PD  
XX  
XX 05-APR-2000; 2000US-00543681.  
PF  
XX  
XX 09-APR-1999; 99US-0128706P.  
PR  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PA  
XX  
XX Breton GL;  
PI  
XX  
XX WPI; 2003-695291/82.  
DR  
XX  
XX N-PSDB; ADF00272.  
PT  
XX  
XX New Proteus mirabilis polypeptides and polynucleotides, useful as  
PT reagents for diagnosis of bacterial disease, as components of  
PT antibacterial vaccines, as targets for antibacterial drugs, or as  
PT biocontrol agents for plants.  
XX  
XX Disclosure; SEQ ID NO 4729; 870pp; English.  
XX  
XX The invention relates to new Proteus mirabilis polypeptides and  
XX polynucleotides. The invention also relates to antibodies against the  
XX polypeptides, methods for producing the polypeptides, a method of  
XX generating vaccines for immunising an individual against P. mirabilis, a  
XX method for evaluating a compound for the ability to bind a P. mirabilis  
XX polypeptide and a method for screening test compounds for anti-bacterial  
XX activity. The polypeptides and polynucleotides are useful as molecular  
XX targets for diagnosing, preventing and treating pathological conditions  
XX resulting from bacterial infection, as reagents for diagnosis of  
XX bacterial diseases, as components of antibacterial vaccines, as targets  
XX for antibacterial drugs or as bio-control agents for plants. This  
XX sequence represents a Proteus mirabilis polypeptide of the invention.  
XX  
XX Sequence 537 AA;  
SQ  
Query Match 39.4%; Score 50; DB 7; Length 537;  
Best Local Similarity 36.4%; Pred. No. 3.4e+02;  
Matches 8; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

OY 3 KMAADNGTIVTEELKOLLEQWNL 24  
 DB 111 KRVYNGSASLEDEPPELLEDKWHL 132

## RESULT 43

AA19080  
 ID AAB19080 standard; protein; 545 AA.

AC AAB19080;

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of a 60 kDa protein from Campylobacter jejuni.

KM Antigenic protein; flagellales mutant; vaccine; poultry; Campylobacter.

OS Campylobacter jejuni.

PN EP1043029-A1.

PD 11-OCT-2000.

PF 03-APR-2000; 2000EP-00201203.

PR 09-APR-1999; 99EP-00201086.

XX (ALKU) AKZO NOBEL NV.

PI Jacobs AAC, Van Den Bosch JF, Nuijten PWM;

DR WPI; 2000-589147/56.

XX Novel Campylobacter antigenic proteins, useful for the production of

PT vaccines for protecting poultry form Campylobacter infection.

XX Disclosure; Page 12-14; 21pp; English.

CC The present sequence represents a 60 kDa protein of Campylobacter jejuni.

CC The protein is antigenic, and is visible on a Western blot of C. jejuni

CC protein after incubation of the blot with antibodies against a

CC flagellales mutant of C. jejuni but not visible after incubation with

CC antibodies against wild type C. jejuni. The proteins are used to produce

CC vaccines which are useful for protecting animals, especially poultry,

CC against Campylobacter, especially C. jejuni

SQ Sequence 545 AA;

Query Match 39.4%; Score 50; DB 3; Length 545;

Best Local Similarity 41.7%; Pred. No. 3.4e+02;

Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 2 KMAADNGTIVTEELKOLLEQWNLV 25

DB 166 EKVGKDGIVTEEPKSIINDELNV 189

## RESULT 44

ABM83407  
 ID ABM83407 standard; protein; 554 AA.

AC ABM83407;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pproteins SEQ ID NO:3656.

KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

OS Homo sapiens.

PN WO2004023973-A2.

XX 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthshorne TA, Suchorolski MT, Altus CM, Pits SJ, Rider LV;

PI Mooney EM, Deleagane AM, Panesar IS, Bannville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirtan ES;

PI Lu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patuay S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN42059.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders, endocrine

CC autoimmune/inflammatory disorder, developmental disorders, or

CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dthp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dthp protein of the

CC invention. Note: The sequence data for this patent is not represented in

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm

SQ Sequence 554 AA;

Query Match 39.4%; Score 50; DB 8; Length 554;

Best Local Similarity 55.6%; Pred. No. 3.5e+02;

Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 KMAADNGTIVTEELKOLLE 20

DB 44 KQLENGEINTEELKQWLE 61

## RESULT 45

ABU48797  
 ID ABU48797 standard; protein; 673 AA.

AC ABU48797;

DT 19-JUN-2003 (first entry)

DE Protein encoded by prokaryotic essential gene #34324.

KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Ureaplasma urealyticum.

PN WO200277183-A2.

XX	03-OCT-2002.
PX	
PF	21-MAR-2002; 2002MO-USO09107.
PR	
PR	21-MAR-2001; 2001US-00815242.
PR	06-SEP-2001; 2001US-00948993.
PR	25-OCT-2001; 2001US-0342923P.
PR	08-FEB-2002; 2002US-00072851.
PR	06-MAR-2002; 2002US-0362699P.
XX	
PA	(ELIT-) ELITRA PHARM INC.
XX	
PI	Mang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;
PI	Wali D, Traawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX	
XI	WPI; 2003-029926/02.
DR	N-PSDB; ACA52667.
XX	
PT	New antisense nucleic acid, useful for identifying proteins or screening
PT	for homologous nucleic acids required for cellular proliferation to
PT	isolate candidate molecules for rational drug discovery programs.
XX	
PS	Claim 25; SEQ ID NO 76721; 1766pp; English.
CC	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC	proliferation or the activity of a gene in an operon required for
CC	proliferation; (7) identifying a compound that influences the activity of
CC	the gene product or that has an activity against a biological pathway
CC	required for proliferation, or that inhibits cellular proliferation; (8)
CC	identifying a gene required for cellular proliferation or the biological
CC	pathway in which a proliferation-required gene or its gene product lies
CC	or a gene on which the test compound that inhibits proliferation of an
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC	compound's activity; (11) a culture comprising strains in which the gene
CC	product is overexpressed or underexpressed; (12) determining the extent
CC	to which each of the strains is present in a culture or collection of
CC	strains; or (13) identifying the target of a compound that inhibits the
CC	proliferation of an organism. The antisense nucleic acids are useful for
CC	identifying proteins or screening for homologous nucleic acids required
CC	for cellular proliferation to isolate candidate molecules for rational
CC	drug discovery programs, or for screening homologous nucleic acids
CC	required for proliferation in cells other than S. aureus, S. typhimurium,
CC	K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC	the target prokaryotic essential genes. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
CC	
SQ	Sequence 673 AA;
	Query March 39 4% Score 50; DB 6; Length 673;
	Best Local Similarity 66.7%; Pred. No. 4.3e+02;
	Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy	12 VEEIKQLLEQNN 23 ::   :
Dd	8 IDELKQKLDQNN 19 ::   :
RESULT 46	
ID	ADB64170 standard; protein; 808 AA.
XC	ADB64170;
XC	

```

ADE71288
ID ADE71288 standard; protein; 867 AA.
XX
AC ADE71288;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel human protein #42.
XX
KM human; novel protein; drug.
XX
OS Homo sapiens.
XX
PN JP2002345493-A.
XX
PD 03-DEC-2002.
XX
PF 29-MAR-2001; 2002JP-00049046.
XX
PR 29-MAR-2001; 2001JP-00095524.
XX
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX
DR WPI; 2003-460885/44.
DR N-PSDB; ADE71226.
XX
PT A gene and a protein encoded by it, used in drugs.
XX
PS Disclosure; Page 189-192; 257pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC human proteins. The DNA and protein sequences of the invention are used
CC in drugs. The present amino acid sequence represents a novel human
CC protein of the invention.
XX
SQ Sequence 867 AA;

Query Match          39.4%; Score 50; DB 7; Length 867;
Best Local Similarity 48.0%; Pred. No. 5.7e+02;
Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 3 KXADNGTITVEBELKQLEQ--MWLV 25
DB 297 KXADGKTTTEBELVLLEBGTWNSI 321

RESULT 48
ABB77073
ID ABB77073 standard; protein; 1803 AA.
XX
AC ABB77073;
XX
DT 15-JUL-2002 (first entry)
XX
DE Euglena gracilis pyruvate:NADP+ oxidoreductase #2.
XX
KM PNO; pyruvate:NADP+ oxidoreductase; antiparasitic; transgenic plant;
KM nicotinamide adenine dinucleotide phosphate; enzyme.
XX
OS Euglena gracilis.
XX
FH Key
FH Peptide 1..37
FT /label= Signal_peptide
FT Protein 38..1803
FT /label= Mature_PNO
XX
PN WO200214522-A1.
XX
PD 21-FEB-2002.
XX
PF 11-AUG-2001; 2001WO-EP009317.
XX

```

```

PR 17-AUG-2000; 2000EP-00117730.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Cirpus P, Lerchl J, Martin W, Rotte C;
XX
DR WPI; 2002-329577/36.
DR N-PSDB; ABL55676.
XX
PT Polynucleotide encoding pyruvate:nicotinamide adenine dinucleotide
PT phosphate+ oxidoreductases and polypeptide for identifying of an agonist
PT or antagonist of PNO activity useful for treating parasite infections.
XX
PS Claim 1; Page 102-105; 112pp; English.
XX
CC The sequence represents Euglena gracilis pyruvate:NADP+ oxidoreductase.
CC CC The invention relates to a novel polynucleotide encoding pyruvate:
CC nicotinamide adenine dinucleotide phosphate (NADP)+ oxidoreductases
CC (PNO). The PNO of the invention has antiparasitic activity. The
CC polynucleotide and polypeptide are useful for production of transgenic
CC plants, plant cells or plant tissue
XX
SQ Sequence 1803 AA;

Query Match          39.4%; Score 50; DB 5; Length 1803;
Best Local Similarity 47.8%; Pred. No. 1.2e+03;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 1 KXKMDNGTITVEBELKQLEQWN 23
DB 963 EKXVADGGLTTL--LAQWLDQWN 983

RESULT 49
ABB77072
ID ABB77072 standard; protein; 1805 AA.
XX
AC ABB77072;
XX
DT 15-JUL-2002 (first entry)
XX
DE Euglena gracilis pyruvate:NADP+ oxidoreductase #1.
XX
KM PNO; pyruvate:NADP+ oxidoreductase; antiparasitic; transgenic plant;
KM nicotinamide adenine dinucleotide phosphate; enzyme.
XX
OS Euglena gracilis.
XX
FH Key
FH Peptide 1..39
FT /label= Signal_peptide
FT Protein 40..1805
FT /label= Mature_PNO
XX
PN WO200214522-A1.
XX
PD 21-FEB-2002.
XX
PF 11-AUG-2001; 2001WO-EP009317.
XX
PR 17-AUG-2000; 2000EP-00117730.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Cirpus P, Lerchl J, Martin W, Rotte C;
XX
DR WPI; 2002-329577/36.
XX
PT Polynucleotide encoding pyruvate:nicotinamide adenine dinucleotide
PT phosphate+ oxidoreductases and polypeptide for identifying of an agonist
PT or antagonist of PNO activity useful for treating parasite infections.
XX
PS Claim 1; Fig 5A; 112pp; English.
XX

```



Job time : 154.511 secs

XX The sequence represents Euglena gracilis pyruvate:NADP+ oxidoreductase.  
 CC The invention relates to a novel polynucleotide encoding pyruvate:  
 CC nicotinamide adenine dinucleotide phosphate (NADP)+ oxidoreductases  
 CC (PNO). The PNO of the invention has antiparasitic activity. The  
 CC polynucleotide and polypeptide are useful for production of transgenic  
 CC plants, plant cells or plant tissue

SQ Sequence 1805 AA;

Query Match 39.4%; Score 50; DB 5; Length 1805;  
 Best Local Similarity 47.8%; Pred. No. 1.2e+03;

Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 1 KKKMADNGTIVTEELKOLLEQWN 23

Db 965 EKKVADGELTTL--LAQWLQDWN 985

RESULT 50

ADN04333

ID ADN04333 standard; protein; 2000 AA.

XX ADN04333;

DT 01-JUL-2004 (first entry)

DE Antiparasitic protein sequence #361.

XX antiparasitic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX PN. WO2004028479-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.

XX (GETH ) GENENTECH INC.

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WT;

XX WI TP;

XX WPI; 2004-305105/28.

XX N-PSDB; ADN04332.

XX New PRO nucleic acid or polypeptide, useful for preparing a

XX pharmaceutical composition for diagnosing or treating psoriasis in a

XX Claim 9; SEQ ID NO 727; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for

XX creating psoriasis or a sequence having at least 80% identity to the

XX above sequences. The nucleic acid is useful for preparing a composition

XX for diagnosing or treating psoriasis in a mammal. This sequence

XX corresponds to one of the polypeptides of the invention.

SQ Sequence 2000 AA;

QY 2 KKMADNGTIVTEELKOLLEQWN 22

Db 1828 KKLSDDWTKGKEIQRLQAF 1848

Search completed: May 11, 2005, 21:22:54

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 21:13:34 ; Search time 25 Seconds  
(without alignments)  
96.217 Million cell updates/sec

Title: US-10-712-812-6  
Perfect score: 127  
Sequence: 1 KKKMADNGTIVEELKQLLEQMNLY 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	48.8	376	2	TS1170
2	55	43.3	206	1	TVH00A
3	53	41.7	351	2	E97225
4	52	40.9	206	1	TV0JRA
5	52	40.9	206	1	JN0622
6	52	40.9	545	2	G81328
7	51	40.2	105	2	T22980
8	51	40.2	344	2	D83894
9	51	40.2	626	2	S35311
10	51	40.2	626	2	AC1619
11	50	40.2	264	2	AG1256
12	50	39.4	264	2	T38795
13	50	39.4	294	2	T25085
14	50	39.4	323	2	C64087
15	50	39.4	536	1	JC6129
16	50	39.4	550	2	S35309
17	50	39.4	673	2	P82930
18	50	39.4	819	2	S61217
19	50	39.4	882	2	S41034
20	50	39.4	1030	2	A32612
21	50	39.4	1325	2	T14790
22	50	39.4	1472	2	A35715
23	50	39.4	2477	1	SUC8A
24	49	38.6	35	2	S16552
25	49	38.6	218	2	S50566
26	49	38.6	462	2	B32840
27	49	38.6	475	2	B27671
28	49	38.6	485	2	C97022
29	49	38.6	506	2	AC0845

30	49	38.6	529	2	A65051	ygaA protein - Esc
31	49	38.6	529	2	E91074	probable 2-compone
32	49	38.6	529	2	D85919	probable 2-compone
33	49	38.6	534	1	A44152	3',5'-cyclic-nucle
34	49	38.6	535	1	A44151	3',5'-cyclic-nucle
35	49	38.6	535	1	A46378	3',5'-cyclic-nucle
36	49	38.6	643	1	H64119	threonine-tRNA lig
37	48	37.8	159	1	S56237	glucosamine-phosph
38	48	37.8	299	2	D83010	probable binding p
39	48	37.8	309	2	T23021	hypothetical prote
40	48	37.8	312	2	AC0897	TDC operon transcr
41	48	37.8	312	2	AG2311	hypothetical prote
42	48	37.8	423	2	T29549	ATP-dependent RNA
43	48	37.8	441	2	AB1290	ATP-dependent RNA
44	48	37.8	442	2	AH1661	hypothetical prote
45	48	37.8	447	2	P90248	hypothetical prote
46	48	37.8	462	2	S52528	UUA1 protein - yea
47	48	37.8	914	2	B75017	alanyl-tRNA synth
48	48	37.8	1273	2	T42405	sax-3 protein - Ca
49	48	37.8	1964	2	A59282	nonmuscle myosin I
50	47.5	37.4	294	2	S60545	envelope polypept
51	47.5	37.4	294	2	S60524	envelope polypept
52	47	37.0	190	2	T08258	conserved hypotet
53	47	37.0	281	2	T01445	hypothetical prote
54	47	37.0	407	2	S27774	transforming prote
55	47	37.0	472	2	H05053	hypothetical prote
56	47	37.0	627	2	B83692	hypothetical prote
57	47	37.0	659	2	S74435	arginine decarboxy
58	47	37.0	667	2	S75959	nitrate transport
59	47	37.0	749	2	JC7729	replication protei
60	47	37.0	1067	2	T06312	hypothetical prote
61	47	37.0	1198	2	D96723	hypothetical prote
62	46.5	36.6	201	2	E97339	HAD superfamily hy
63	46.5	36.6	428	2	G82238	adenosylmethionine
64	46.5	36.6	594	2	A82913	hypothetical prote
65	46	36.2	118	2	E90178	hypothetical prote
66	46	36.2	335	2	F72404	flagellar motor sw
67	46	36.2	340	2	EG9527	hypothetical prote
68	46	36.2	420	2	C71407	hypothetical prote
69	46	36.2	473	2	T50420	nonerythroid alpha
70	46	36.2	474	2	H72403	glycine dehydrogen
71	46	36.2	475	2	A27671	spectrin alpha cha
72	46	36.2	477	2	E64595	hypothetical prote
73	46	36.2	477	2	F71918	hypothetical prote
74	46	36.2	544	2	I40731	heat shock protein
75	46	36.2	544	2	B41479	60K heat shock pro
76	46	36.2	544	2	UJ0117	hspB protein - Chl
77	46	36.2	544	2	B81556	60 kDa chaperonin
78	46	36.2	544	2	F86507	heat shock protein
79	46	36.2	544	2	S19023	chaperonin GroEL -
80	46	36.2	544	2	D81709	60 kDa chaperonin
81	46	36.2	544	2	A71555	probable hsp-60 -
82	46	36.2	560	2	AB2043	chaperonin GroEL
83	46	36.2	963	2	B83502	ribonucleoside red
84	45.5	35.8	88	2	AB2591	conserved hypotet
85	45.5	35.8	88	2	B97373	hypothetical prote
86	45.5	35.8	138	2	H90461	hypothetical prote
87	45.5	35.8	206	1	E64317	hypothetical prote
88	45.5	35.8	422	1	AD0141	adenosylmethionine
89	45.5	35.8	490	2	T08873	calcium-dependent
90	45.5	35.8	644	2	T02366	hypothetical prote
91	45.5	35.8	759	2	D89946	hypothetical prote
92	45.5	35.8	3488	2	T74418	protein-export mem
93	45	35.4	104	2	F90183	hypothetical prote
94	45	35.4	106	2	FN0468	hypothetical prote
95	45	35.4	118	2	G70478	hypothetical prote
96	45	35.4	128	2	C69183	hypothetical prote
97	45	35.4	150	2	T47315	hypothetical prote
98	45	35.4	207	2	A69349	conserved hypotet
99	45	35.4	226	2	S37434	membrane glycoprot
100	45	35.4	226	2	D49591	membrane protein M
101	45	35.4	260	1	A38585	deoxycytidine kina
102	45	35.4	307	2	T45998	hypothetical prote

103	45	35.4	318	2	T43492	hypothetical prote	176	43.5	34.3	501	2	G85097	hypothetical prote
104	45	35.4	376	2	S55892	endo-1,4-beta-xylo	177	43.5	34.3	516	2	T33061	hypothetical prote
105	45	35.4	401	2	E72213	probable 2,3-bisph	178	43.5	34.3	571	2	T00835	calcium-dependent
106	45	35.4	459	2	H82426	probable regulator	179	43.5	34.3	635	2	T49694	hypothetical prote
107	45	35.4	468	2	F82012	hypothetical prote	180	43.5	34.3	761	2	B69797	transcription regu
108	45	35.4	470	2	T11049	hypothetical prote	181	43.5	34.3	1165	2	S58236	pyruvate (flavodox
109	45	35.4	473	2	T15998	hypothetical prote	182	43	33.9	71	2	E98040	degenerative trans
110	45	35.4	514	2	T10938	calcium-dependent	183	43	33.9	80	2	B82267	exodeoxyribonuclea
111	45	35.4	543	2	S70013	chaperonin-like pr	184	43	33.9	145	2	A56085	regulatory protein
112	45	35.4	546	2	S36237	chaperonin groEL -	185	43	33.9	146	2	D83676	transcription regu
113	45	35.4	546	2	B71986	60kDa chaperone -	186	43	33.9	163	2	G69035	hypothetical prote
114	45	35.4	560	1	DOCGA	NAO-diphthamide AD	187	43	33.9	178	2	AG0049	hypothetical prote
115	45	35.4	560	1	DOCGPO	NAO-diphthamide AD	188	43	33.9	184	2	S41960	ras-related GTP-bi
116	45	35.4	755	2	T47806	hypothetical prote	189	43	33.9	184	2	I55401	ras-related protei
117	45	35.4	897	2	AC2001	hypothetical prote	190	43	33.9	186	2	F89831	hypothetical prote
118	45	35.4	1052	2	T17093	intraluminal subti	191	43	33.9	192	2	S16509	DNA-invertase - St
119	45	35.4	1052	2	T17093	hypothetical prote	192	43	33.9	197	2	S11781	DNA-invertase - St
120	45	35.4	1549	2	T21809	hypothetical prote	193	43	33.9	199	2	A44033	ubiquinol-cytochro
121	45	35.4	1596	2	T00057	genome polyprotein	194	43	33.9	237	2	D97801	hypothetical prote
122	45	35.4	1696	2	R10057	conserved hypoteth	195	43	33.9	267	2	H69373	hypothetical prote
123	44.5	35.0	146	2	G90201	transcription regu	196	43	33.9	278	2	T24444	hypothetical prote
124	44.5	35.0	260	2	A80330	hypothetical prote	197	43	33.9	279	2	B72255	dimethyladenosine
125	44.5	35.0	271	2	A82209	rRNA (adenine-N6,N	198	43	33.9	292	2	D85863	probable regulator
126	44.5	35.0	280	2	G68881	hypothetical prote	199	43	33.9	292	2	B91019	probable transcrip
127	44.5	35.0	314	2	G37050	DNA-methyltransfer	200	43	33.9	306	2	A48118	major epidermal ca
128	44.5	35.0	532	2	S22262	transcription fact	201	43	33.9	322	2	S52032	triase-phosphate 1
129	44.5	35.0	536	2	T05500	calcium-dependent	202	43	33.9	325	2	T32838	hypothetical prote
130	44.5	35.0	852	2	T12016	envelope glycoprot	203	43	33.9	336	2	S74424	sphx protein - Syn
131	44.5	35.0	1384	2	S78132	DNA-directed RNA p	204	43	33.9	353	2	T15429	hypothetical prote
132	44.5	35.0	3770	2	A40889	delta-(U-alpha-ami	205	43	33.9	364	2	A84099	hypothetical prote
133	44	34.6	100	2	D86891	hypothetical prote	206	43	33.9	370	2	A49360	pyruvate dehydroge
134	44	34.6	151	2	D86891	hypothetical prote	207	43	33.9	379	2	H84398	phosphate ABC tran
135	44	34.6	182	2	B70335	hypothetical prote	208	43	33.9	382	2	F82428	iron-containing al
136	44	34.6	183	2	A96606	conserved hypoteth	209	43	33.9	389	2	A86706	hypothetical prote
137	44	34.6	186	2	F82508	unknown protein F1	210	43	33.9	394	2	D83002	multidrug resistan
138	44	34.6	258	2	A59369	hypothetical prote	211	43	33.9	399	2	A82351	DNA/pantothenate m
139	44	34.6	271	2	A30592	ubiquinol-cytochro	212	43	33.9	404	2	S76573	transcription init
140	44	34.6	308	1	F69752	33K cytoskeletal p	213	43	33.9	414	2	G70360	hypothetical prote
141	44	34.6	407	2	T24951	5-dehydro-4-deoxyg	214	43	33.9	420	2	AH2225	two-component sens
142	44	34.6	429	2	D70763	hypothetical prote	215	43	33.9	460	2	D70435	hypothetical prote
143	44	34.6	443	2	B75165	threonine ammonia-	216	43	33.9	468	2	D85828	gluconate-6-phosph
144	44	34.6	443	2	B75165	signal recognition	217	43	33.9	468	2	F90982	gluconate-6-phosph
145	44	34.6	500	2	A71874	hypothetical prote	218	43	33.9	469	2	A72377	6-phosphogluconate
146	44	34.6	511	2	H89758	histidine ammonia-	219	43	33.9	473	2	D83508	two-component resp
147	44	34.6	540	2	D81192	chaperonin, 60 kD	220	43	33.9	481	2	UQ1147	N-acetylilmuramoyl-L
148	44	34.6	553	2	D84133	hypothetical prote	221	43	33.9	499	2	AH0485	proteobacterial prote
149	44	34.6	555	2	S12639	ATP-binding protei	222	43	33.9	510	2	B70368	L-aspartate oxidas
150	44	34.6	571	2	C70353	succinate dehydrog	223	43	33.9	521	2	B71717	hypothetical prote
151	44	34.6	601	2	C81044	hypothetical prote	224	43	33.9	526	2	B86149	TlN6.20 protein -
152	44	34.6	603	2	G82738	gamma-glutamyltran	225	43	33.9	539	2	S22342	chaperonin HSP60 -
153	44	34.6	611	1	S62811	oligoendopeptidase	226	43	33.9	541	2	S68249	chaperonin groEL, h
154	44	34.6	750	2	S34683	hypothetical prote	227	43	33.9	543	2	F97232	heat shock protein
155	44	34.6	919	2	B83212	probable sensor/re	228	43	33.9	543	2	B41872	hypothetical prote
156	44	34.6	940	2	B81852	probable type III	229	43	33.9	543	2	T30186	chaperonin groEL-2
157	44	34.6	1019	2	F70342	cation efflux syst	230	43	33.9	552	2	S74322	glutathione-disulf
158	44	34.6	1415	2	C86438	hypothetical prote	231	43	33.9	565	2	T47625	calcium-dependent
159	44	34.6	1577	2	T30858	glycosyltransferas	232	43	33.9	577	2	T51264	CPB60 protein [imp
160	44	34.6	1905	2	T51553	plexin - African c	233	43	33.9	589	2	H90112	proflinaggrin - hum
161	44	34.6	2094	2	S33124	lpr protein - huma	234	43	33.9	591	2	A45135	major capsid prote
162	44	34.6	5369	2	T44807	myosubtilin synth	235	43	33.9	602	2	T13219	calcium-dependent
163	43.5	34.3	209	2	H69901	general stress pro	236	43	33.9	602	2	S60052	arginine decarboxy
164	43.5	34.3	248	2	E90295	hypothetical prote	237	43	33.9	615	2	F45772	arginine decarboxy
165	43.5	34.3	279	2	C90468	hypothetical prote	238	43	33.9	615	2	T18677	hypothetical prote
166	43.5	34.3	279	2	A86312	FLA6.5 protein -	239	43	33.9	642	2	C81345	endopeptidase Clp
167	43.5	34.3	316	2	E90401	hypothetical prote	240	43	33.9	821	1	S76330	alcohol-acetaldehy
168	43.5	34.3	316	2	A99307	hypothetical prote	241	43	33.9	890	2	C98101	transcription fact
169	43.5	34.3	316	2	H90426	hypothetical prote	242	43	33.9	1187	2	T46637	zinc finger protei
170	43.5	34.3	355	2	S74678	hypothetical prote	243	43	33.9	1188	2	T46608	protein F40E12.2 [
171	43.5	34.3	370	2	G97277	glycosyltransferas	244	43	33.9	1245	2	C88104	hypothetical prote
172	43.5	34.3	429	1	UC5005	adenosylmethionine	245	43	33.9	1245	2	T31953	hypothetical prote
173	43.5	34.3	429	1	AG0596	adenosylmethionine	246	43	33.9	1247	2	C89583	protein K0783.1 [i
174	43.5	34.3	467	2	F96773	geranylgeranyl red	247	43	33.9	1374	2	S62524	probable RNA helic
175	43.5	34.3	495	1	S46284	calcium-dependent	248	43	33.9	1495	2	S61023	hypothetical prote

249	42.5	33.5	58	2	T04616	hypothetical prote	322	42	33.1	466	2	T30040	hypothetical prote
250	42.5	33.5	147	2	A29910	myosin calcium-bn	323	42	33.1	482	2	T01659	phosphoglucuronate d
251	42.5	33.5	189	2	S39864	late competence op	324	42	33.1	484	2	T01658	phosphoglucuronate d
252	42.5	33.5	224	2	D89836	hypothetical prote	325	42	33.1	484	2	B33501	myosin heavy chain
253	42.5	33.5	265	2	S73334	probable lipoprote	326	42	33.1	494	2	S75398	lysine-tRNA ligase
254	42.5	33.5	321	2	A63088	conserved hypotet	327	42	33.1	509	2	A61295	Bifunctional phosph
255	42.5	33.5	340	2	PH0217	reverse transcript	328	42	33.1	509	2	AC1667	Bifunctional phosph
256	42.5	33.5	376	2	T16050	hypothetical prote	329	42	33.1	510	2	JC7886	cytochrome P450 92
257	42.5	33.5	428	2	S09134	gene ND4L intron 1	330	42	33.1	521	2	G96543	calcium-dependent
258	42.5	33.5	429	1	XNCCDP	adenosylmethionine	331	42	33.1	529	1	S71774	calcium-dependent
259	42.5	33.5	429	2	E85585	7,8-diaminopelarg	332	42	33.1	553	1	T02139	calcium-dependent
260	42.5	33.5	429	2	D90735	calcium-dependent	333	42	33.1	554	1	T03263	calcium-dependent
261	42.5	33.5	490	1	S71776	probable RNA-direc	334	42	33.1	604	2	G89864	hypothetical prote
262	42.5	33.5	513	2	S21976	hypothetical prote	335	42	33.1	611	2	T21747	hypothetical prote
263	42.5	33.5	523	2	S23347	dihydroxy-acid deh	336	42	33.1	621	2	S10450	myosin heavy chain
264	42.5	33.5	558	2	B99492	flagellar hook-aaa	337	42	33.1	624	2	A55220	penicillin-binding
265	42.5	33.5	666	2	S71032	probable RNA-direc	338	42	33.1	654	2	T17959	hypothetical prote
266	42.5	33.5	685	2	S16783	hypothetical prote	339	42	33.1	667	2	B97012	methy1-accepting c
267	42.5	33.5	821	2	T24728	hypothetical prote	340	42	33.1	674	2	S74506	ribonuclease E - S
268	42.5	33.5	932	2	H86325	hypothetical prote	341	42	33.1	684	2	S60266	novel antigen rece
269	42.5	33.5	1076	2	I39580	ncca protein - Alc	342	42	33.1	692	1	S46953	phosphotransferase
270	42.5	33.5	1481	2	S78373	DNA-directed RNA p	343	42	33.1	712	1	A47331	ribonucleoside-tri
271	42.5	33.5	1601	2	AE2011	hypothetical prote	344	42	33.1	712	2	AC1058	ribonucleoside-tri
272	42.5	33.5	1809	2	S57329	tuberosus sclerosis	345	42	33.1	712	2	G91280	anaerobic ribonuc
273	42.5	33.1	55	2	F56976	transfer complex p	346	42	33.1	712	2	G86121	polypeptide synthet
274	42.5	33.1	82	2	A99836	hypothetical prote	347	42	33.1	750	2	AC3008	hypothetical prote
275	42.5	33.1	82	2	C85694	unknown protein en	348	42	33.1	757	2	T24266	hypothetical prote
276	42.5	33.1	103	2	F69110	hypothetical prote	349	42	33.1	770	2	F88275	barfingcin mxi syn
277	42.5	33.1	134	2	AE2496	transposase Alr714	350	42	33.1	910	2	B89918	2-oxoglutarate deh
278	42.5	33.1	135	2	T29428	hypothetical prote	351	42	33.1	979	2	E72236	clostritpain-relate
279	42.5	33.1	158	2	A72562	hypothetical prote	352	42	33.1	1125	2	T30298	dynamin heavy chain
280	42.5	33.1	159	2	T10826	probable resistanc	353	42	33.1	1169	2	A64505	pl15 homolog - Met
281	42.5	33.1	159	2	T10837	conserved resistanc	354	42	33.1	1203	2	B55094	chromosomal protei
282	42.5	33.1	172	2	G69087	conserved hypotet	355	42	33.1	1268	2	A49674	flightless-I homol
283	42.5	33.1	185	2	G69626	ribosome recycling	356	42	33.1	1286	2	A88396	protein M01E10.2 (
284	42.5	33.1	189	2	B69044	conserved hypotet	357	42	33.1	1305	2	T00670	probable inositol
285	42.5	33.1	190	2	F69187	epoxidase - Methan	358	42	33.1	1365	1	RN1VC2	DNA-directed RNA p
286	42.5	33.1	191	2	T10620	probable calcium-b	359	42	33.1	1409	2	T29594	hypothetical prote
287	42.5	33.1	204	2	T25760	hypothetical prote	360	42	33.1	1583	2	AB2137	hypothetical prote
288	42.5	33.1	207	2	E38625	GTP-binding protei	361	42	33.1	1733	2	D70887	probable polyketid
289	42.5	33.1	222	2	H82169	phage shock protei	362	42	33.1	1938	2	UC5421	smooth muscle myos
290	42.5	33.1	225	2	AF0219	basal-body rod mod	363	42	33.1	1972	1	A41604	myosin heavy chain
291	42.5	33.1	229	1	B43685	nonstructural - Sen	364	42	33.1	1972	2	UC5420	smooth muscle myos
292	42.5	33.1	230	1	JC2582	somatolactin - Sen	365	42	33.1	3026	2	T28431	varian surface pr
293	42.5	33.1	244	2	E72364	ABC transporter. A	366	42	33.1	3759	2	A35085	trithorax protein
294	42.5	33.1	282	2	H70671	probable oxidoredu	367	42	32.7	82	2	D64329	hypothetical prote
295	42.5	33.1	290	1	N1AVF	nitrogenase (EC 1.	368	42	32.7	184	2	T40305	hypothetical prote
296	42.5	33.1	292	2	S60950	probable membrane	369	42	32.7	202	2	H69902	nitroreductase hom
297	42.5	33.1	297	2	H72670	hypothetical prote	370	42	32.7	226	1	H69474	conserved hypotet
298	42.5	33.1	312	1	QOECRG	tdcA protein - Bac	371	42	32.7	236	2	A86075	probable transcript
299	42.5	33.1	312	2	B85973	transcription acti	372	42	32.7	236	2	S40817	hypothetical prote
300	42.5	33.1	312	2	F91128	transcription acti	373	42	32.7	236	2	B91228	probable transcript
301	42.5	33.1	321	2	E69147	glycerol-3-phospha	374	42	32.7	239	2	D70359	conserved hypotet
302	42.5	33.1	364	2	T44672	H+-transporting AT	375	42	32.7	255	2	F69962	amino acid ABC tra
303	42.5	33.1	367	1	D70395	conserved hypotet	376	42	32.7	281	2	F69323	ATP phosphoribosyl
304	42.5	33.1	368	2	E97198	probable enzyme wi	377	42	32.7	345	2	S60466	transposase - frui
305	42.5	33.1	374	2	T07887	G box-binding prot	378	42	32.7	428	2	B84964	adenosylmethionine
306	42.5	33.1	376	2	T07882	rRNA-splicing endo	379	42	32.7	450	2	D86356	hypothetical prote
307	42.5	33.1	377	2	A38862	hypothetical prote	380	42	32.7	489	2	H86356	probable UDP-gluc
308	42.5	33.1	379	2	G42543	histidinol-phospha	381	42	32.7	508	1	A43713	calcium-dependent
309	42.5	33.1	389	1	A48329	hypothetical prote	382	42	32.7	532	2	AD2420	hypothetical prote
310	42.5	33.1	390	2	T25996	polymyrase-associ	383	42	32.7	559	2	T09038	NMDH dehydrogenase
311	42.5	33.1	399	1	A43685	hypothetical prote	384	42	32.7	583	2	H84810	hypothetical prote
312	42.5	33.1	407	2	T36204	hypothetical prote	385	42	32.7	634	2	E86880	hypothetical prote
313	42.5	33.1	408	2	A61745	amino transferase h	386	42	32.7	639	1	T02784	calcium-dependent
314	42.5	33.1	412	2	S07537	myosin heavy chain	387	42	32.7	678	2	S56284	hypothetical prote
315	42.5	33.1	420	2	T43932	cell division cont	388	42	32.7	846	1	B84417	envy polypeptin pr
316	42.5	33.1	427	2	C87060	theonine deaminas	389	42	32.7	846	1	VCLJND	cell surface glyco
317	42.5	33.1	431	2	A72549	probable pyruvate	390	42	32.7	852	2	A28459	penicillin-binding
318	42.5	33.1	445	2	H71176	probable signal re	391	42	32.7	886	2	F83862	hypothetical prote
319	42.5	33.1	451	2	S56717	calcium-dependent	392	42	32.7	886	2	S67200	hypothetical prote
320	42.5	33.1	459	2	B86640	argininosuccinate	393	42	32.7	1893	2	A56158	eye development pr
321	42.5	33.1	464	2	T22087	hypothetical prote	394	42	32.7	2123	2	S55089	probable acetyl-Co

395	41.5	32.7	2339	2	A45597	DNA-directed RNA p	468	41	32.3	544	2	S37039	groEL protein - Ba
396	41.5	32.7	3119	2	T18414	protein g377 - mal	469	41	32.3	544	2	T43364	potassium channel
397	41	32.3	71	1	RGB032	GTP-binding regula	470	41	32.3	545	2	TN0509	heat shock protein
398	41	32.3	71	2	JC7290	guanine nucleotide	471	41	32.3	545	2	C95311	groEL2 chaperonin
399	41	32.3	126	2	B82184	hypothetical prote	472	41	32.3	546	2	S34938	heat shock protein
400	41	32.3	140	2	A10114	conserved hypotnet	473	41	32.3	546	2	S65596	heat shock protein
401	41	32.3	150	1	MC2P	calmodulin - flasi	474	41	32.3	546	2	S22347	groEL - Brucella
402	41	32.3	150	2	S18394	trypsin C isoform	475	41	32.3	546	2	T140342	heat shock protein
403	41	32.3	152	2	A11018	SoxR protein limpo	476	41	32.3	546	2	AG3640	60K chaperonin gro
404	41	32.3	154	2	B91259	redox-sensing acti	477	41	32.3	557	2	AC2137	ABC transporter AT
405	41	32.3	154	2	A86100	redox-sensing acti	478	41	32.3	572	2	S58889	collapsin response
406	41	32.3	154	2	US0577	soxR protein - Esc	479	41	32.3	576	2	T43353	potassium channel
407	41	32.3	156	2	T32236	hypothetical prote	480	41	32.3	581	2	T50841	phosphoinositide-s
408	41	32.3	159	2	T32233	hypothetical prote	481	41	32.3	603	2	A84584	acylttransferase (t
409	41	32.3	161	2	S47549	cell division cont	482	41	32.3	622	2	AC1236	acetoin catabolism
410	41	32.3	169	2	D84864	probable calcium b	483	41	32.3	627	2	C98148	transcription regu
411	41	32.3	169	2	H75387	hypothetical prote	484	41	32.3	627	2	A13139	probable ABC trans
412	41	32.3	172	2	G69432	hypothetical prote	485	41	32.3	630	2	AC1309	hypothetical prote
413	41	32.3	206	2	S73817	type I restriction	486	41	32.3	640	2	T32885	hypothetical prote
414	41	32.3	211	2	T32591	MADS-box protein A	487	41	32.3	695	2	T13639	probable tail-host
415	41	32.3	214	2	T00879	hypothetical prote	488	41	32.3	749	2	H82691	topoisomerase IV s
416	41	32.3	240	2	T22210	hypothetical prote	489	41	32.3	754	2	G83025	topoisomerase IV s
417	41	32.3	253	1	F71233	hypothetical prote	490	41	32.3	765	2	S76795	hypothetical prote
418	41	32.3	260	2	S73040	hypothetical prote	491	41	32.3	772	2	D75002	chemotaxis histidi
419	41	32.3	280	2	F67668	hypothetical prote	492	41	32.3	784	2	G95112	exoribonuclease, V
420	41	32.3	292	2	AG0791	probable transcrip	493	41	32.3	784	2	F97981	exoribonuclease R
421	41	32.3	296	2	I52860	smooth muscle myos	494	41	32.3	785	2	A82123	chemotaxis protein
422	41	32.3	307	2	B69837	hypothetical prote	495	41	32.3	818	2	H83904	hypothetical prote
423	41	32.3	325	2	B83165	hypothetical prote	496	41	32.3	821	2	H84600	probable vacuolar
424	41	32.3	329	2	G72319	smooth muscle myos	497	41	32.3	831	2	H84368	MCM / cell divisio
425	41	32.3	330	2	I65768	response regulator	498	41	32.3	838	1	A40995	glucosylceramidase
426	41	32.3	338	2	G71220	hypothetical prote	499	41	32.3	843	2	T13334	starch phosphoryla
427	41	32.3	344	2	G75260	hypothetical prote	500	41	32.3	847	2	AG1949	probable tail-host
428	41	32.3	344	2	T48827	hypothetical prote	501	41	32.3	864	2	S71741	hypothetical prote
429	41	32.3	364	2	T25086	hypothetical prote	502	41	32.3	864	2	AG1949	DNA ligase (ATP) (
430	41	32.3	364	2	T09011	probable transpos	503	41	32.3	883	2	B95237	pyruvate dehydroge
431	41	32.3	383	2	AB1567	teichoic acid bios	504	41	32.3	895	2	A55514	alanine-tRNA ligas
432	41	32.3	390	2	AC2169	molybdopterin bios	505	41	32.3	913	2	C71455	diTP protein - yea
433	41	32.3	398	2	A64390	N-acetylornithine	506	41	32.3	943	2	S59317	hypothetical prote
434	41	32.3	410	2	AE2621	conserved hypotnet	507	41	32.3	949	2	T38543	leukotoxin A - Pas
435	41	32.3	410	2	B97403	hypothetical prote	508	41	32.3	953	1	B30169	glycine cleavage s
436	41	32.3	416	2	C47017	probable transcrip	509	41	32.3	954	2	AP2756	glycine cleavage s
437	41	32.3	416	2	AF2017	RNA polymerase sig	510	41	32.3	954	2	B97537	protein-tyrosine k
438	41	32.3	416	2	F71869	hypothetical prote	511	41	32.3	1154	2	A39577	myelin transcripti
439	41	32.3	443	2	H96841	hypothetical prote	512	41	32.3	1182	2	T30189	microcystin synthe
440	41	32.3	444	2	E90192	DNA repair protein	513	41	32.3	1271	2	T43269	hypothetical prote
441	41	32.3	448	2	C82936	signal recognition	514	41	32.3	1411	2	S55123	hypothetical prote
442	41	32.3	455	2	H89896	hypothetical prote	515	41	32.3	1525	2	T14961	hypothetical prote
443	41	32.3	455	2	H71028	hypothetical prote	516	41	32.3	1557	2	T29132	hypothetical prote
444	41	32.3	456	2	F81215	signal recognition	517	41	32.3	1613	2	A43081	vitellogenin vit-2
445	41	32.3	456	2	B81792	signal recognition	518	41	32.3	1613	2	F89528	protein vit-2 [imp
446	41	32.3	461	2	S50864	avermectin-sensiti	519	41	32.3	1732	2	E71442	hypothetical prote
447	41	32.3	465	2	D83598	probable zinc prot	520	41	32.3	1795	2	T30332	avirulence protein
448	41	32.3	468	2	I41250	phosphogluconat d	521	41	32.3	1819	2	D97033	uncharacterized pr
449	41	32.3	472	1	B53236	transcription fact	522	41	32.3	2396	2	T13714	kkapo gene protei
450	41	32.3	472	1	AD1889	adenylate cyclase	523	40.5	31.9	85	2	C69418	hypothetical prote
451	41	32.3	478	1	S73919	pet112 protein hom	524	40.5	31.9	98	2	D95371	hypothetical prote
452	41	32.3	486	1	S57786	phosphogluconat d	525	40.5	31.9	156	2	A83952	hypothetical prote
453	41	32.3	486	2	AC2424	hypothetical prote	526	40.5	31.9	165	2	AG2184	hypothetical prote
454	41	32.3	492	2	S50554	hypothetical prote	527	40.5	31.9	234	2	S27956	arginine-rich prot
455	41	32.3	495	2	T20754	hypothetical prote	528	40.5	31.9	243	2	S43887	restriction endonu
456	41	32.3	520	2	C84774	probable calcium-d	529	40.5	31.9	243	2	F81130	type II restrictio
457	41	32.3	525	2	D70747	probable effh prote	530	40.5	31.9	243	2	H86487	hypothetical prote
458	41	32.3	534	2	H82244	sensor histidine k	531	40.5	31.9	261	2	B97589	1-2,3-butanediol d
459	41	32.3	537	2	AC2259	transposase all363	532	40.5	31.9	261	2	AC2810	short chain dehydr
460	41	32.3	538	2	H72367	groEL protein - Th	533	40.5	31.9	269	2	S60521	envelope polyprote
461	41	32.3	538	2	A70485	single-strand-DNA-	534	40.5	31.9	299	2	S60552	envelope polyprote
462	41	32.3	541	2	JN0511	heat shock protein	535	40.5	31.9	299	2	S60551	envelope polyprote
463	41	32.3	541	2	JN0512	heat shock protein	536	40.5	31.9	299	2	S60523	envelope polyprote
464	41	32.3	541	2	S72614	chaperonin 60 - Th	537	40.5	31.9	299	2	S60554	envelope polyprote
465	41	32.3	542	2	F95967	probable heat choc	538	40.5	31.9	299	2	S60553	DNA repair protein
466	41	32.3	544	1	B43827	chaperonin groEL -	539	40.5	31.9	331	2	E90121	GTP-binding protei
467	41	32.3	544	2	B82048	chaperonin, 60 Kd	540	40.5	31.9	427	2	F87465	

541	40.5	31.9	452	2	S10840	gene ND4L intron p
542	40.5	31.9	459	2	T39668	amino transferase -
543	40.5	31.9	479	2	F86356	TL6E15.2 protein -
544	40.5	31.9	523	2	C62289	exopolysphatase
545	40.5	31.9	614	2	T33149	hypothetical prote
546	40.5	31.9	685	2	S65974	conserved hypotet
547	40.5	31.9	808	2	H64474	hypothetical prote
548	40.5	31.9	866	2	A11466	phosphoenolpyruv
549	40.5	31.9	897	2	G02529	dynein heavy chain
550	40.5	31.9	912	2	T31223	tag protein homol
551	40.5	31.9	1343	2	T20718	hypothetical prote
552	40.5	31.9	1518	2	A44811	glucosyltransferas
553	40.5	31.9	1634	2	E64410	DNA-directed DNA p
554	40.5	31.9	1784	2	A49420	tuberos sclerosi
555	40.5	31.9	3746	1	VGPIV3	alpha-aminoadipyl-
556	40.5	31.9	3791	1	VGPIV8	alpha-aminoadipyl-
557	40.5	31.9	4644	1	A38905	dynein heavy chain
558	40.5	31.9	4677	1	T31345	hypothetical prote
559	40.5	31.9	50	2	E48518	PEB1 3'-region hyp
560	40.5	31.5	64	2	H81811	hypothetical prote
561	40.5	31.5	65	2	E97099	hypothetical prote
562	40.5	31.5	66	2	B87516	hypothetical prote
563	40.5	31.5	86	2	D67774	hypothetical prote
564	40.5	31.5	88	2	E75144	hypothetical prote
565	40.5	31.5	102	2	F69475	conserved hypotet
566	40.5	31.5	116	1	A69043	conserved hypotet
567	40.5	31.5	134	2	T22275	hypothetical prote
568	40.5	31.5	134	2	F72638	hypothetical prote
569	40.5	31.5	150	2	H86194	hypothetical prote
570	40.5	31.5	151	2	A97008	transcription regu
571	40.5	31.5	154	2	G85041	probable calmodul
572	40.5	31.5	155	2	G83774	hypothetical prote
573	40.5	31.5	156	2	T16066	hypothetical prote
574	40.5	31.5	177	2	U01691	gamma B protein -
575	40.5	31.5	177	2	H83323	hypothetical prote
576	40.5	31.5	188	2	B82370	Sua5/Yic10/YidC fam
577	40.5	31.5	190	2	A90354	conserved hypotet
578	40.5	31.5	191	1	W6WLR1	E6 protein - rhesu
579	40.5	31.5	192	2	T17331	hypothetical prote
580	40.5	31.5	194	2	E69999	hypothetical prote
581	40.5	31.5	198	2	T20305	hypothetical prote
582	40.5	31.5	204	2	S65256	hypothetical prote
583	40.5	31.5	211	2	H70443	rRNA methylase Spo
584	40.5	31.5	218	2	G81423	hypothetical prote
585	40.5	31.5	229	1	D33685	nonstructural prot
586	40.5	31.5	231	1	D64170	hypothetical prote
587	40.5	31.5	231	2	H70157	hypothetical prote
588	40.5	31.5	231	2	B83060	hypothetical prote
589	40.5	31.5	235	2	A81515	probable phosphopr
590	40.5	31.5	248	2	T04170	MADS box protein -
591	40.5	31.5	250	2	G81365	probable ABC-type
592	40.5	31.5	269	2	B97113	protein serine/thr
593	40.5	31.5	270	2	A42882	motility protein (
594	40.5	31.5	291	2	D90491	ABC transporter, A
595	40.5	31.5	294	2	B86731	hypothetical prote
596	40.5	31.5	296	1	J02155	nitrogenase (Ec 1.
597	40.5	31.5	306	2	A81238	aspartate carboxyl
598	40.5	31.5	307	2	S16390	auxin-induced prot
599	40.5	31.5	315	2	AH0897	probable carboxydr
600	40.5	31.5	327	2	A11422	hypothetical prote
601	40.5	31.5	328	2	C90196	conserved hypotet
602	40.5	31.5	332	2	AF3265	asparaginase (Ec 3
603	40.5	31.5	333	2	H82245	glyceraledehyde 3-p
604	40.5	31.5	336	2	D71016	probable chlorodex
605	40.5	31.5	339	2	H75187	hypothetical prote
606	40.5	31.5	340	2	D97170	probable nucleosid
607	40.5	31.5	341	2	A75313	DNA-directed RNA p
608	40.5	31.5	341	2	T45124	hypothetical prote
609	40.5	31.5	345	2	D75116	thioredoxin reduct
610	40.5	31.5	351	2	A87716	uroporphyrinogen d
611	40.5	31.5	352	1	S76448	transcription releas
612	40.5	31.5	373	2	E90241	soluble hydrogenas
613	40.5	31.5	374	2	E70346	mannosyltransferas
614	40.5	31.5	377	2	S44844	K6H7.4 protein -
615	40.5	31.5	382	2	S58138	gene 8 protein - p
616	40.5	31.5	386	2	G97316	NADH-dependent but
617	40.5	31.5	389	2	C62027	conserved hypotet
618	40.5	31.5	389	2	C86597	CT712 hypothetical
619	40.5	31.5	391	2	S31416	pyruvate dehydroge
620	40.5	31.5	391	2	T20752	hypothetical prote
621	40.5	31.5	394	2	S57332	NADH2 dehydrogenas
622	40.5	31.5	394	2	S46437	NADH2 dehydrogenas
623	40.5	31.5	399	2	C43685	polymerase-associ
624	40.5	31.5	401	2	C71483	probable nifS-rela
625	40.5	31.5	416	2	T25101	hypothetical prote
626	40.5	31.5	418	2	T39279	probable homocitra
627	40.5	31.5	425	2	T16159	carboxyl-terminol
628	40.5	31.5	427	2	A53964	hypothetical prote
629	40.5	31.5	433	2	S74753	hypothetical prote
630	40.5	31.5	438	2	S62453	transcription regu
631	40.5	31.5	442	2	D70315	signal recognition
632	40.5	31.5	445	2	T36069	signal recognition
633	40.5	31.5	446	2	C64205	signal recognition
634	40.5	31.5	446	2	B47154	hypothetical prote
635	40.5	31.5	448	2	T32575	C4 dicarboxylate c
636	40.5	31.5	450	2	H82495	hypothetical prote
637	40.5	31.5	451	2	T21036	membrane associat
638	40.5	31.5	455	2	H97237	hypothetical prote
639	40.5	31.5	459	2	F75049	hypothetical prote
640	40.5	31.5	462	2	G96506	phosphogluconate d
641	40.5	31.5	468	1	D8ECC6	phosphogluconate d
642	40.5	31.5	468	2	I62465	d phosphogluconate d
643	40.5	31.5	468	2	I62463	transcription fact
644	40.5	31.5	469	1	TVH082	hypothetical 53K p
645	40.5	31.5	470	1	S65655	hypothetical 53K p
646	40.5	31.5	470	2	P91291	probable regulator
647	40.5	31.5	470	2	H86132	probable regulator
648	40.5	31.5	478	2	C70416	trigger factor tig
649	40.5	31.5	479	2	S65466	xylose isomerase (
650	40.5	31.5	479	2	T49871	peroxisomal Ca-dep
651	40.5	31.5	485	2	A84859	probable cytochrom
652	40.5	31.5	485	2	AF1575	acetaldehyde dehyd
653	40.5	31.5	486	2	AC1222	acetaldehyde dehyd
654	40.5	31.5	487	1	S71770	calcium-dependent
655	40.5	31.5	493	2	A33809	calcium-dependent
656	40.5	31.5	502	2	T14286	embryonic callus
657	40.5	31.5	505	2	F71266	probable cytochrom
658	40.5	31.5	506	2	F71895	hypothetical prote
659	40.5	31.5	508	2	AB2236	probable tpr prote
660	40.5	31.5	511	1	E89775	2',3'-cyclic-nucle
661	40.5	31.5	511	2	T05363	phosphogluconate d
662	40.5	31.5	513	1	T02259	calcium-dependent
663	40.5	31.5	513	2	S48981	hypothetical prote
664	40.5	31.5	513	2	S53392	probable membrane
665	40.5	31.5	531	1	T02993	calcium-dependent
666	40.5	31.5	533	1	S56652	calcium-dependent
667	40.5	31.5	536	2	T23346	hypothetical prote
668	40.5	31.5	538	2	T08874	calcium-dependent
669	40.5	31.5	540	1	T01989	calcium-dependent
670	40.5	31.5	541	2	S61301	heat shock protein
671	40.5	31.5	541	2	AB2320	heat shock protein
672	40.5	31.5	544	2	S70667	heat shock protein
673	40.5	31.5	544	2	S61302	heat shock protein
674	40.5	31.5	544	2	S61300	heat shock protein
675	40.5	31.5	544	2	C81021	chaperonin, 60 kDa
676	40.5	31.5	544	2	S61303	heat shock protein
677	40.5	31.5	544	2	H81964	chaperonin 60KD bu
678	40.5	31.5	547	2	H87334	chaperonin, 60 kDa
679	40.5	31.5	548	2	B84932	chaperonin, 60 kDa
680	40.5	31.5	548	2	B42281	symblonin symL - p
681	40.5	31.5	548	2	H95066	helicase, probable
682	40.5	31.5	550	2	T10393	chitinase (EC 3.2.
683	40.5	31.5	554	2	T25992	hypothetical prote
684	40.5	31.5	564	2	F86879	arginine-cRNA liga
685	40.5	31.5	572	2	JC5316	dihydropyrimidinas
686	40.5	31.5	573	2	T40474	hypothetical prote

687	40	31.5	581	1	S71170	phosphoinositide-s
688	40	31.5	582	2	H97326	methy1-accepting c
689	40	31.5	584	2	T08678	hypothetical prote
690	40	31.5	601	2	T38200	spliceosome associ
691	40	31.5	606	2	B69805	conserved hypotnet
692	40	31.5	608	2	H72292	hypothetical prote
693	40	31.5	619	2	B81117	dihydroxy-acid deh
694	40	31.5	624	2	A84150	hypothetical prote
695	40	31.5	629	2	A65636	plastin, intestina
696	40	31.5	633	2	AH1598	acyltransferase (t
697	40	31.5	642	2	S59306	probable membrane
698	40	31.5	645	2	B64444	hypothetical prote
699	40	31.5	647	2	C71534	probable transglyc
700	40	31.5	650	2	I49523	tumor necrosis fac
701	40	31.5	656	2	JC7222	77K muscle-derived
702	40	31.5	680	2	H90558	hypothetical prote
703	40	31.5	744	2	A70385	DNA gyrase A subun
704	40	31.5	774	2	A28392	penicillin amidase
705	40	31.5	777	2	T21048	hypothetical prote
706	40	31.5	796	2	D97065	transketolase [lmp
707	40	31.5	810	1	I40508	transketolase [lmp
708	40	31.5	819	1	B72128	endopeptidase Ia (
709	40	31.5	819	2	B86494	lon ATP-dependent
710	40	31.5	844	2	S77363	hypothetical prote
711	40	31.5	845	2	I48176	synaptonemal compl
712	40	31.5	868	2	S65186	NIP80 protein - ye
713	40	31.5	880	2	AC2108	alanyl-cRNA synthe
714	40	31.5	969	2	T23256	hypothetical prote
715	40	31.5	976	2	S40697	processing endopro
716	40	31.5	1002	2	T46033	receptor protein k
717	40	31.5	1007	2	S48535	rho-type GTPase-ac
718	40	31.5	1013	2	A69226	type I restriction
719	40	31.5	1021	2	AC2202	hypothetical prote
720	40	31.5	1039	2	A12284	translational initia
721	40	31.5	1054	2	D70425	conserved hypotnet
722	40	31.5	1097	2	AD2572	hypothetical prote
723	40	31.5	1116	2	D97001	probable membrane
724	40	31.5	1136	2	AH1227	different proteins
725	40	31.5	1154	2	S69206	regulator protein
726	40	31.5	1232	2	T43027	neural cell adhesi
727	40	31.5	1295	2	T21720	hypothetical prote
728	40	31.5	1334	2	AB1775	hypothetical prote
729	40	31.5	1441	1	GNVUSV	M polyprotein prec
730	40	31.5	1607	2	T04583	TWV resistance pro
731	40	31.5	1690	2	T35694	ATP dependent DNA
732	40	31.5	1979	1	S03166	mpoasin heavy chain
733	40	31.5	2150	1	S27802	zinc finger protei
734	40	31.5	2150	2	T19450	hypothetical prote
735	40	31.5	2186	2	T13169	liggrin - fruit fl
736	40	31.5	3006	2	T28625	variant-specific s
737	40	31.5	3190	2	T13828	CREB-binding prote
738	40	31.5	3228	2	T21381	hypothetical prote
739	40	31.5	4930	2	B69679	polyketide synthet
740	40	31.5	5126	2	S40450	translucine receptor
741	40	31.5	5149	2	B83345	probable non-ribos
742	40	31.1	78	2	B97045	hypothetical prote
743	39.5	31.1	135	2	AB1429	hypothetical prote
744	39.5	31.1	139	2	S63353	hypothetical prote
745	39.5	31.1	169	2	C89919	hypothetical prote
746	39.5	31.1	192	1	KUS888	calcium-binding hypotnet
747	39.5	31.1	206	2	AD1898	urase accessory p
748	39.5	31.1	208	2	D69744	hypothetical prote
749	39.5	31.1	240	2	D75203	hypothetical prote
750	39.5	31.1	284	1	S74516	(adenine-N6, N6-) -d
751	39.5	31.1	291	2	A70475	H+-transporting tw
752	39.5	31.1	301	2	S60532	envelope polypote
753	39.5	31.1	301	2	S60531	envelope polypote
754	39.5	31.1	301	2	AB1307	dehydrogenases and
755	39.5	31.1	306	2	AB1518	hypothetical prote
756	39.5	31.1	309	2	F70217	conserved hypotnet
757	39.5	31.1	314	2	D89958	catabolic control
758	39.5	31.1	317	2	S54548	hypothetical prote
759	39.5	31.1	347	2	C90412	2-isopropylmalate
760	39.5	31.1	368	2	S54575	hypothetical prote
761	39.5	31.1	424	1	AB4905	inhibin beta-A cha
762	39.5	31.1	424	1	S31440	inhibin beta-A cha
763	39.5	31.1	425	1	S50898	inhibin beta-A cha
764	39.5	31.1	425	1	I47072	inhibin beta-A cha
765	39.5	31.1	426	1	B24248	inhibin beta-A cha
766	39.5	31.1	481	2	B86356	hypothetical prote
767	39.5	31.1	482	2	T33651	hypothetical prote
768	39.5	31.1	490	2	D84592	hypothetical prote
769	39.5	31.1	503	2	T52172	probable cytochrom
770	39.5	31.1	548	2	AC0871	probable integrase
771	39.5	31.1	552	2	T33511	hypothetical prote
772	39.5	31.1	552	2	UC4030	DnaJ-like protein
773	39.5	31.1	567	2	T33650	hypothetical prote
774	39.5	31.1	575	2	H72752	probable dihydroxy
775	39.5	31.1	657	2	C71905	probable outer mem
776	39.5	31.1	660	2	F64608	conserved hypotnet
777	39.5	31.1	662	2	G89909	transketolase [lmp
778	39.5	31.1	672	2	S75001	hypothetical prote
779	39.5	31.1	707	2	T42239	probable phosphopr
780	39.5	31.1	722	2	VCPVCN	coat protein VP1 -
781	39.5	31.1	722	2	T34072	hypothetical prote
782	39.5	31.1	732	1	JU0132	acylaminoacyl-pept
783	39.5	31.1	732	1	S07624	coat protein VP1 -
784	39.5	31.1	737	1	VCPVCD	coat protein VP1 -
785	39.5	31.1	748	1	VCPVCP	phytochrome-like p
786	39.5	31.1	751	2	AD2168	probable sucrose s
787	39.5	31.1	809	2	T06497	DNA polymerase I (
788	39.5	31.1	875	2	AB1270	hypothetical prote
789	39.5	31.1	877	2	S76394	preprotein translo
790	39.5	31.1	888	2	S78288	hypothetical prote
791	39.5	31.1	1113	2	H84105	hypothetical prote
792	39.5	31.1	1281	2	I48123	p-glycoprotein iso
793	39.5	31.1	1331	1	XORTDH	xanthine dehydroge
794	39.5	31.1	2364	2	I40884	cytochrome L - Clo
795	39.5	31.1	2396	2	B38651	orf Ia protein - L
796	39	30.7	40	2	I39944	regulatory extrace
797	39	30.7	46	2	A26929	sacQ protein - Bac
798	39	30.7	75	2	I39157	GTP-binding regula
799	39	30.7	75	2	UC4339	GTP-binding regula
800	39	30.7	79	1	KLPGI	calcium-binding pr
801	39	30.7	81	2	F90454	hypothetical prote
802	39	30.7	89	2	A54314	calcyclin - mouse
803	39	30.7	89	2	E47758	retrovirus-related
804	39	30.7	90	2	S27011	calcyclin - rat
805	39	30.7	90	2	B28363	calcyclin - rat
806	39	30.7	92	2	B69408	transcription regu
807	39	30.7	95	1	LUPG10	calpactin I light
808	39	30.7	95	2	T12718	hypothetical prote
809	39	30.7	97	2	UC1139	calpactin I light
810	39	30.7	97	2	B28489	calpactin I light
811	39	30.7	103	2	D83678	hypothetical prote
812	39	30.7	105	2	B86755	prophage p12 prote
813	39	30.7	114	2	B86353	protein F2E2.12 [i
814	39	30.7	119	1	A69441	conserved hypotnet
815	39	30.7	119	2	B84085	arsenate reductase
816	39	30.7	122	2	T04090	probable thioredox
817	39	30.7	122	2	A45385	translation repres
818	39	30.7	127	2	B97269	hypothetical prote
819	39	30.7	132	2	S76503	hypothetical prote
820	39	30.7	148	2	G70312	transcription term
821	39	30.7	148	2	A99268	conserved hypotnet
822	39	30.7	149	2	A33353	calcium-binding pr
823	39	30.7	151	2	S62426	hypothetical prote
824	39	30.7	155	2	T13308	hypothetical prote
825	39	30.7	158	2	UC5434	larva muscle tropo
826	39	30.7	158	2	A83937	tropomin C-1 - gia
827	39	30.7	161	2	F70381	glycine cleavage s
828	39	30.7	166	2	A45119	basic helix-loop-h
829	39	30.7	167	2	A55438	transcription fact
830	39	30.7	167	2	T43621	hypothetical prote
831	39	30.7	176	2	T30025	hypothetical prote
832	39	30.7	178	2	T22802	hypothetical prote



833	39	30.7	180	2	575356	sensory transducti
834	39	30.7	185	2	H88709	protein C43c2.3 [i
835	39	30.7	185	2	H90540	hypothetical prote
836	39	30.7	188	2	AB0044	elongation factor
837	39	30.7	190	2	C84152	hypothetical prote
838	39	30.7	192	2	B86679	prophage p11 prote
839	39	30.7	204	2	C84122	thymidine kinase (
840	39	30.7	208	2	B70208	conserved hypotet
841	39	30.7	209	2	A97011	probable Zn-finger
842	39	30.7	208	2	S09885	hypothetical prote
843	39	30.7	211	2	AB0118	hypothetical prote
844	39	30.7	219	2	F70474	conserved hypotet
845	39	30.7	229	2	T18629	hypothetical prote
846	39	30.7	231	2	B69756	ABC transporter (A
847	39	30.7	233	2	T41263	hypothetical prote
848	39	30.7	238	2	F81221	probable phosphata
849	39	30.7	238	2	AB6068	probable phosphata
850	39	30.7	238	2	D37841	hypothetical 27.1k
851	39	30.7	240	2	AC1921	hypothetical prote
852	39	30.7	247	2	C71229	hypothetical prote
853	39	30.7	248	2	T20037	hypothetical prote
854	39	30.7	257	2	T23332	hypothetical prote
855	39	30.7	260	2	A55122	deoxycytidine kina
856	39	30.7	260	2	A10934	glutamate racemase
857	39	30.7	262	2	A99417	conserved hypotet
858	39	30.7	269	2	C82080	dihydrodipicolinat
859	39	30.7	270	2	S67389	conserved hypotet
860	39	30.7	278	2	AB1266	probable biotin sy
861	39	30.7	280	1	PRSAEA	epidermolysin toxi
862	39	30.7	282	2	T44699	probable oxidoredu
863	39	30.7	286	2	C82143	conserved hypotet
864	39	30.7	297	2	S52726	syntaxin-4 - human
865	39	30.7	298	2	E48213	syntaxin 4 - rat
866	39	30.7	300	2	S60558	envelope polyprote
867	39	30.7	300	2	S60526	envelope polyprote
868	39	30.7	301	2	G01817	syntaxin 5 - human
869	39	30.7	301	2	F48213	syntaxin 5 - rat
870	39	30.7	303	2	AF1304	aspartate carboxamoy
871	39	30.7	303	2	AF1676	aspartate carboxamoy
872	39	30.7	303	2	S34966	rflQ protein - Shi
873	39	30.7	303	2	B37850	cell division prot
874	39	30.7	309	2	B82137	transcription regu
875	39	30.7	312	2	T20932	hypothetical prote
876	39	30.7	314	2	C90038	hypothetical prote
877	39	30.7	315	2	AB4598	probable triosepho
878	39	30.7	323	2	UT0755	ethylene-forming e
879	39	30.7	323	2	AB6184	hypothetical prote
880	39	30.7	324	2	G69515	transcription regu
881	39	30.7	325	2	AC1333	conjugated bile ac
882	39	30.7	334	2	B69888	GMP-binding protei
883	39	30.7	334	2	B86226	hypothetical prote
884	39	30.7	335	2	E72324	conserved hypotet
885	39	30.7	336	2	T03999	A1c1 protein homol
886	39	30.7	338	2	D72327	heat shock operon
887	39	30.7	342	2	I51547	probable RNA-bind
888	39	30.7	342	2	S14432	heterogeneous ribo
889	39	30.7	343	2	AB2105	hypothetical prote
890	39	30.7	344	2	B84204	hypothetical prote
891	39	30.7	345	2	AB1311	malate dehydrogena
892	39	30.7	346	2	AH3358	pyruvate dehydroge
893	39	30.7	346	2	C98156	probable l-malate
894	39	30.7	347	2	I51546	probable RNA-bind
895	39	30.7	353	2	A11558	N-syndecan - rat (
896	39	30.7	356	2	A12317	two-component hydr
897	39	30.7	362	2	A47211	protein kinase BRK
898	39	30.7	362	2	A49506	MSM1 protein - Yea
899	39	30.7	369	2	F81125	glutamate 5-kinase
900	39	30.7	369	2	B81895	probable glutamate
901	39	30.7	371	2	T02284	hypothetical prote
902	39	30.7	374	2	H75002	methyl-accepting c
903	39	30.7	383	2	AG1216	hypothetical prote
904	39	30.7	384	2	AA4146	syndecan-3 - chick
905	39	30.7	387	1	BRADY4	41k fiber protein
906	39	30.7	389	1	DEGPA	pyruvate dehydroge
907	39	30.7	390	1	DEHUPA	pyruvate dehydroge
908	39	30.7	390	1	DETRP1	pyruvate dehydroge
909	39	30.7	390	1	DETRPA	pyruvate dehydroge
910	39	30.7	390	2	S23506	pyruvate dehydroge
911	39	30.7	390	2	B69483	hypothetical prote
912	39	30.7	391	2	A82801	conserved hypotet
913	39	30.7	393	2	S04408	hydroxyneurosporen
914	39	30.7	393	2	B81438	helicase-like prot
915	39	30.7	394	2	H97825	elongation factor
916	39	30.7	394	2	F82507	proteinase VCA0045
917	39	30.7	398	2	A59371	Ig V-region-like B
918	39	30.7	405	1	A64314	corrinoid/iron-gu1
919	39	30.7	406	1	F86576	Nifs-related amino
920	39	30.7	406	2	G72047	nifs-related amino
921	39	30.7	407	2	B83873	hypothetical prote
922	39	30.7	408	2	AB0103	probable regulator
923	39	30.7	412	2	H90244	hypothetical prote
924	39	30.7	413	2	AE2163	hypothetical prote
925	39	30.7	416	2	T13514	adenosylhomocyste
926	39	30.7	417	2	S58193	adenosylhomocyste
927	39	30.7	424	2	E64450	hypothetical prote
928	39	30.7	425	2	S17759	protein kinase, ca
929	39	30.7	429	2	AB2936	hypothetical prote
930	39	30.7	429	2	E98346	hypothetical prote
931	39	30.7	431	2	AB1150	histidyl-tRNA synt
932	39	30.7	433	2	A69735	phage P88X termina
933	39	30.7	442	2	C90224	B-adenosyl-L-homoc
934	39	30.7	442	2	B82936	hemolysin U0072 [i
935	39	30.7	445	2	D64067	hypothetical prote
936	39	30.7	452	2	UC4100	hydroxyindole O-me
937	39	30.7	453	2	AD0400	signal recognition
938	39	30.7	453	2	F82702	conserved hypotet
939	39	30.7	455	2	T29555	hypothetical prote
940	39	30.7	456	2	C71402	probable glucosylc
941	39	30.7	456	2	E86903	hypothetical prote
942	39	30.7	465	1	T03024	calcium-dependent
943	39	30.7	469	2	B70486	hypothetical prote
944	39	30.7	472	1	A53236	transcription fact
945	39	30.7	472	2	AB1246	6-phosphogluconate
946	39	30.7	472	2	AD1609	probable glucosylc
947	39	30.7	475	2	C72538	probable cysteinyl
948	39	30.7	476	2	D71200	probable glutamate
949	39	30.7	479	1	A42241	glycine hydroxymet
950	39	30.7	482	2	B69629	spore germination
951	39	30.7	485	2	F90182	conserved hypotet
952	39	30.7	488	2	AB7660	hypothetical prote
953	39	30.7	494	2	E70352	anthranilate synth
954	39	30.7	503	2	A97802	n utilization subs
955	39	30.7	503	2	H71659	transcription term
956	39	30.7	514	2	F64019	hypothetical prote
957	39	30.7	516	2	S44181	carboxypeptidase D
958	39	30.7	531	2	D85059	probable calcium d
959	39	30.7	532	2	T14335	protein kinase, ca
960	39	30.7	532	2	PN0108	RNA-directed RNA p
961	39	30.7	534	2	T23425	hypothetical prote
962	39	30.7	536	2	S62110	lysophospholipase
963	39	30.7	539	2	AS4294	cell division cont
964	39	30.7	542	2	JN0661	heat shock protein
965	39	30.7	542	2	S32106	groEL protein - Ia
966	39	30.7	542	2	B86674	60 kD chaperonin [
967	39	30.7	542	2	AD1333	class I heat-shock
968	39	30.7	542	2	AC1704	class I heat-shock
969	39	30.7	545	2	T43893	DNA gyrase chain A
970	39	30.7	545	2	S47530	chaperonin groEL -
971	39	30.7	545	2	D69679	polyketide synthas
972	39	30.7	547	2	F82763	60kDa chaperonin X
973	39	30.7	547	2	I40331	Cn60 protein (Gro
974	39	30.7	548	2	AG0064	60 kDa chaperonin
975	39	30.7	549	2	UC2564	heat shock protein
976	39	30.7	550	2	S52901	heat shock protein
977	39	30.7	553	2	F96982	fission threonyl-tr
978	39	30.7	554	2	T05476	calcium-dependent

```

979 39 30.7 554 2 T43466 hypothetical prote
980 39 30.7 555 2 AG1914 carbon dioxide con
981 39 30.7 557 2 E95945 probable urocanate
982 39 30.7 559 2 C84137 transcription regu
983 39 30.7 561 2 S71597 carboxylase (
984 39 30.7 564 2 C94188 hypothetical prote
985 39 30.7 566 2 A72254 methyl-accepting c
986 39 30.7 573 1 A32800 chaperonin GroEL p
987 39 30.7 573 1 HHMS60 chaperonin groEL p
988 39 30.7 573 1 HHRT60 chaperonin groEL p
989 39 30.7 573 2 A34173 mitochondrial proc
990 39 30.7 573 2 AD2361 flavoprotein (limp
991 39 30.7 583 2 S57721 csbp protein - C1o
992 39 30.7 587 2 T14360 H+-exporting ATPas
993 39 30.7 595 2 G64233 dnaK-type molecula
994 39 30.7 595 2 S73733 dnaK-type molecula
995 39 30.7 597 2 A32440 RNA-directed RNA p
996 39 30.7 597 2 T45676 hypothetical prote
997 39 30.7 601 2 T46084 CDPK-related prote
998 39 30.7 605 2 T50842 phospholipase C2 l
999 39 30.7 606 2 T11909 NADH2 dehydrogenas
1000 39 30.7 608 2 T03476 conserved hypothet

```

## ALIGNMENTS

## RESULT 1

TS1170 homocitrate synthase (EC 4.1.3.21) [validated] - Thermus aquaticus

C/Species: Thermus aquaticus  
C/Date: 28-Jul-2000 #sequence\_revision 28-Jul-2000 #text\_change 09-Jul-2004

C/Accession: T51170

R/Kosuge, T.; Hoshino, T.

submitted to the EMBL Data Library, October 1998

A/Description: Lysoine is synthesized through the alpha-aminoadipate pathway in Thermus

A/Reference number: 225321

A/Accession: T51170

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-376 <KOS>

A/Cross-references: UNIPROT:O87198; EMBL:AB018379; PDB:BAA33785.1

A/Experimental source: strain HB27

C/Genetics:

A/Gene: lys20

C/Function: A/Description: EC 4.1.3.21 [validated, MUID:99085673]

A/Superfamily: hydroxymethylglutaryl-CoA lyase

C/Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase

```

Query Match          48.8%; Score 62; DB 2; Length 376;
Best Local Similarity 47.6%; Pred. No. 1.5;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

```

QY 2 KKMADNGTIVTEELKQLLEQW 22

Db 353 KALADRGQLTEELDRIRRW 373

## RESULT 2

TVHUA

transforming protein ralA - human

N/Alternate names: GTP-binding protein ral

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004

C/Accession: S04596; A34387

R/Chardin, P.; Tavittian, A.

Nucleic Acids Res. 17, 4380, 1989

A/Title: Coding sequences of human ralA and ralB cDNAs.

A/Reference number: S04596; MUID:89296492; PMID:2662142

A/Accession: S04596

A/Molecule type: mRNA

A/Residues: 1-206 <CHA>

```

A/Cross-references: UNIPROT:P11233; GB:X15014; NID:935845; PDB:CAA33118.1; PID:935846
R/Polakis, P.G.; Weber, R.F.; Nevins, B.; Didsbury, J.R.; Evans, T.; Snyderman, R.
J. Biol. Chem. 264, 16383-16389, 1989
A/Title: Identification of the ral and rac1 gene products, low molecular mass GTP-binding
A/Reference number: A34387; MUID:89380251; PMID:2550440
A/Accession: A34387
A/Molecule type: mRNA
A/Residues: 1, 'VDYL', 3-206 <POL>
A/Cross-references: GB:M29893; NID:9190849; PDB:AAA6542.1; PID:9190850
A/Note: parts of this sequence were confirmed by peptide sequencing
C/Genetics:
A/Gene: GDB:RALA
A/Cross-references: GDB:120723; OMIM:179550
A/Map position: 7pter-7cen
C/Superfamily: ras transforming protein; translation elongation factor Tu homology
C/Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleoti
F/15-130/Domain: translation elongation factor Tu homology <RTU>
F/21-28/Region: nucleotide-binding motif A (P-loop)
F/127-130/Region: GTP-binding NKXD motif
F/157-159/Region: GTP-binding SAK/L motif
F/27,28,46,127,128,130,157/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #stat
F/203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
F/203/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

```

```

Query Match          43.3%; Score 55; DB 1; Length 206;
Best Local Similarity 41.7%; Pred. No. 6.7;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 KKMADNGTIVTEELKQLLEQW 24

Db 128 KSDLEKROVSVEAKRRAQOMNV 151

## RESULT 3

E97225

carbamoylphosphate synthase small chain [imported] - Clostridium acetobutylicum

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C/Accession: E97225

R/Nolling, J.; Bretton, G.; Ometchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: E97225

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-351 <KIR>

A/Cross-references: UNIPROT:Q97FT3; GB:AE001437; PDB:AAK0592.1; PID:915025673; GSPDB:GT

A/Experimental source: Clostridium acetobutylicum ATCC824

C/Genetics:

A/Gene: CAC2645

C/Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbamo

```

Query Match          41.7%; Score 53; DB 2; Length 351;
Best Local Similarity 37.5%; Pred. No. 21;
Matches 9; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

```

QY 2 KKMADNGTIVTEELKQLLEQW 25

Db 127 KCIISNGELSTELKRMADSNIV 150

## RESULT 4

TVCDRA

transforming protein ral - cotton-top tamarin

C/Species: Saguinus oedipus (cotton-top tamarin)

C/Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 19-Jan-2001

C/Accession: A25261; A24893

R/Chardin, P.; Tavittian, A.

EMBO J. 5, 2203-2208, 1986

A/Title: The ral gene: a new ras related gene isolated by the use of a synthetic probe.

A/Reference number: A91050; MUID:87053859; PMID:3023062

A/Accession: A25261  
A/Molecule type: mRNA  
A/Residues: 1-206 <CRA>  
A/Cross-references: EMBL:X04328; NID:G38256; PIND:CAA27859.1; PID:G38257  
C/Genetics:  
A/Gene: ral  
C/Superfamily: ras transforming protein; translation elongation factor Tu homology  
C/Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleot  
F/15-130/Domain: translation elongation factor Tu homology <ETU>  
F/21-28/Region: nucleotide-binding motif A (P-loop)  
F/127-130/Region: GTP-binding NKXD motif  
F/157-159/Region: GTP-binding SAK/L motif  
F/27,28,46,127,128,130,157/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta  
F/203/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted  
F/203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 40.9%; Score 52; DB 1; Length 206;  
Best Local Similarity 37.5%; Pred. No. 17;  
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Oy 1 KKKKADNGTITVEELKQLLEQNL 24  
Db 128 KSDLEDKQVSVBEAKRADQMN 151

RESULT 5  
JN0622  
GTP-binding protein ral A - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: JN0622  
R/Milley, G.M.; Vagstad, M.; Rim, S.; Denker, J.K.  
Biochem. Biophys. Res. Commun. 194, 552-559, 1993  
A/Title: Isolation of cDNA clones and tissue expression of rat ral A and ral B GTP-bind  
A/Reference number: JN0622; MUID:93326173; PMID:7687439  
A/Accession: JN0622  
A/Molecule type: mRNA  
A/Residues: 1-206 <MIL>  
A/Cross-references: UNIPROT:P05810; GB:L19698; NID:G310209; PIND:AAA42003.1; PID:G310210  
C/Genetics:  
A/Gene: ral A  
C/Superfamily: ras transforming protein; translation elongation factor Tu homology  
C/Keywords: GTP binding; nucleotide binding; P-loop; proto-oncogene; transforming protei  
F/15-130/Domain: translation elongation factor Tu homology <ETU>  
F/21-28/Region: nucleotide-binding motif A (P-loop)  
F/127-130/Region: GTP-binding NKXD motif  
F/157-159/Region: GTP-binding SAK/L motif  
F/27,28,46,127,128,130,157/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 40.9%; Score 52; DB 2; Length 206;  
Best Local Similarity 37.5%; Pred. No. 17;  
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Oy 1 KKKKADNGTITVEELKQLLEQNL 24  
Db 128 KSDLEDKQVSVBEAKRADQMN 151

RESULT 6  
G81328  
60 kD chaperonin (cpn60) Cj1221 [imported] - Campylobacter jejuni (strain NCTC 11168)  
C/Species: Campylobacter jejuni  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: G81328  
R/Perkhill, J.; Wren, B.W.; Murgall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
Nature 403, 665-668, 2000  
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy  
A/Reference number: A81250; MUID:20150912; PMID:10688204  
A/Accession: G81328  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-545 <PAR>

A/Cross-references: UNIPROT:O69289; GB:A1139077; GB:A1111168; NID:96968444; PIND:CA87347  
A/Experimental source: serotype O2, strain NCTC 11168  
C/Genetics:  
A/Gene: groEL; Cj1221  
C/Superfamily: chaperonin groEL

Query Match 40.9%; Score 52; DB 2; Length 545;  
Best Local Similarity 41.7%; Pred. No. 45;  
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Oy 2 KKKADNGTITVEELKQLLEQNL 25  
Db 166 EKVKGDVITVEAKSINDELNV 189

RESULT 7  
T22980  
hypothetical protein F59B10.6 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T22980  
R/Lloyd, C.  
submitted to the EMBL Data Library, March 1995  
A/Reference number: Z19646  
A/Accession: T22980  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-105 <MIL>  
A/Cross-references: UNIPROT:Q09954; EMBL:Z48716; PIND:CA88600.1; GSPDB:GN00020; CESP:F5  
A/Experimental source: clone F59B10  
C/Genetics:  
A/Gene: CESP:F59B10.6  
A/Map position: 2  
A/Introns: 54/2; 75/2

Query Match 40.2%; Score 51; DB 2; Length 105;  
Best Local Similarity 36.0%; Pred. No. 11;  
Matches 9; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Oy 1 KKKKADNGTITVEELKQLLEQNL 25  
Db 60 EKKIENGVARSKELQRLDPAVYKI 84

RESULT 8  
D83894  
hypothetical protein BH1956 [imported] - Bacillus halodurans (strain C-125)  
C/Species: Bacillus halodurans  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C/Accession: D83894  
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A/Reference number: A83650; MUID:20512582; PMID:11058132  
A/Accession: D83894  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-344 <STO>  
A/Cross-references: UNIPROT:Q9YBH1; GB:AP001513; GB:BA000004; NID:G10174345; PIND:BA0056  
A/Experimental source: strain C-125  
C/Genetics:  
A/Gene: BH1956

Query Match 40.2%; Score 51; DB 2; Length 344;  
Best Local Similarity 41.4%; Pred. No. 38;  
Matches 12; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Oy 4 MADNGTITVEE-----LKQLLEQNL 24  
Db 273 MGDNGATVGENKEQALVLDLRLLPEPKI 301

RESULT 9



Oy 1 KKKMADNGTIVEB---LKOLLEQWN 23  
 ||:|||||:  
 Db 243 KKRMBDTLTPLEKTKHWOLOEQWN 269

## RESULT 14

C64087  
 exopolysphatase ppx homolog - Haemophilus influenzae (strain Rd KW20)  
 C:Species: Haemophilus influenzae  
 C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
 C:Accession: C64087  
 R:Feleischman, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
 R:Goeynne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman, J.  
 R:D.M.; Brandon, R.C.; Fine, L.D.; Fritschman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.  
 Science 269, 496-512, 1995  
 A:Authors: Ghemm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A:Reference number: A64000; MUID:95350630; PMID:7542800  
 A:Accession: C64087  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-323 <TIGR>  
 A:Cross-references: UNIPROT:P44828; GB:U32752; GB:L42023; NID:G1573692; PIDN:AAC22355.1;

Query Match 39.4%; Score 50; DB 2; Length 323;  
 Best Local Similarity 66.7%; Pred. No. 48;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 7 NGTITVEELKOLLEQ 21  
 |||||:  
 Db 238 NGTITVEELKOLLEQ 252

## RESULT 15

UC6129  
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp  
 A:Alternative names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
 C:Accession: UC6129; G02260  
 R:Jiang, X.; Li, J.; Paikind, M.; Epstein, P.M.  
 Proc. Natl. Acad. Sci. U.S.A. 93, 11236-11241, 1996  
 A:Title: Inhibition of calmodulin-dependent phosphodiesterase induces apoptosis in human  
 A:Reference number: UC6129; MUID:97008163; PMID:8855339  
 A:Accession: UC6129  
 A:Molecule type: mRNA  
 A:Residues: 1-536 <JIA>  
 A:Cross-references: UNIPROT:Q01064; GB:U56976; NID:G1621591; PIDN:AACS0769.1; PID:G16215  
 A:Experimental source: lymphoblastoid B-cell  
 R:Houslay, M.D.; Erdogan, S.; Rena, G.; Sullivan, M.  
 submitted to the EMBL Data Library, November 1995  
 A:Reference number: H00937  
 A:Accession: G02260  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 201-203, 'W', 205-358, 'S', 360-384 <HOU>  
 A:Cross-references: EMBL:U40584; NID:G1110534; PID:G1110535  
 C:Comment: This enzyme is a useful target for inducing the death of leukemic cells, and  
 C:Genetics:  
 A:Gene: GDB:PDE1B; PDE31B  
 A:Cross-references: GDB:120264; OMIM:171891  
 A:Map position: 16p13.11  
 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent, 3',5'  
 C:Keywords: alternative splicing; calmodulin binding; GMP binding; phosphoric diester h  
 P:22-439/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 39.4%; Score 50; DB 1; Length 536;  
 Best Local Similarity 55.6%; Pred. No. 81;  
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 3 KKMADNGTIVEELKOLLE 20  
 ||:|||||:  
 Db 44 KOLNENIIEELKKNLE 61

## RESULT 16

S35309  
 heat shock protein groEL2 - Bradyrhizobium japonicum  
 C:Species: Bradyrhizobium japonicum  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
 C:Accession: S35309  
 R:Fiicher, H.M.; Babet, M.; Kaepar, T.; Acuna, G.; Arigoni, F.; Hennecke, H.  
 EMBO J. 12, 2901-2912, 1993  
 A:Title: One member of a groEL-like chaperonin multigene family in Bradyrhizobium japon  
 A:Reference number: S35308; MUID:93327780; PMID:8101485  
 A:Accession: S35309  
 A:Molecule type: DNA  
 A:Residues: 1-550 <FIS>  
 A:Cross-references: UNIPROT:P35861; EMBL:Z22604; NID:G312977; PIDN:CAA80318.1; PID:G3129  
 C:Genetics:  
 A:Gene: groEL2  
 C:Superfamily: chaperonin groEL  
 C:Keywords: molecular chaperone

Query Match 39.4%; Score 50; DB 2; Length 550;  
 Best Local Similarity 45.8%; Pred. No. 83;  
 Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Oy 2 KKMADNGTIVEELKOLLEQWNLY 25  
 ||:|||||:  
 Db 167 KKVNGEVITVEEAKSLETELEV 190

## RESULT 17

F82930  
 DNA ligase Utl121 [imported] - Ureaplasma urealyticum  
 C:Species: Ureaplasma urealyticum  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 12-Jul-2004  
 C:Accession: F82930  
 R:Glasz, J.I.; Lefkowitz, E.J.; Glasz, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to GenBank, February 2000  
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min  
 A:Reference number: A82870  
 A:Accession: F82930  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-673 <GLA>  
 A:Cross-references: GB:AE002113; GB:AF222894; NID:G6899078; PIDN:AAF30527.1; GSPDB:GN001  
 A:Experimental source: serovar 3; biovar 1  
 C:Genetics:  
 A:Gene: lig; Utl121  
 A:Genetic code: SGC3  
 C:Superfamily: NAD+-dependent DNA ligase, ligA type

Query Match 39.4%; Score 50; DB 2; Length 673;  
 Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 12 VEELKOLLEQWN 23  
 ||:|||||:  
 Db 8 IDEELKOLLEQWN 19

## RESULT 18

S61217  
 spectrin alpha II chain - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 18-Sep-1997 #sequence\_revision 18-Sep-1997 #text\_change 29-Sep-1999  
 C:Accession: S61217  
 R:Kalamiraki, P.; Gazzotti, P.  
 submitted to the EMBL Data Library, August 1995  
 A:Description: Structural and functional characterization of the calmodulin and calpain  
 A:Reference number: S61217  
 A:Accession: S61217  
 A:Status: preliminary  
 A:Molecule type: mRNA

A;Residues: 1-819 <KAL>  
A;Cross-references: EMBL:X90845  
C;Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/  
C;Keywords: EF hand  
F;284-389/Domain: spectrin/dystrophin repeat homology <SP12>

Query Match 39.4%; Score 50; DB 2; Length 819;  
Best Local Similarity 47.6%; Pred. No. 1.2e+02;  
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KKMADNGTITVEELKQLEQW 22  
Db 774 KKLSDNTIGQEELIQRLAQF 794

## RESULT 19

hypothetical protein R10E12.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C;Accession: S41034

R;Smith, A.

submitted to the EMBL Data Library, January 1994

A;Accession: S41034

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-882 <SM1>

A;Cross-references: UNIPROT:Q81115; EMBL:Z29561; NID:9450897; PID:9450898

C;Genetics:

A;Intons: 72/2; 324/3; 359/1; 400/2; 722/1; 743/1; 782/1; 818/1

Query Match 39.4%; Score 50; DB 2; Length 882;  
Best Local Similarity 47.6%; Pred. No. 1.3e+02;  
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 5 ADNGTITVEELKQLEQW 25  
Db 548 ATGETDTYRQLRQPMSCNNEV 568

## RESULT 20

spectrin alpha chain, nonerythroid - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 09-Jul-2004

C;Accession: A32612

R;Hong, W.; Doyle, D.

J. Biol. Chem. 264, 12758-12764, 1989

A;Title: Cloning and analysis of cDNA clones for rat kidney alpha-spectrin.

A;Reference number: A32612; MUID:89327227; PMID:2753883

A;Accession: A32612

A;Molecule type: mRNA

A;Residues: 1-1030 <HON>

A;Cross-references: UNIPROT:P16086; GB:J04828; NID:9203013; PID:AAA40770.1; PID:9203014

C;Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/  
C;Keywords: actin binding; cytoskeleton; EF hand

F;47-152/Domain: spectrin/dystrophin repeat homology <SP12>

F;799-904/Domain: spectrin/dystrophin repeat homology <SP19>

F;913-1019/Domain: spectrin/dystrophin repeat homology <SP20>

Query Match 39.4%; Score 50; DB 2; Length 1030;  
Best Local Similarity 47.6%; Pred. No. 1.6e+02;  
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KKMADNGTITVEELKQLEQW 22  
Db 537 KKLSDNTIGQEELIQRLAQF 557

## RESULT 21

hypothetical protein DKFp564P0562.1 - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: U14790  
R;Blum, H.; Baerach, S.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, August 1999

Query Match 39.4%; Score 50; DB 2; Length 1325;  
Best Local Similarity 47.6%; Pred. No. 2e+02;  
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KKMADNGTITVEELKQLEQW 22  
Db 817 KKLSDNTIGQEELIQRLAQF 837

## RESULT 22

fodrin alpha chain - human

C;Species: Homo sapiens (man)

C;Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 09-Jul-2004

C;Accession: A35715; A28580; I52382; A61369; G01810; S54877; S65689

R;Moon, R.T.; McMahon, A.P.

J. Biol. Chem. 265, 4427-4433, 1990

A;Title: Generation of diversity in nonerythroid spectrins. Multiple polypeptides are pr

A;Reference number: A35715; MUID:90170948; PMID:2307671

A;Accession: A35715

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2472 <MOO>

A;Cross-references: UNIPROT:Q13813; GB:J05243; NID:9179105; PID:AAA51790.1; PID:9179106

R;McMahon, A.P.; Giebelhaus, D.H.; Champion, J.E.; Balles, J.A.; Lacey, S.; Carrillo, B.;

Differantiation 34, 68-78, 1987

A;Title: cDNA cloning, sequencing and chromosome mapping of a non-erythroid spectrin, hu

A;Reference number: A28580; MUID:87277023; PMID:3038643

A;Accession: A28580

A;Molecule type: mRNA

A;Residues: 676-1594 <MCN>

R;McMahon, A.P.; Moon, R.T.

Biochem. Soc. Trans. 15, 804-807, 1987

A;Title: Structure and evolution of a non-erythroid spectrin, human alpha-fodrin.

A;Reference number: I52382; MUID:88083942; PMID:3631949

A;Accession: I52382

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 676-1594 <RES>

A;Cross-references: GB:M24773; NID:9537330; PID:AAA52468.1; PID:9537331

R;Mutha, S.; Langston, A.; Bonifas, J.M.; Epstein Jr., E.H.

U. Invest. Dermatol. 97, 383-388, 1991

A;Title: Biochemical identification of alpha-fodrin and protein 4.1 in human keratinocy.

A;Reference number: A61369; MUID:91341201; PMID:1875039

A;Accession: A61369

A;Molecule type: mRNA

A;Residues: 'R',1595-1610,'E',1612-1614,'P',1616-1624,'S',1626-1638,'P',1640,'E',1642-16

2-1813,'R',1815-1820,'K',1822-1844,'V',1846-1850 <MUT>

A;Note: the sequence in Fig. 4 is inconsistent with the sequence in Fig. 3 at several po

R;Morrow, J.S.

submitted to the EMBL Data Library, May 1995

A;Reference number: G08473

A;Accession: G01810

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A:Residues: 811-1299, 'I', 1301-1529 <MOR>  
 A:Cross-references: EMBL:X1263966; NID:g836668; PIDD:AAE0364.1; PTD:g836669  
 R:Lundberg, S.; Bjoerk, J.; Loeftvenberg, L.; Backmann, L.  
 Submitted to the EMBL Data Library, May 1995  
 A:Description: Cloning and characterization of two putative calcium-binding sites in human  
 A:Reference number: S54877  
 A:Accession: N55877  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 2059-2312, 'P', 2314-2346, 'EF', 2349-2433 <LNU>  
 A:Cross-references: EMBL:X86901  
 R:Lundberg, S.; Bjoerk, J.; Loeftvenberg, L.; Backman, L.  
 Eur. J. Biochem. 230, 658-665, 1995  
 A:Title: Cloning, expression and characterization of two putative calcium-binding sites  
 A:Reference number: S65689; MUID:95331304; PMID:7607240  
 A:Accession: S65689  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 2330-2346, 'EF', 2349-2406 <LU2>  
 A:Cross-references: EMBL:X86901  
 A:Gene: GDB:SPTPANI  
 C:Genetics:  
 A:Map position: 9q34.1-9q34.1  
 C:Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin,  
 C:Keywords: actin binding; EF hand  
 F:466-571/Domain: spectrin/dystrophin repeat homology <SP5>  
 F:572-676/Domain: spectrin/dystrophin repeat homology <SP6>  
 F:677-782/Domain: spectrin/dystrophin repeat homology <SP7>  
 F:974-1021/Domain: SH3 homology <SH3>  
 F:2000-2195/Domain: spectrin/dystrophin repeat homology <SP19>  
 F:2204-2310/Domain: spectrin/dystrophin repeat homology <SP20>  
 F:2333-2355/Domain: calmodulin repeat homology <EF1>  
 F:2366-2398/Domain: calmodulin repeat homology <EF2>  
  
 Query Match 39.4%; Score 50; DB 2; Length 2472;  
 Best Local Similarity 47.6%; Pred. NO. 3.9e+02;  
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
  
 QY 2 KKMADNGTITVEELKQLLEQW 22  
 Db 1828 KKLSDNMTIGKEFIQRLAQF 1848  
 ||::|||::|||::|||:  
  
 RESULT 23  
 SCSHA  
 A:Alternat names: calspectin alpha chain; fodrin alpha chain  
 C:Species: Gallus gallus (chicken)  
 C:Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text\_change 09-Jul-2004  
 C:Accession: A30122; A31866; A22723; S02425; S03190  
 R:Maenlein, V.M.; Saraste, M.; Salven, P.; Eiraema, M.; Holm, L.; Lehto, V.P.  
 J. Cell Biol. 108, 1177-1178, 1989  
 A:Reference number: A30122  
 A:Contents: erratum  
 A:Accession: A30122  
 A:Molecule type: mRNA  
 A:Residues: 1-2477 <MAS>  
 A:Cross-references: UNIPROT:P07751; GB:X14519  
 R:Maenlein, V.M.; Saraste, M.; Salven, P.; Eiraema, M.; Holm, L.; Lehto, V.P.  
 J. Cell Biol. 108, 79-93, 1989  
 A:Title: Primary structure of the brain alpha-spectrin.  
 A:Reference number: A31866; MUID:89093238; PMID:2910879  
 A:Accession: A31866  
 A:Molecule type: mRNA  
 A:Residues: 1-2477 <MA2>  
 A:Cross-references: EMBL:X13701  
 A:Note: residues 1880-2359 are shown between residues 1399 and 1400 in Fig. 2  
 C:Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/dystrophin  
 C:Keywords: actin binding; calcium binding; cytoskeleton; duplication; EF hand; heterodimer  
 F:43-147/Domain: spectrin/dystrophin repeat homology <SP1>  
 F:148-253/Domain: spectrin/dystrophin repeat homology <SP2>  
 F:254-359/Domain: spectrin/dystrophin repeat homology <SP3>

```

F.360-465/Domain: spectrin/dystrophin repeat homology <SP4>
F.466-571/Domain: spectrin/dystrophin repeat homology <SP5>
F.572-676/Domain: spectrin/dystrophin repeat homology <SP6>
F.677-782/Domain: spectrin/dystrophin repeat homology <SP7>
F.783-888/Domain: spectrin/dystrophin repeat homology <SP8>
F.889-973/Domain: spectrin/dystrophin repeat homology <SP9>
F.974-1021/Domain: SH3 homology <SH3>
F.1090-1231/Domain: spectrin/dystrophin repeat homology #status atypical <SP10>
F.1232-1337/Domain: spectrin/dystrophin repeat homology <SP11>
F.1338-1443/Domain: spectrin/dystrophin repeat homology <SP12>
F.1444-1549/Domain: spectrin/dystrophin repeat homology <SP13>
F.1550-1661/Domain: spectrin/dystrophin repeat homology <SP14>
F.1662-1767/Domain: spectrin/dystrophin repeat homology <SP15>
F.1768-1873/Domain: spectrin/dystrophin repeat homology <SP16>
F.1874-1979/Domain: spectrin/dystrophin repeat homology <SP17>
F.1980-2086/Domain: spectrin/dystrophin repeat homology <SP18>
F.2095-2200/Domain: spectrin/dystrophin repeat homology <SP19>
F.2209-2315/Domain: spectrin/dystrophin repeat homology <SP20>
F.2316-2360/Domain: spectrin/dystrophin repeat homology <SP21>
F.2371-2403/Domain: calmodulin repeat homology <EF1>
F.2371-2403/Domain: calmodulin repeat homology <EF2>

Query Match          39.4%; Score 50; DB 1; Length 2477;
Best Local Similarity 47.6%; Pred. No. 3.5e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

      2 KKMADNGTITVEELKQLLEQW 22
      ||::|||::|||::|||::|
Db      1833 KKLSDNTIGKEIKIQRLQAF 1853

RESULT 24
S16552
hypotheetical protein - Yersinia enterocolitica
C:Species: Yersinia enterocolitica
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S16552
R:Seoane, A.; Garcia Lobo, J.M.
Mol. Gen. Genet. 228, 215-220, 1991
A:Title: Nucleotide sequence of a new class A beta-lactamase gene from the chromosome of
A:Reference number: S16552; MUID:91360067; PMID:1886608
A:Accession: S16552
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-36 <SEO>
A:Cross-references: EMBL:X57074

Query Match          38.6%; Score 49; DB 2; Length 36;
Best Local Similarity 58.8%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

      2 KKMADNGTITVEELKQL 18
      ||::|||::|||::|||::|
Db      14 KKLDEGRTTSEYQQL 30

RESULT 25
S50566
hypotheetical protein YER063w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50566
R:Idetrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612.
A:Reference number: S50427
A:Accession: S50566
A:Cross-references: UNIPROT:P40040; EMBL:U18813; NID:G1381127; PID:G603299; GSPDB:GN0000
A:Molecule type: DNA
A:Residues: 1-218 <DIR>
C:Genetics:
A:Gene: SGD:THO1; MIPS:YER063w
A:Cross-references: SGD:S0000865
A:Map position: 5R

```





A/Reidues: 1-529 <BLAT>  
 A/Cross-references: UNIPROT:P37013; GB:AE000354; GB:U00096; NID:G2367149; PIDN:AACT5751.  
 A/Experimental source: strain K-12, substrain MG1655  
 C/Genetics:  
 A/Gene: ygaA  
 C/Superfamily: Response regulator (sigma54-dependent transcriptional activator), FhlA ty  
 F/212-434/Domain: RNA polymerase sigma factor interaction domain homology <SFI>

Query Match 38.6%; Score 49; DB 2; Length 529;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVBELKOL 18  
 Db 299 KFEWADNGTFLDELIGEL 316

RESULT 31  
 B91074  
 Probable 2-component transcription regulator [imported] - Escherichia coli (strain O157:  
 C/Species: Escherichia coli  
 C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C/Accession: B91074  
 R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc  
 A/Reference number: A99629; MUID:21156231; PMID:11258796  
 A/Accession: B91074  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Reidues: 1-529 <HAY>  
 A/Cross-references: UNIPROT:O8X854; GB:BA000007; PIDN:BAH36988.1; PID:G13363036; GSPDB:C  
 A/Experimental source: strain O157:H7, substrain RMD 0509952  
 C/Genetics:  
 A/Gene: EC63565  
 C/Superfamily: Response regulator (sigma54-dependent transcriptional activator), FhlA ty

Query Match 38.6%; Score 49; DB 2; Length 529;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVBELKOL 18  
 Db 299 KFEWADNGTFLDELIGEL 316

RESULT 32  
 D85919  
 Probable 2-component transcription regulator ygaA [imported] - Escherichia coli (strain  
 C/Species: Escherichia coli  
 C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C/Accession: D85919  
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A/Reference number: A85460; MUID:21074935; PMID:11206551  
 A/Accession: D85919  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Reidues: 1-529 <STO>  
 A/Cross-references: UNIPROT:Q8X854; GB:AE005174; NID:G12517154; PIDN:AA657816.1; GSPDB:C  
 A/Experimental source: strain O157:H7, substrain EDL933  
 C/Genetics:  
 A/Gene: ygaA  
 C/Superfamily: Response regulator (sigma54-dependent transcriptional activator), FhlA ty

Query Match 38.6%; Score 49; DB 2; Length 529;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KKKMADNGTIVBELKOL 18

Db 299 KFEWADNGTFLDELIGEL 316

RESULT 33  
 A44162  
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63k gp  
 N/Alternate names: 63k calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
 C/Accession: A44162; B40283  
 R/Bentley, J.K.; Kadlec, A.; Sherbert, C.H.; Seger, D.; Sonnenburg, W.K.; Charbonneau,  
 J. Biol. Chem. 267, 18676-18682, 1992  
 A/Title: Molecular cloning of cDNA encoding a "63"-kDa calmodulin-stimulated phosphodies  
 A/Reference number: A44162; MUID:92406781; PMID:1326531  
 A/Accession: A44162  
 A/Molecule type: mRNA  
 A/Reidues: 1-534 <BEN>  
 A/Cross-references: UNIPROT:Q01061; GB:M94867; NID:G162782; PIDN:AAA74558.1; PID:G162783  
 A/Experimental source: brain  
 A/Note: sequence extracted from NCBI backbone (NCBI:P113352)  
 R/Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.  
 Biochemistry 30, 7940-7947, 1991  
 A/Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nuc  
 A/Reference number: A40283; MUID:91329366; PMID:1651112  
 A/Accession: B40283  
 A/Molecule type: Protein  
 A/Reidues: 29-45,'IP',48,'R',50-52,'IS',55-85,196-215,277,'D',279,'T',281-287,'T',289-2  
 A/Experimental source: brain  
 C/Comment: This enzyme is a useful target for inducing the death of leukemic cells, and  
 C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
 C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h  
 F/220-437/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 38.6%; Score 49; DB 1; Length 534;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 KMDNGTIVBELKOL 20  
 Db 43 KOLENGEVNIEELKONLE 60

RESULT 34  
 A44161  
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63k gp  
 N/Alternate names: 63k calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
 C/Accession: A44161  
 R/Repaske, D.R.; Swinnen, J.V.; Jin, S.L.; Van Wyk, J.J.; Condt, M.  
 J. Biol. Chem. 267, 18683-18688, 1992  
 A/Title: A polymerase chain reaction strategy to identify and clone cyclic nucleotide ph  
 A/Reference number: A44161; MUID:92406782; PMID:1326532  
 A/Accession: A44161  
 A/Molecule type: mRNA  
 A/Reidues: 1-535 <REP>  
 A/Cross-references: UNIPROT:Q01066; GB:M94537; NID:G203266; PIDN:AAA16530.1; PID:G203269  
 A/Experimental source: brain  
 A/Note: sequence extracted from NCBI backbone (NCBI:P113357)  
 C/Comment: This enzyme is a useful target for inducing the death of leukemic cells, and  
 C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
 C/Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester h  
 F/221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 38.6%; Score 49; DB 1; Length 535;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 KMDNGTIVBELKOL 20  
 Db 43 KOLENGEVNIEELKONLE 60

## RESULT 35

A46378

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp

N:Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1

C:Species: Mus musculus (house mouse)

C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

A:Accession: A46378; B44161

R:Polli, J.W.; Kincaid, R.L.

Proc. Natl. Acad. Sci. U.S.A. 89, 11079-11083, 1992

A:Title: Molecular cloning of DNA encoding a calmodulin-dependent phosphodiesterase enri

A:Reference number: A46378; MUID:99066388; PMID:1332068

A:Accession: A46378

A:Molecule type: mRNA; protein

A:Residues: 1-535 &lt;POL&gt;

A:Cross-references: UNIPROT:Q01065; GB:L01695; NID:9200269; PIDN:AAA39902.1; PID:9200270

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBI:118901, NCBI:118903)

R:Repaske, D.R.; Swinnen, J.V.; Jin, S.L.; Van Wyk, J.J.; Conti, M.

U. Biol. Chem. 267, 18683-18688, 1992

A:Title: A polymerase chain reaction strategy to identify and clone cyclic nucleotide ph

A:Reference number: A44161; MUID:92406782; PMID:1326532

A:Accession: B44161

A:Molecule type: mRNA

A:Residues: 221-223, R', 225-336 &lt;REP&gt;

A:Cross-references: GB:M94538; NID:9192368; PIDN:AAA3767.1; PID:9192369

A:Note: sequence extracted from NCBI backbone (NCBI:113365)

C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'

C:Keywords: alternative splicing; calmodulin binding; GMP binding; phosphoric diester h

F;21-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology &lt;CNP&gt;

Query Match 38.6%; Score 49; DB 1; Length 535;

Best Local Similarity 50.0%; Pred. No. 1.1e+02;

Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 KMAADNGTTFVEELKQLE 20

Db 43 KQLENGEVAIEELKKNLE 60

## RESULT 36

H64119

threonine-tRNA ligase (EC 6.1.1.3) - Haemophilus influenzae

N:Alternate names: threonyl-tRNA synthetase

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004

A:Accession: H64119

R:Flaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.Y.; Glodek, A.; Kelley, J.M.; Meidman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:9550630; PMID:7542800

A:Accession: H64119

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-643 &lt;TIG&gt;

A:Cross-references: UNIPROT:P43014; GB:U32816; GB:L42023; NID:91574193; PIDN:AAC23014.1;

A:Experimental source: strain Rd KW20

C:Genetics: A:Gene: thrS

C:Function: A:Description: activates L-threonine and transfers it to the specific tRNA

A:Pathway: protein biosynthesis

A:Note: belongs to class-II synthetases

C:Superfamily: threonine-tRNA ligase

C:Keywords: aminacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 38.6%; Score 49; DB 2; Length 643;

Best Local Similarity 52.6%; Pred. No. 1.3e+02;

Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 2 KMAADNGTTFVEELKQLE 20

Db 611 KQADLSTFVEEFAELK 629

## RESULT 37

S56237

glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) [validated] - Yeast (Saccharomyces

N:Alternate names: phosphoglucosamine acetylase; phosphoglucosamine transacetylase; prote

C:Species: Saccharomyces cerevisiae

C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004

A:Accession: S56237; S48321; S62296

R:Murakami, Y.; Naitou, M.; Hagihara, H.; Shibata, T.; Ozawa, M.; Sasamura, S.I.; Sasamu

submitted to the EMBL Data Library, May 1995

A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cer

A:Reference number: S56186

A:Accession: S56237

A:Molecule type: DNA

A:Residues: 1-159 &lt;MUR&gt;

A:Cross-references: UNIPROT:P43577; EMBL:D50617; NID:9836685; PIDN:BA09221.1; PID:983677

R:Churcher, C.

submitted to the EMBL Data Library, September 1994

A:Reference number: S48310

A:Accession: S48321

A:Molecule type: DNA

A:Residues: 1-111, 'ASS' &lt;CHU&gt;

A:Cross-references: EMBL:Z46255; NID:9559925; PIDN:CA086352.1; PID:9559937; GSPDB:GN00006

R:Murakami, Y.

submitted to the EMBL Data Library, December 1994

A:Reference number: S62230

A:Accession: S62296

A:Molecule type: DNA

A:Residues: 1-159 &lt;MUR&gt;

A:Cross-references: EMBL:D44596; NID:91100783; PIDN:BA08000.1; PID:91100787

C:Genetics:

A:Gene: SGD:GNA1; GNA1; MIPS:YFL017C

A:Cross-references: MIPS:YFL017C; SGD:S0001877

A:Map position: 6L

C:Function: A:Description: EC 2.3.1.4 [validated, MUID:99085039]; glucosamine-phosphate N-acetyltran

A:Note: phosphoglucosamine acetyltransferase activity has been shown in vitro, by incubat

acetylglucosamine is produced from glucosamine 6-phosphate, indicating that 142-Phe and

C:Superfamily: Saccharomyces glucosamine-phosphate N-acetyltransferase

C:Keywords: acyltransferase; coenzyme A

Query Match 37.8%; Score 48; DB 1; Length 159;

Best Local Similarity 40.9%; Pred. No. 42;

Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Oy 2 KMAADNGTTFVEELKQLEON 23

Db 25 KVLTFVTTFEESFKLIKW 46

## RESULT 38

DB3010

probable binding protein component of ABC transporter PA5082 [imported] - Pseudomonas ae

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

A:Accession: DB3010

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lasky, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: DB3010

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-299 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9HUAL; GB:AE004921; GB:AE004091; NID:99951372; PIDN:AA0846

A:Experimental source: strain PA01  
C:Gene: PA5082

Query Match 37.8%; Score 48; DB 2; Length 299;  
Best Local Similarity 81.8%; Pred. No. 81;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 KKMADNGTITV 12  
||:|||||:  
DB 30 KKVADNGTITL 40

#### RESULT 39

T23021  
hypochemical protein H01G02.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T23021

R:Kershaw, J.

submitted to the EMBL Data Library, March 1997  
A:Reference number: Z19655

A:Accession: T23021

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-309 <WIL>

A:Cross-references: UNIPROT:O17902; EMBL:Z92847; PIDN:GAB07421.1; GSPDB:GN00022; CESP:HO

A:Experimental source: clone H01G02

C:Gene: CESP:H01G02.1

A:Map position: 4

A:introns: 20/1; 52/3; 121/1; 162/3; 238/2

Query Match 37.8%; Score 48; DB 2; Length 309;  
Best Local Similarity 40.9%; Pred. No. 84;  
Matches 9; Conservative 9; Mismatches 2; Indels 2; Gaps 1;

OY 4 MADNGTIVE--ELKQLEQWN 23  
:|||||:|:|:|:|:|:  
DB 154 IAFNGTIVEMDQVEKIDWMS 175

#### RESULT 40

AC0897

TDC operon transcription activator STY3428 [imported] - *Salmonella enterica* subsp. enter

C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh

A:Note: this species has also been called *Salmonella typhi*

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C:Accession: AC0897

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,

ch, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AC0897

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-312 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD07769.1; PID:gl6504318; GSPDB:GN00176

C:Gene: STY3428

C:Superfamily: regulatory protein 11v

Query Match 37.8%; Score 48; DB 2; Length 312;  
Best Local Similarity 52.2%; Pred. No. 85;  
Matches 12; Conservative 1; Mismatches 8; Indels 2; Gaps 1;

OY 2 KKMADNGTITVBEKQLEQWN 24  
||:|||||:|:|:|:|:|:  
DB 179 KSRCTGTITLESMD--EQWAL 199

#### RESULT 41

AG2311

hypochemical protein alr4046 [imported] - *Nostoc* sp. (strain PCC 7120)

C:Species: *Nostoc* sp. PCC 7120

A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C:Accession: AG2311

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritsugu,

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AG2311

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-335 <KUR>

A:Cross-references: UNIPROT:O8YFZ4; GB:BA000019; PIDN:BA075745.1; PID:gl7133181; GSPDB:G

A:Experimental source: strain PCC 7120

C:Gene: alr4046

C:Superfamily: glutathione S-transferase

Query Match 37.8%; Score 48; DB 2; Length 335;  
Best Local Similarity 43.5%; Pred. No. 91;  
Matches 10; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

OY 3 KKMADNGTITV--BEKQLEQWN 23  
:|||||:|:|:|:|:|:  
DB 172 EFAKSTLNLVBEKQIDWVN 194

#### RESULT 42

T29549  
hypochemical protein ZK377.3 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T29549

R:Nhan, M.; Hawkins, J.

submitted to the EMBL Data Library, February 1997

A:Description: The sequence of *C. elegans* cosmid ZK377.

A:Reference number: Z20639

A:Accession: T29549

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-423 <NHA>

A:Cross-references: EMBL:U88183; PIDN:AB52658.1; GSPDB:GN00028; CESP:ZK377.3

A:Experimental source: strain Bristol N2; clone ZK377

C:Gene: ZK377.3

A:Map position: X

A:introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match 37.8%; Score 48; DB 2; Length 423;  
Best Local Similarity 40.0%; Pred. No. 1.2e+02;  
Matches 8; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKMADNGTITVBEKQLE 20  
:|||||:|:|:|:|:|:  
DB 368 RTKVSPGTITIEVRQVDE 387

#### RESULT 43

AB1280

ATP-dependent RNA helicase homolog lmo1722 [imported] - *Listeria monocytogenes* (strain

C:Species: *Listeria monocytogenes*

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AB1280

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeat, O.; Entian, K.D.; Fathi, H.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

C.; Schluerer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.  
 A:Reference number: AB1077; MUID:21537279; PMID:11679669  
 A:Accession: AB1290  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-441 <GLA>  
 A:Cross-references: UNIPROT:Q8Y6G5; GB:NC\_003210; PIDN:CAC99800.1; PID:G16411176; GSPDB:C:Genetics:  
 A:Experimental source: strain EGD-e  
 A:Gene: lmo1722  
  
 Query Match 37.8%; Score 48; DB 2; Length 441;  
 Best Local Similarity 52.2%; Pred. No. 1.2e+02;  
 Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
  
 Oy 1 KKKWADNGTIVEELKQLLEQWN 23  
 |||:|||||  
 Db 135 KIKMHEIKTITLDECDQLLRQEN 157  
  
 RESULT 44  
 AH1661  
 AIP-dependent RNA helicases homolog lln1833 [imported] - *Listeria innocua* (strain C1p111)  
 C:Species: *Listeria innocua*  
 C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: AH1661  
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fahn, H.; Jones, L.W.; Kaye, U.  
 Science 294, 849-852, 2001  
 A:Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madheno, E.; Maicournam, A.; Maok, C.; Schluerer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.  
 A:Reference number: AB1077; MUID:21537279; PMID:11679669  
 A:Accession: AH1661  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-442 <GLA>  
 A:Cross-references: UNIPROT:Q92AT6; GB:AL592022; PIDN:CAC97064.1; PID:G16414335; GSPDB:C:Genetics:  
 A:Experimental source: strain C1p11262  
 A:Gene: lln1833  
  
 Query Match 37.8%; Score 48; DB 2; Length 442;  
 Best Local Similarity 52.2%; Pred. No. 1.2e+02;  
 Matches 12; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
  
 Oy 1 KKKWADNGTIVEELKQLLEQWN 23  
 |||:|||||  
 Db 135 KIKMHEIKTITLDECDQLLRQEN 157  
  
 RESULT 45  
 F90248  
 hypochemical protein srp54 [imported] - *Sulfolobus solfataricus*  
 C:Species: *Sulfolobus solfataricus*  
 C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
 C:Accession: F90248  
 R:Sheng, Q.; Singu, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Anayez, M.U.; Chanat, J.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Tni-Ngoc, H.P.; Redder, F.; Jett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
 submitted to GenBank, April 2001  
 A:Description: *Sulfolobus solfataricus* complete genome.  
 A:Reference number: AB9139  
 A:Accession: F90248  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-447 <KUR>  
 A:Cross-references: UNIPROT:Q97ZE7; GB:AB006641; NID:G13814155; PIDN:AAK41245.1; GSPDB:C:Genetics:  
 A:Gene: srp54  
 C:Superfamily: signal recognition particle 5k protein

```

Query Match          37.8%; Score 48; DB 2; Length 447;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches            8; Conservative          9; Mismatches      5; Indels          0; Gaps          0;

QY      2 KKMAADNGTIVTEELKQLEQNLV 23
Db      401 RRIAGSGLEVEERLELMEYN 422

RESULT 46
S52528
UNAI protein - yeast (Saccharomyces cerevisiae)
NAlternate names: protein LPA14w; protein YP8132.10; protein YPL003w
CSpecies: Saccharomyces cerevisiae
C.Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C.Accession: S52528; S59690
R.Badock, K.; Churcher, C.
Submitted to the EMBL Data Library, February 1995
A.Reference number: S52519
A.Accession: S52528
A.Molecule type: DNA
A.Residues: 1-462 <BAD>
A.Cross-references: UNIPROT:Q12059; EMBL:Z48483; NID:g9683777; PID:g683787; MIPS:YPL003w
A.Experimental source: strain AB972
R.Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storme, R.K.; Vo, D.H.; Wa
Submitted to the EMBL Data Library, August 1995
A.Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A.Reference number: S59677
A.Accession: S59690
A.Molecule type: DNA
A.Residues: 1-462 <HAL>
A.Cross-references: EMBL:U3335; NID:g965076; PID:g965090; MIPS:YPL003w
C.Genetics:
A.Gene: SGD:UNAI; UNAI
A.Cross-references: SGD:S0005924
A.Map position: 16L

Query Match          37.8%; Score 48; DB 2; Length 462;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches            7; Conservative          8; Mismatches      1; Indels          0; Gaps          0;

QY      6 DNGTIVTEELKQLEQ 21
Db      213 NNGRITIDQMKKVLQD 228

RESULT 47
B75017
alanyl-tRNA synthetase (alaS) PAB1245 - Pyrococcus abyssi (strain Orsay)
CSpecies: Pyrococcus abyssi
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Accession: B75017
R.anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A.Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A.Reference number: B75017
A.Accession: B75017
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-914 <KAM>
A.Cross-references: UNIPROT:Q9UY36; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5057
A.Experimental source: strain Orsay
C.Genetics:
A.Gene: PAB1245
C.Superfamily: alanyl-tRNA ligase

Query Match          37.8%; Score 48; DB 2; Length 914;
Best Local Similarity 36.0%; Pred. No. 2.5e+02;
Matches            9; Conservative          9; Mismatches      7; Indels          0; Gaps          0;

QY      1 KKMAADNGTIVTEELKQLEQNLV 25
:|||||:|:|||||:::|:|:

```

Db 314 RKKVAEKYISVEELEKAIKPEYELI 338

## RESULT 48

sax-3 protein - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: T42405

R/Zaller, J.A.; Yi, B.A.; Bargmann, C.I.

Cell 92, 217-227, 1998

A/Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp

A/Reference number: 222160; MUID:98117250; PMID:9458046

A/Accession: T42405

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1273 <ZAL>

A/Cross-references: UNIPROT:O44928; EMBL:AF041053; NID:G2804779; PIDN:AAC38848.1; PID:92

C/Genetics:

A/Note: sax-3

C/Function:

A/Description: sax-3 function is required at the time of axon guidance

Query Match 37.8%; Score 48; DB 2; Length 1273;

Best Local Similarity 40.0%; Pred. No. 3.6e+02;

Matches 8; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKKMADNGTIVBELKQLE 20

Db 369 RTKVSPGTGLTIEVRYQYDE 388

RESULT 49

nonmuscle myosin II heavy chain A - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004

C/Accession: A59282

R/BhacI, Dey, N.; Taira, M.; Conti, M.A.; Nooruddin, H.; Adellestein, R.S.

Mech. Dev. 78, 33-36, 1998

A/Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus e

A/Reference number: A59282; MUID:98077683; PMID:9858676

A/Accession: A59282

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1964 <BHA>

A/Cross-references: UNIPROT:O93522; GB:AF055895; NID:G3660671; PIDN:AAC83556.1; PID:G366

A/Experimental source: cell line XC

C/Superfamily: myosin heavy chain; myosin motor domain homology

F/84-764/Domain: myosin motor domain homology <MMO>

Query Match 37.8%; Score 48; DB 2; Length 1964;

Best Local Similarity 56.5%; Pred. No. 5.6e+02;

Matches 13; Conservative 6; Mismatches 2; Indels 2; Gaps 2;

OY 1 KKKMADN-GTI-TVEELKQLEQ 21

Db 1370 KKKMDENVGSLTIVBELKKKLLQK 1392

RESULT 50

860545

envelope polypeptide gp41 - human immunodeficiency virus type 1 (isolate CI-45-1) (fragm

C/Species: human immunodeficiency virus type 1, HIV-1

A/Variant: isolate CI-45-1

C/Date: 20-Jul-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S60545

R/Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;

AIDS 8, 21-26, 1994

A/Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d

A/Reference number: S60521; MUID:94280700; PMID:8011235

A/Accession: S60545

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-294 <JAN>

A/Cross-references: UNIPROT:O76190; EMBL:X72047; NID:G468669; PIDN:CAAS0930.1; PID:G4686

A/Experimental source: isolate CI-45-1

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993

C/Genetics:

A/Gene: env

C/Superfamily: type B retrovirus env polypeptide

C/Keywords: AIDS; glycoprotein; immunodeficiency; polypeptide

Query Match 37.4%; Score 47.5; DB 2; Length 294;

Best Local Similarity 45.0%; Pred. No. 93;

Matches 9; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

OY 7 NGTITVE-ELKQLEOMNLY 25

Db 136 NGTITLQCKIKQIVNMOKV 155

Search completed: May 11, 2005, 21:23:16

Job time : 31 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: May 11, 2005, 21:15:49 ; Search time 120.745 Seconds  
(without alignments)  
106.025 Million cell updates/sec

Title: US-10-712-812-6

Perfect score: 127

Sequence: 1 KKKMADNGITVEELKQLEQMNLY 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

Uniprot 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	88.2	143	2	Q6ARI0 SARS corona
2	112	88.2	143	2	Q6ARI4 SARS corona
3	112	88.2	143	2	Q6ARI8 SARS corona
4	112	88.2	143	2	Q6ARI2 SARS corona
5	112	88.2	143	2	Q6ARI6 SARS corona
6	112	88.2	143	2	Q6ARI4 SARS corona
7	112	88.2	143	2	Q6ARI8 SARS corona
8	112	88.2	143	2	Q6ARI2 SARS corona
9	112	88.2	143	2	Q6ARI6 SARS corona
10	112	88.2	143	2	Q6ARI0 SARS corona
11	112	88.2	143	2	Q6ARI4 SARS corona
12	112	88.2	143	2	Q6ARI8 SARS corona
13	112	88.2	143	2	Q6ARI2 SARS corona
14	112	88.2	143	2	Q6ARI6 SARS corona
15	112	88.2	143	2	Q6ARI0 SARS corona
16	112	88.2	143	2	Q6ARI4 SARS corona
17	112	88.2	143	2	Q6ARI8 SARS corona
18	112	88.2	221	1	Q6ARI2 SARS corona
19	112	88.2	221	1	Q6ARI6 SARS corona
20	112	88.2	221	2	Q6ARI0 SARS corona
21	112	88.2	221	2	Q6ARI4 SARS corona
22	112	88.2	221	2	Q6ARI8 SARS corona
23	112	88.2	221	2	Q6ARI2 SARS corona
24	112	88.2	221	2	Q6ARI6 SARS corona
25	112	88.2	221	2	Q6ARI0 SARS corona
26	112	88.2	221	2	Q6ARI4 SARS corona
27	112	88.2	221	2	Q6ARI8 SARS corona
28	112	88.2	221	2	Q6ARI2 SARS corona
29	112	88.2	221	2	Q6ARI6 SARS corona
30	112	88.2	221	2	Q6ARI0 SARS corona
31	112	88.2	221	2	Q6ARI4 SARS corona

32	112	88.2	221	2	Q6ARI4 SARS corona
33	112	88.2	221	2	Q6ARI8 SARS corona
34	112	88.2	221	2	Q6ARI2 SARS corona
35	112	88.2	221	2	Q6ARI6 SARS corona
36	112	88.2	221	2	Q6ARI0 SARS corona
37	112	88.2	221	2	Q6ARI4 SARS corona
38	112	88.2	221	2	Q6ARI8 SARS corona
39	112	88.2	221	2	Q6ARI2 SARS corona
40	112	88.2	221	2	Q6ARI6 SARS corona
41	112	88.2	221	2	Q6ARI0 SARS corona
42	112	88.2	221	2	Q6ARI4 SARS corona
43	108	85.0	221	2	Q6ARI8 SARS corona
44	108	85.0	221	2	Q6ARI2 SARS corona
45	106	83.5	143	2	Q6ARI6 SARS corona
46	62	48.8	376	1	HOSC_THER2
47	57	44.9	184	2	Q6ARI4 SARS corona
48	55.5	43.7	409	2	Q6ARI8 SARS corona
49	55	43.3	206	1	RALA_HUMAN
50	55	43.3	229	2	Q6ARI2 SARS corona
51	54	42.5	446	1	SR54_SULAC
52	54	42.5	458	2	Q6ARI6 SARS corona
53	54	42.5	767	2	Q6ARI0 SARS corona
54	53.5	42.1	512	2	Q6ARI4 SARS corona
55	53	41.7	82	2	Q6ARI8 SARS corona
56	53	41.7	184	2	Q6ARI2 SARS corona
57	53	41.7	184	2	Q6ARI6 SARS corona
58	53	41.7	262	2	Q6ARI0 SARS corona
59	53	41.7	279	2	Q6ARI4 SARS corona
60	53	41.7	351	1	CARA_CLOAB
61	53	41.7	527	2	Q6ARI8 SARS corona
62	53	41.7	547	1	CH60_WOLRE
63	53	41.7	895	2	Q6ARI2 SARS corona
64	52.5	41.3	213	2	Q6ARI6 SARS corona
65	52.5	41.3	490	2	Q6ARI0 SARS corona
66	52	40.9	185	2	Q6ARI4 SARS corona
67	52	40.9	185	2	Q6ARI8 SARS corona
68	52	40.9	185	2	Q6ARI2 SARS corona
69	52	40.9	206	1	RALA_CALJA
70	52	40.9	206	1	RALA_MOUSE
71	52	40.9	206	1	RALA_RAT
72	52	40.9	206	2	Q6ARI4 SARS corona
73	52	40.9	401	2	Q6ARI8 SARS corona
74	52	40.9	410	2	Q6ARI2 SARS corona
75	52	40.9	545	1	CH60_CAMJE
76	52	40.9	16367	2	Q6ARI6 SARS corona
77	51.5	40.6	352	2	Q6ARI0 SARS corona
78	51	40.2	184	2	Q6ARI4 SARS corona
79	51	40.2	184	2	Q6ARI8 SARS corona
80	51	40.2	203	1	VR1A_HUMAN
81	51	40.2	217	2	Q6ARI2 SARS corona
82	51	40.2	326	2	Q6ARI6 SARS corona
83	51	40.2	545	1	Q6ARI0 SARS corona
84	51	40.2	545	1	Q6ARI4 SARS corona
85	51	40.2	545	1	Q6ARI8 SARS corona
86	51	40.2	545	1	Q6ARI2 SARS corona
87	51	40.2	545	1	Q6ARI6 SARS corona
88	51	40.2	545	1	Q6ARI0 SARS corona
89	51	40.2	545	1	Q6ARI4 SARS corona
90	51	40.2	545	1	Q6ARI8 SARS corona
91	51	40.2	545	1	Q6ARI2 SARS corona
92	51	40.2	545	1	Q6ARI6 SARS corona
93	51	40.2	545	1	Q6ARI0 SARS corona
94	51	40.2	545	1	Q6ARI4 SARS corona
95	50.5	39.8	193	2	Q6ARI8 SARS corona
96	50.5	39.8	203	2	Q6ARI2 SARS corona
97	50.5	39.8	203	2	Q6ARI6 SARS corona
98	50.5	39.8	203	2	Q6ARI0 SARS corona
99	50.5	39.8	218	2	Q6ARI4 SARS corona
100	50.5	39.8	342	2	Q6ARI8 SARS corona
101	50.5	39.8	450	2	Q6ARI2 SARS corona
102	50.5	39.8	451	2	Q6ARI6 SARS corona
103	50.5	39.8	451	2	Q6ARI0 SARS corona
104	50.5	39.8	852	2	Q6ARI4 SARS corona

105	50.5	39.8	852	2	Q9DQ10	Q9dq10 human immun	178	49	38.6	536	2	Q9BE16	Q9be16 macaca fasc
106	50	39.4	149	2	O8ENU0	O8enu0 oceanobacil	179	49	38.6	643	1	SYT_HAEIN	P33014 haemophilus
107	50	39.4	174	2	O6Z2J1	O6z2j1 oryza sativ	180	49	38.6	648	1	CH6B_DROME	Cyp55 dirosophila
108	50	39.4	184	2	O8KUZ5	O8kuz5 uncultured	181	49	38.6	1744	2	Q9R055	Q9r095 rattus norv
109	50	39.4	184	2	O6BH71	O6bh71 clostridium	182	49	38.6	2788	2	Q7WRX9	Q7wrx9 anabaena ci
110	50	39.4	184	2	O6BH72	O6bh72 clostridium	183	49	38.6	4416	2	Q9J3F3	Q9j3f3 murine hepa
111	50	39.4	264	1	YES4_SCHPO	O11171 scizosacch	184	49	38.6	4416	2	Q9J3F8	Q9j3f8 m replicase
112	50	39.4	274	1	O8RI36	O8ri36 fusobacteri	185	49	38.6	7124	1	R1AB_CVM2	Q9pya3 m replicase
113	50	39.4	294	2	O94072	O94072 caenorhabdi	186	48.5	38.2	163	2	Q9MWT4	Q9mwt4 human immun
114	50	39.4	300	2	Q7WVC9	Q7wvc9 actinetobact	187	48.5	38.2	174	2	Q7OCJ8	Q7ocj8 human immun
115	50	39.4	300	2	Q9F7D7	Q9f7d7 actinetobact	188	48.5	38.2	179	2	Q9DVP8	Q9dvp8 human immun
116	50	39.4	323	1	PXP_HAEIN	P44828 haemophilus	189	48.5	38.2	185	2	O5S132	O5s132 mus musculu
117	50	39.4	516	2	Q96KP3	Q96kp3 homo sapien	190	48.5	38.2	193	2	Q7ZN14	Q7zn14 human immun
118	50	39.4	531	2	O98974	O98974 ritzobium 1	191	48.5	38.2	195	2	Q7ORQ3	Q7orq3 human immun
119	50	39.4	536	1	CN1B_HUMAN	Q01064 homo sapien	192	48.5	38.2	195	2	Q7ORQ6	Q7orq6 human immun
120	50	39.4	546	1	CH60_MOLSU	Q7mae3 wolinnella s	193	48.5	38.2	203	2	O8AD00	O8ad00 human immun
121	50	39.4	549	1	CH62_BRAVA	P33861 bradyrhizob	194	48.5	38.2	206	2	Q7SUT3	Q7sut3 human immun
122	50	39.4	673	2	O9PR23	O9pr23 ureaplasma	195	48.5	38.2	211	2	Q7ZNS9	Q7zn99 human immun
123	50	39.4	846	2	O8N270	O8n270 homo sapien	196	48.5	38.2	842	2	Q7O895	Q7o895 human immun
124	50	39.4	846	2	O8I114	O8i114 caenorhabdi	197	48.5	38.2	842	2	Q73340	Q73340 human immun
125	50	39.4	861	1	P058_CAEEL	P34552 caenorhabdi	198	48.5	38.2	855	2	O6UFC3	O6ufc3 human immun
126	50	39.4	868	2	O6ALT6	O6alt6 deesulfoale	199	48.5	38.2	872	2	O9IUD0	O9iuz0 human immun
127	50	39.4	882	2	O8I115	O8i115 caenorhabdi	200	48.5	38.2	872	2	Q9IUD1	Q9iuz1 human immun
128	50	39.4	1118	2	Q7R2P7	Q7r2p7 giardia lam	201	48	37.8	119	2	O6PRV2	O6prv2 cuturnix co
129	50	39.4	1325	2	Q9UG16	Q9ug16 homo sapien	202	48	37.8	125	2	O05614	O05614 pseudomonas
130	50	39.4	1458	1	SPCN_MOUSE	P16546 mus musculu	203	48	37.8	126	2	P84137	P84137 bacillus st
131	50	39.4	1803	1	PNO_EUGER	O94i05 euglena gra	204	48	37.8	127	2	O8CBJ3	O8cbj3 mus musculu
132	50	39.4	2443	1	Q96J17	Q96j17 homo sapien	205	48	37.8	159	1	GNAL_YEAST	P43577 saccharomyc
133	50	39.4	2452	2	Q7Z6M5	Q7z6m5 homo sapien	206	48	37.8	159	1	O8KHT8	O8kht8 uncultured
134	50	39.4	2452	2	O6IRK8	O6irk8 rattus norv	207	48	37.8	184	2	O8KIA7	O8kia7 uncultured
135	50	39.4	2472	1	SPCN_HUMAN	Q13813 homo sapien	208	48	37.8	184	2	O8KP73	O8kp73 veillonella
136	50	39.4	2472	1	SPCN_RAT	P16086 rattus norv	209	48	37.8	184	2	O8KUZ1	O8kuz1 uncultured
137	50	39.4	2477	1	SPCN_CHICK	P07751 gallus gal1	210	48	37.8	184	2	O8KV10	O8kv10 uncultured
138	50	39.4	4091	2	Q7QAT8	Q7qa48 anopheles g	211	48	37.8	184	2	O8KV16	O8kv16 uncultured
139	50	39.4	13536	2	Q83VS0	O83vs0 pseudomonas	212	48	37.8	184	2	O8KVA2	O8kva2 uncultured
140	49.5	39.0	143	2	O6T702	O6t702 symbiodacte	213	48	37.8	184	2	O8KVA4	O8kva4 uncultured
141	49.5	39.0	177	2	Q9QRL9	Q9qrl9 human immun	214	48	37.8	184	2	O8KVA5	O8kva5 uncultured
142	49.5	39.0	201	2	O8US59	O8us59 human immun	215	48	37.8	184	2	O8KVB6	O8kvb6 uncultured
143	49.5	39.0	203	2	O70521	O70521 human immun	216	48	37.8	184	2	O8KVB8	O8kvb8 uncultured
144	49.5	39.0	203	2	O70528	O70528 human immun	217	48	37.8	184	2	O8KVC3	O8kvc3 uncultured
145	49.5	39.0	208	2	O8Q7K0	O8q7k0 human immun	218	48	37.8	184	2	O8KVC6	O8kvc6 uncultured
146	49.5	39.0	573	2	O6FY31	O6fy31 candida gla	219	48	37.8	184	2	O8KVS5	O8kvs5 uncultured
147	49.5	39.0	855	2	O8UL72	O8ul72 human immun	220	48	37.8	184	2	O8KVS5	O8kvs5 uncultured
148	49.5	39.0	897	2	O99786	O99786 cache valle	221	48	37.8	184	2	O8KVS5	O8kvs5 uncultured
149	49.5	39.0	897	2	O91ZG4	O91z94 cache valle	222	48	37.8	184	2	O8KVS6	O8kvs6 uncultured
150	49.5	39.0	897	2	O791N3	O791n3 strephylcoc	223	48	37.8	184	2	O8KVS8	O8kvs8 uncultured
151	49	38.6	118	2	Q99MNS	O99mns rattus norv	224	48	37.8	184	2	O8KV16	O8kv16 uncultured
152	49	38.6	123	2	O9X5T5	O9x5t5 streptomyc	225	48	37.8	184	2	O8KV12	O8kv12 uncultured
153	49	38.6	143	2	O961X6	O961x6 homo sapien	226	48	37.8	184	2	O8KVL5	O8kvl5 uncultured
154	49	38.6	180	2	O70NT8	O70nt8 helicobacte	227	48	37.8	184	2	O8KVP5	O8kvp5 uncultured
155	49	38.6	183	2	O65WMP2	O65wp2 manheimia	228	48	37.8	184	2	O8KVO4	O8kvo4 uncultured
156	49	38.6	184	2	O8KVL5	O8kvl5 uncultured	229	48	37.8	184	2	O8KVO8	O8kvo8 uncultured
157	49	38.6	184	2	O8KV26	O8kv26 uncultured	230	48	37.8	184	2	O68GZ5	O68gz5 ruminococcu
158	49	38.6	184	2	O8KVQ0	O8kvq0 uncultured	231	48	37.8	184	2	O68GZ7	O68gz7 ruminococcu
159	49	38.6	218	1	TH01_YEAST	P40040 saccharomyc	232	48	37.8	184	2	O68GZ9	O68gz9 ruminococcu
160	49	38.6	431	2	O74KY2	O74ky2 lactobacill	233	48	37.8	184	2	O68H01	O68h01 ruminococcu
161	49	38.6	458	2	O6PDPS	O6pdp5 mus musculu	234	48	37.8	184	2	O68H40	O68h40 eubacterium
162	49	38.6	462	1	TRPE_LBPBI	P20463 leptospira	235	48	37.8	184	2	O68H45	O68h45 eubacterium
163	49	38.6	473	1	LCBI_HUMAN	O15269 homo sapien	236	48	37.8	184	2	O68H56	O68h56 eubacterium
164	49	38.6	475	2	O14917	O14917 homo sapien	237	48	37.8	184	2	O68H59	O68h59 clostridium
165	49	38.6	485	1	SYE_CLOAB	O91kc9 clostridium	238	48	37.8	184	2	O68H62	O68h62 clostridium
166	49	38.6	495	2	O9DBS6	O9db86 mus musculu	239	48	37.8	184	2	O68H80	O68h80 butyrivibri
167	49	38.6	504	1	NORR_ECOS7	O8x854 escherichia	240	48	37.8	184	2	O65H00	O65h00 bacillus 11
168	49	38.6	504	1	NORR_ECOS6	O8x856 escherichia	241	48	37.8	184	2	O74076	O74076 human immun
169	49	38.6	504	1	NORR_ECOS1	P37013 escherichia	242	48	37.8	217	1	VT1A_MOUSE	O91i51 rattus norv
170	49	38.6	504	1	NORR_SHIFL	P59402 shigella fl	243	48	37.8	224	1	VT1A_RAT	O37049 porcine epi
171	49	38.6	506	1	NORR_SALTI	O8x4c6 salmonella	244	48	37.8	226	2	O37351	O37351 porcine epi
172	49	38.6	506	1	NORR_SALTY	O8xmj8 salmonella	245	48	37.8	226	2	O72839	O72839 porcine epi
173	49	38.6	512	2	O6DBR9	O6dbr9 erwinia car	246	48	37.8	226	2	O610S8	O610s8 porcine epi
174	49	38.6	513	2	O6NUL7	O6nul7 homo sapien	247	48	37.8	226	2	O610S8	O610s8 porcine epi
175	49	38.6	534	1	CN1B_BOVIN	O01061 bos taurus	248	48	37.8	235	1	O8TS68	O8ts68 methanosarc
176	49	38.6	535	1	CN1B_MOUSE	O01065 mus musculu	249	48	37.8	254	1	WI12_CAEEL	O22306 caenorhabdi
177	49	38.6	535	1	CN1B_RAT	O01066 rattus norv	250	48	37.8	294	2	O6BEU9	O6beu9 caenorhabdi



251	48	37.8	299	2	Q84SQ1	Q84eq1 oryza sativ	324	47.5	37.4	294	2	Q76190	Q76190 human immun
252	48	37.8	299	2	Q9HUA1	Q9Hua1 pseudomonas	325	47.5	37.4	342	2	Q91U83	Q91u83 human immun
253	48	37.8	309	2	Q17902	Q17902 caenorhabdi	326	47.5	37.4	405	2	Q66LA6	Q66la6 human immun
254	48	37.8	312	2	Q82KX3	Q82Kx3 salmonella	327	47.5	37.4	486	2	Q72WJ2	Q72wj2 human immun
255	48	37.8	335	2	Q8YFZ4	Q8Yfz4 anabaena sp	328	47.5	37.4	495	2	Q748Z6	Q748z6 human immun
256	48	37.8	338	2	Q7WZ12	Q7Wz12 haemophilus	329	47.5	37.4	583	2	Q8EP19	Q8ep19 human immun
257	48	37.8	428	2	Q7XT74	Q7Xt74 oryza sativ	330	47.5	37.4	846	2	Q6BBR0	Q6bbR0 human immun
258	48	37.8	441	2	Q8Y6G5	Q8Y6g5 listeria mo	331	47.5	37.4	849	2	Q8J9B8	Q8j9B8 human immun
259	48	37.8	442	2	Q92AT6	Q92At6 listeria in	332	47.5	37.4	861	2	Q6XJ54	Q6xj54 human immun
260	48	37.8	442	2	Q71YU6	Q71Yu6 listeria mo	333	47.5	37.4	863	2	Q6UPP6	Q6upP6 human immun
261	48	37.8	446	2	Q8D2V4	Q8D2v4 wigglewort	334	47.5	37.4	869	2	Q8ULP9	Q8ulP9 human immun
262	48	37.8	447	1	SR54_SULSO	SR54 sulfolobus	335	47.5	37.4	874	2	Q8UL68	Q8ul68 human immun
263	48	37.8	457	1	Q74IW2	Q74Iw2 saccharomy	336	47.5	37.4	874	2	Q8UL68	Q8ul68 human immun
264	48	37.8	462	1	UTAI_YEAST	Q12059 utai yeast	337	47.5	37.4	1119	2	Q6TUP9	Q6tup9 ratuce norv
265	48	37.8	517	2	Q63OH3	Q63Oh3 bacillus ce	338	47.5	37.0	184	2	Q8KVA1	Q8kva1 uncultured
266	48	37.8	517	2	Q81JMS	Q81Jms bacillus an	339	47.5	37.0	184	2	Q8KVE4	Q8kve4 uncultured
267	48	37.8	517	2	Q6HAK8	Q6Hak8 bacillus th	340	47.5	37.0	184	2	Q68G17	Q68g17 rhinococcu
268	48	37.8	530	2	Q72X14	Q72X14 bacillus ce	341	47.5	37.0	184	2	Q68H43	Q68h43 eubacterium
269	48	37.8	536	2	Q814J7	Q814j7 bacillus ce	342	47.5	37.0	184	2	Q68H67	Q68h67 clostridium
270	48	37.8	540	2	Q8FP25	Q8Fp25 corynebacte	343	47.5	37.0	186	2	Q8KVD7	Q8kvd7 uncultured
271	48	37.8	553	2	Q9WGG2	Q9Wg2 hyphantha	344	47.5	37.0	186	2	Q8KXV5	Q8kxv5 uncultured
272	48	37.8	594	2	Q8BMV1	Q8Bmv1 oceanobacil	345	47.5	37.0	190	2	Q54554	Q54554 halobacteri
273	48	37.8	647	2	Q8CA10	Q8Ca10 mus musculu	346	47.5	37.0	199	2	Q7MV58	Q7mv58 porphyromon
274	48	37.8	654	2	Q975S3	Q975s3 sulfolobus	347	47.5	37.0	215	1	AROD_METKA	Q8cy76 methanopyru
275	48	37.8	856	2	Q6APR6	Q6Apr6 desulfotale	348	47.5	37.0	281	2	Q48759	Q48759 arabidopsis
276	48	37.8	914	1	SYA_PYRAP	Q9Y36 pyrococcus	349	47.5	37.0	312	2	Q8ZLW0	Q8zlw0 salmonella
277	48	37.8	1027	2	Q9WPP5	Q9Wp5 chimpazee	350	47.5	37.0	370	2	Q6MR14	Q6mr14 belliovibri
278	48	37.8	1213	2	Q8IC20	Q8Ic20 plasmodium	351	47.5	37.0	407	1	MYC_ASTVU	Q71103 acetabias vu
279	48	37.8	1269	2	Q01632	Q01632 caenorhabdi	352	47.5	37.0	453	2	Q8BLT3	Q8blt3 mus musculu
280	48	37.8	1273	2	Q44928	Q44928 caenorhabdi	353	47.5	37.0	459	2	Q7MEF6	Q7mef6 vibrio vuln
281	48	37.8	1662	2	Q6A070	Q6A070 mus musculu	354	47.5	37.0	459	2	Q87HY2	Q87hy2 vibrio para
282	48	37.8	1964	2	Q93522	Q93522 xenopus lae	355	47.5	37.0	459	2	Q8D7E7	Q8d7e7 vibrio vuln
283	48	37.8	4437	2	Q8GCP3	Q8Gcp3 streptomyce	356	47.5	37.0	472	2	Q98OR0	Q98or0 mycoplasma
284	47.5	37.4	149	2	Q9YD13	Q9Yd13 diosiphila	357	47.5	37.0	493	2	Q732A5	Q732a5 bacillus ce
285	47.5	37.4	155	2	Q73383	Q73383 human immun	358	47.5	37.0	493	2	Q8A2P4	Q8a2P4 bacteroides
286	47.5	37.4	156	2	Q91W68	Q91w68 human immun	359	47.5	37.0	508	2	Q6HUN5	Q6hun5 bacillus an
287	47.5	37.4	168	2	Q8Q2G9	Q8Q2g9 human immun	360	47.5	37.0	510	2	Q636N5	Q636n5 bacillus ce
288	47.5	37.4	171	2	Q7OR72	Q7Or72 human immun	361	47.5	37.0	510	2	Q8R8K4	Q8r8K4 thermoaer
289	47.5	37.4	178	2	Q99F39	Q99F39 human immun	362	47.5	37.0	510	2	Q732T5	Q732t5 bacillus ce
290	47.5	37.4	184	2	Q8Q1U2	Q8Q1u2 human immun	363	47.5	37.0	510	2	Q81WP5	Q81wp5 bacillus an
291	47.5	37.4	184	2	Q8Q1U3	Q8Q1u3 human immun	364	47.5	37.0	510	2	Q6HF24	Q6hf24 bacillus th
292	47.5	37.4	184	2	Q8Q1U4	Q8Q1u4 human immun	365	47.5	37.0	553	2	Q7MBB4	Q7mbb4 glieobacter
293	47.5	37.4	184	2	Q8Q1U5	Q8Q1u5 human immun	366	47.5	37.0	577	2	Q9ST62	Q9st62 solanum tub
294	47.5	37.4	184	2	Q8Q1U6	Q8Q1u6 human immun	367	47.5	37.0	608	2	Q42620	Q42620 magnaporthe
295	47.5	37.4	184	2	Q8Q1U7	Q8Q1u7 human immun	368	47.5	37.0	627	2	Q9KPY2	Q9kpy2 bacillus ha
296	47.5	37.4	184	2	Q8Q1U8	Q8Q1u8 human immun	369	47.5	37.0	657	2	Q8APL5	Q8apl5 chimpazee
297	47.5	37.4	184	2	Q8Q1U9	Q8Q1u9 human immun	370	47.5	37.0	659	1	SPA2_SYNY3	P72587 synechocyst
298	47.5	37.4	184	2	Q8Q1V0	Q8Q1v0 human immun	371	47.5	37.0	667	2	Q5462	Q5462 synechocyst
299	47.5	37.4	184	2	Q8Q1V1	Q8Q1v1 human immun	372	47.5	37.0	689	2	Q89ZV9	Q89zv9 bacteroides
300	47.5	37.4	184	2	Q90C08	Q90C08 human immun	373	47.5	37.0	749	2	Q9RPM1	Q9rfn1 lactobacill
301	47.5	37.4	186	2	Q7SKV1	Q7SKv1 human immun	374	47.5	37.0	759	1	BURL_THBAC	Q9hja4 thermoplasm
302	47.5	37.4	195	2	Q7ORC5	Q7ORc5 human immun	375	47.5	37.0	804	2	Q8A7T2	Q8a7T2 bacteroides
303	47.5	37.4	196	2	Q9JBU5	Q9JbJ5 human immun	376	47.5	37.0	863	2	Q76148	Q76148 anopheles s
304	47.5	37.4	197	2	Q6SUT1	Q6Sut1 human immun	377	47.5	37.0	867	2	Q7OEU3	Q7oEj3 anopheles g
305	47.5	37.4	199	2	Q7SKT3	Q7SKt3 human immun	378	47.5	37.0	999	2	Q6GIM3	Q6gim3 bartonella
306	47.5	37.4	199	2	Q7ZNI0	Q7Zni0 human immun	379	47.5	37.0	1066	2	Q93W58	Q93w58 phaseolus v
307	47.5	37.4	202	2	Q8J8T0	Q8J8t0 human immun	380	47.5	37.0	1067	2	Q98Z57	Q98z57 arabidopsis
308	47.5	37.4	202	2	Q90N01	Q90N01 human immun	381	47.5	37.0	1198	2	Q04538	Q04538 arabidopsis
309	47.5	37.4	202	2	Q8AL44	Q8Al44 human immun	382	47.5	37.0	1290	2	Q9S1A7	Q9s1A7 microcycetis
310	47.5	37.4	203	2	Q8J8H4	Q8J8h4 human immun	383	47.5	37.0	1291	2	Q8RGT3	Q8rGT3 microcycetis
311	47.5	37.4	211	2	Q6RHL9	Q6Rhl9 human immun	384	47.5	37.0	1291	2	Q9RAN9	Q9ran9 microcycetis
312	47.5	37.4	205	2	Q8J8I6	Q8J8i6 human immun	385	47.5	37.0	2156	2	Q81DB7	Q81db7 bacillus ce
313	47.5	37.4	208	2	Q8Q0J1	Q8Q0j1 human immun	386	47.5	37.0	2816	2	Q8G983	Q8g983 oscillatori
314	47.5	37.4	209	2	Q8US45	Q8Us45 human immun	387	47.5	37.0	4467	2	Q9J3B9	Q9j3B9 murine hepa
315	47.5	37.4	210	2	Q70QW2	Q70Qw2 human immun	388	47.5	37.0	4470	2	Q66WN5	Q66wn5 murine hepa
316	47.5	37.4	211	2	Q70QW4	Q70Qw4 human immun	389	47.5	37.0	7176	1	RIAB_CVMA5	P6342 m replicase
317	47.5	37.4	211	2	Q8AD04	Q8Ad04 human immun	390	47.5	37.0	7178	2	Q66WN6	Q66wn6 murine hepa
318	47.5	37.4	216	2	Q70QO1	Q70Qo1 human immun	391	46.5	36.6	79	2	Q70493	Q70493 human immun
319	47.5	37.4	217	2	Q70Q81	Q70Q81 human immun	392	46.5	36.6	104	2	Q78877	Q78877 human immun
320	47.5	37.4	219	2	Q7ZBA3	Q7Zba3 human immun	393	46.5	36.6	104	2	Q78881	Q78881 human immun
321	47.5	37.4	221	2	Q7ZP24	Q7Zp24 human immun	394	46.5	36.6	159	2	Q9JBS7	Q9jeb7 human immun
322	47.5	37.4	224	2	Q7ZME5	Q7Zme5 human immun	395	46.5	36.6	161	2	Q70R49	Q70r49 human immun
323	47.5	37.4	294	2	Q76168	Q76168 human immun	396	46.5	36.6	162	2	Q70QK1	Q70qk1 human immun

397	46.5	36.6	168	2	06J4B0	06J4B0	human	immun	470	46.5	36.6	402	2	06ELA3	06ELA3	human	immun		
398	46.5	36.6	169	2	070QZ6	070QZ6	human	immun	471	46.5	36.6	409	2	041635	041635	human	immun		
399	46.5	36.6	169	2	070R29	070R29	human	immun	472	46.5	426	087QW7	087QW7	vibrio para	087QW7	vibrio para			
400	46.5	36.6	176	2	070R40	070R40	human	immun	473	46.5	36.6	428	2	06LPR1	06LPR1	photobacter			
401	46.5	36.6	183	2	09DVA1	09DVA1	human	immun	474	46.5	36.6	428	2	09KSZ5	09KSZ5	vibrio chol			
402	46.5	36.6	190	2	08US55	08US55	human	immun	475	46.5	36.6	429	2	07MLV1	07MLV1	vibrio vuln			
403	46.5	36.6	191	2	070R37	070R37	human	immun	476	46.5	36.6	462	2	082VU0	082VU0	nitrosomona			
404	46.5	36.6	194	2	091VV5	091VV5	human	immun	477	46.5	36.6	486	2	08RC59	08RC59	thermoanaer			
405	46.5	36.6	195	2	070525	070525	human	immun	478	46.5	36.6	588	2	0655G1	0655G1	tyza sativ			
406	46.5	36.6	195	2	07ZND6	07ZND6	human	immun	479	46.5	36.6	594	2	09POM8	09POM8	ureaplasma			
407	46.5	36.6	195	2	09QNX2	09QNX2	human	immun	480	46.5	36.6	801	2	09MMV9	09MMV9	human	immun		
408	46.5	36.6	196	2	070R78	070R78	human	immun	481	46.5	36.6	847	2	09MTS1	09MTS1	human	immun		
409	46.5	36.6	197	2	06SU01	06SU01	human	immun	482	46.5	36.6	849	2	09YKT4	09YKT4	human	immun		
410	46.5	36.6	197	2	06SU03	06SU03	human	immun	483	46.5	36.6	849	2	09YKT7	09YKT7	human	immun		
411	46.5	36.6	197	2	06SU08	06SU08	human	immun	484	46.5	36.6	850	2	09QBR2	09QBR2	human	immun		
412	46.5	36.6	197	2	06SU09	06SU09	human	immun	485	46.5	36.6	858	2	06UFG9	06UFG9	human	immun		
413	46.5	36.6	197	2	06SU10	06SU10	human	immun	486	46.5	36.6	858	2	073293	073293	human	immun		
414	46.5	36.6	197	2	06SU12	06SU12	human	immun	487	46.5	36.6	1366	2	08KN79	08KN79	streptococc			
415	46.5	36.6	197	2	06SUW3	06SUW3	human	immun	488	46.5	36.6	1366	2	08P2F2	08P2F2	streptococc			
416	46.5	36.6	197	2	09DVI5	09DVI5	human	immun	489	46.5	36.6	1372	2	087BN3	087BN3	chaetosphe			
417	46.5	36.6	198	2	07SKS3	07SKS3	human	immun	490	46.5	36.6	1373	1	RPC2	CHAGL	wolfinella s			
418	46.5	36.6	199	2	07SU41	07SU41	human	immun	491	46.5	36.2	90	2	07MS15	90	2	07RM11	07RM11	plasmodium
419	46.5	36.6	199	2	08ALM1	08ALM1	human	immun	492	46.5	36.2	100	2	08S313	08S313	populus tre			
420	46.5	36.6	200	1	COAE_BACAN	COAE_BACAN			493	46.5	36.2	114	2	Y352	SUISO	bulfolobus			
421	46.5	36.6	200	2	0633I3	0633I3	Bacillus an		494	46.5	36.2	118	1	06RJZ7	06RJZ7	capetium an			
422	46.5	36.6	200	2	06HCU7	06HCU7	Bacillus ce		495	46.5	36.2	124	2	06M9J5	06M9J5	parachlamyd			
423	46.5	36.6	201	2	097D99	097D99	clostridium		496	46.5	36.2	124	2	09JGU5	09JGU5	puteilla xy			
424	46.5	36.6	201	2	0619D6	0619D6	human	immun	497	46.5	36.2	131	2	08KH65	08KH65	uncultured			
425	46.5	36.6	201	2	07SU31	07SU31	human	immun	498	46.5	36.2	184	2	08KH90	08KH90	uncultured			
426	46.5	36.6	201	2	07SU33	07SU33	human	immun	499	46.5	36.2	184	2	08KH39	08KH39	uncultured			
427	46.5	36.6	201	2	07SU42	07SU42	human	immun	500	46.5	36.2	184	2	08KH184	08KH184	uncultured			
428	46.5	36.6	202	2	07ZP14	07ZP14	human	immun	501	46.5	36.2	184	2	08KV31	08KV31	uncultured			
429	46.5	36.6	202	2	08AL57	08AL57	human	immun	502	46.5	36.2	184	2	08KV49	08KV49	uncultured			
430	46.5	36.6	202	2	070518	070518	human	immun	503	46.5	36.2	184	2	08KV63	08KV63	uncultured			
431	46.5	36.6	203	2	070522	070522	human	immun	504	46.5	36.2	184	2	08KV65	08KV65	uncultured			
432	46.5	36.6	203	2	070529	070529	human	immun	505	46.5	36.2	184	2	08KV72	08KV72	uncultured			
433	46.5	36.6	203	2	07SU52	07SU52	human	immun	506	46.5	36.2	184	2	08KV87	08KV87	uncultured			
434	46.5	36.6	203	2	07SU04	07SU04	human	immun	507	46.5	36.2	184	2	08KV98	08KV98	uncultured			
435	46.5	36.6	203	2	07SU19	07SU19	human	immun	508	46.5	36.2	184	2	08KV98	08KV98	uncultured			
436	46.5	36.6	203	2	08AL98	08AL98	human	immun	509	46.5	36.2	184	2	08KV90	08KV90	uncultured			
437	46.5	36.6	204	2	070540	070540	human	immun	510	46.5	36.2	184	2	08KV97	08KV97	uncultured			
438	46.5	36.6	205	2	07SKV0	07SKV0	human	immun	511	46.5	36.2	184	2	08KV82	08KV82	uncultured			
439	46.5	36.6	206	2	07SU37	07SU37	human	immun	512	46.5	36.2	184	2	08KV61	08KV61	uncultured			
440	46.5	36.6	206	2	07SU35	07SU35	human	immun	513	46.5	36.2	184	2	08KV70	08KV70	uncultured			
441	46.5	36.6	206	2	07SU58	07SU58	human	immun	514	46.5	36.2	184	2	08KV80	08KV80	uncultured			
442	46.5	36.6	206	2	07SU18	07SU18	human	immun	515	46.5	36.2	184	2	08KV11	08KV11	uncultured			
443	46.5	36.6	206	2	07SU12	07SU12	human	immun	516	46.5	36.2	184	2	08KV11	08KV11	uncultured			
444	46.5	36.6	207	2	06SU58	06SU58	human	immun	517	46.5	36.2	184	2	08KV11	08KV11	uncultured			
445	46.5	36.6	209	2	07SU68	07SU68	human	immun	518	46.5	36.2	184	2	08KV98	08KV98	uncultured			
446	46.5	36.6	214	2	07SU34	07SU34	human	immun	519	46.5	36.2	184	2	08KV90	08KV90	uncultured			
447	46.5	36.6	215	2	08J9D8	08J9D8	human	immun	520	46.5	36.2	184	2	08KV97	08KV97	uncultured			
448	46.5	36.6	218	2	07SU00	07SU00	human	immun	521	46.5	36.2	184	2	06BH36	06BH36	lactobacill			
449	46.5	36.6	218	2	07SU01	07SU01	human	immun	522	46.5	36.2	184	2	06BH41	06BH41	eubacterium			
450	46.5	36.6	218	2	09WLR7	09WLR7	human	immun	523	46.5	36.2	184	2	06BH42	06BH42	eubacterium			
451	46.5	36.6	220	2	07SU44	07SU44	human	immun	524	46.5	36.2	184	2	06BH68	06BH68	clostridium			
452	46.5	36.6	220	2	07ZMF5	07ZMF5	human	immun	525	46.5	36.2	185	2	06BS72	06BS72	uncultured			
453	46.5	36.6	223	2	07SU39	07SU39	human	immun	526	46.5	36.2	185	2	06J157	06J157	chlamydia p			
454	46.5	36.6	265	2	09WIR3	09WIR3	human	immun	527	46.5	36.2	186	2	08KV01	08KV01	uncultured			
455	46.5	36.6	276	2	09WE10	09WE10	human	immun	528	46.5	36.2	216	2	08CTQ3	08CTQ3	staphylococ			
456	46.5	36.6	277	2	08D8M8	08D8M8	vibrio vuln		529	46.5	36.2	229	2	08ECT2	08ECT2	shewanella			
457	46.5	36.6	278	2	076212	076212	human	immun	530	46.5	36.2	229	2	06LVS1	06LVS1	methanococc			
458	46.5	36.6	288	2	073316	073316	human	immun	531	46.5	36.2	229	2	06ZWT8	06ZWT8	homo sapien			
459	46.5	36.6	301	2	070212	070212	human	immun	532	46.5	36.2	292	2	07Z6A8	07Z6A8	homo sapien			
460	46.5	36.6	327	2	0871A9	0871A9	vibrio para		533	46.5	36.2	292	2	0896D1	0896D1	clostridium			
461	46.5	36.6	328	2	091U84	091U84	human	immun	534	46.5	36.2	298	2	0892F7	0892F7	clostridium			
462	46.5	36.6	347	2	07ZP53	07ZP53	human	immun	535	46.5	36.2	306	2	08XLD5	08XLD5	clostridium			
463	46.5	36.6	358	2	08QD00	08QD00	human	immun	536	46.5	36.2	335	1	FLIG_THEMEA	FLIG_THEMEA	thermoga			
464	46.5	36.6	359	2	P87967	P87967	human	immun	537	46.5	36.2	336	1	09GFE1	09GFE1	hinterleuk			
465	46.5	36.6	359	2	08OAZ6	08OAZ6	human	immun	538	46.5	36.2	340	1	YM21_ARCFU	YM21_ARCFU	archaeoglob			
466	46.5	36.6	359	2	08OAZ7	08OAZ7	human	immun	539	46.5	36.2	382	2	069BD1	069BD1	campylobact			
467	46.5	36.6	359	2	08QD01	08QD01	human	immun	540	46.5	36.2	382	2	069BT1	069BT1	campylobact			
468	46.5	36.6	386	2	08Q843	08Q843	human	immun	541	46.5	36.2	401	2	08VR20	08VR20	chlamydophi			
469	46.5	36.6	386	2	08Q846	08Q846	human	immun	542	46.5	36.2	401	2	090HW7	090HW7	human	immun		

543	46	36.2	403	2	Q9BPM3	Q9BPM3	toxoplasma	616	45.5	35.8	194	2	Q6VG99	Q6VG99	human	immun
544	46	36.2	408	2	Q83WK4	Q83WK4	chlamydia p	617	45.5	35.8	195	2	Q7ZNG0	Q7ZNG0	human	immun
545	46	36.2	417	2	Q59792	Q59792	chlamydia p	618	45.5	35.8	196	2	Q68ID5	Q68ID5	human	immun
546	46	36.2	419	2	Q972U4	Q972U4	sulfolobus	619	45.5	35.8	196	2	Q9JB10	Q9JB10	human	immun
547	46	36.2	420	2	Q23306	Q23306	arabidopsis	620	45.5	35.8	196	2	Q9JB11	Q9JB11	human	immun
548	46	36.2	433	2	Q944M2	Q944M2	arabidopsis	621	45.5	35.8	196	2	Q9JB12	Q9JB12	human	immun
549	46	36.2	449	2	Q63611	Q63611	bacillus ce	622	45.5	35.8	196	2	Q9JB10	Q9JB10	human	immun
550	46	36.2	449	2	Q732M5	Q732M5	bacillus ce	623	45.5	35.8	196	2	Q9JBK0	Q9JBK0	human	immun
551	46	36.2	449	2	Q819W2	Q819W2	bacillus ce	624	45.5	35.8	197	2	Q6SUT5	Q6SUT5	human	immun
552	46	36.2	449	2	Q81WJ2	Q81WJ2	bacillus an	625	45.5	35.8	197	2	Q6SUT4	Q6SUT4	human	immun
553	46	36.2	449	2	Q6HEX0	Q6HEX0	bacillus th	626	45.5	35.8	197	2	Q6SUT5	Q6SUT5	human	immun
554	46	36.2	460	1	IR44_HUMAN	IR44_HUMAN	Q9HWZ3	627	45.5	35.8	197	2	Q6SUT6	Q6SUT6	human	immun
555	46	36.2	463	2	Q8BSN1	Q8BSN1	Q9BSN1	628	45.5	35.8	197	2	Q9JB11	Q9JB11	human	immun
556	46	36.2	473	2	Q90990	Q90990	gallus gall	629	45.5	35.8	198	2	Q841L4	Q841L4	human	immun
557	46	36.2	474	1	Q63633	Q63633	thermotoga	630	45.5	35.8	198	2	Q9JBC6	Q9JBC6	human	immun
558	46	36.2	475	2	Q63633	Q63633	rattus norv	631	45.5	35.8	199	2	Q70543	Q70543	human	immun
559	46	36.2	477	2	Q68960	Q68960	helicobacte	632	45.5	35.8	199	2	Q7ZN11	Q7ZN11	human	immun
560	46	36.2	477	2	Q25326	Q25326	helicobacte	633	45.5	35.8	199	2	Q9JBD1	Q9JBD1	human	immun
561	46	36.2	477	2	Q92LM7	Q92LM7	helicobacte	634	45.5	35.8	200	1	COAE_BACR	COAE_BACR	human	immun
562	46	36.2	480	2	Q8G4H4	Q8G4H4	blifidobacte	635	45.5	35.8	200	1	COAE_BACR	COAE_BACR	human	immun
563	46	36.2	497	2	Q98680	Q98680	chlamydia p	636	45.5	35.8	200	2	Q6J9C1	Q6J9C1	human	immun
564	46	36.2	497	2	Q9X4G4	Q9X4G4	chlamydia p	637	45.5	35.8	201	2	Q6J9C1	Q6J9C1	human	immun
565	46	36.2	497	2	Q9X4G5	Q9X4G5	chlamydia p	638	45.5	35.8	201	2	Q9JBD8	Q9JBD8	human	immun
566	46	36.2	513	2	Q6T1H2	Q6T1H2	oryza sativ	639	45.5	35.8	202	2	Q9JB18	Q9JB18	human	immun
567	46	36.2	513	2	Q7X8Q5	Q7X8Q5	oryza sativ	640	45.5	35.8	202	2	Q9JB19	Q9JB19	human	immun
568	46	36.2	533	2	Q6KCS3	Q6KCS3	nicotiana p	641	45.5	35.8	202	2	Q9JB11	Q9JB11	human	immun
569	46	36.2	539	1	CH61_BRAJA	CH61_BRAJA	bradyrhizob	642	45.5	35.8	202	2	Q9JB12	Q9JB12	human	immun
570	46	36.2	542	2	Q7VC71	Q7VC71	prochloroco	643	45.5	35.8	203	2	Q6SUN1	Q6SUN1	human	immun
571	46	36.2	543	1	CH60_CHLMU	CH60_CHLMU	chlamydia m	644	45.5	35.8	203	2	Q9JBB6	Q9JBB6	human	immun
572	46	36.2	543	1	CH60_CHLTR	CH60_CHLTR	chlamydia t	645	45.5	35.8	203	2	Q9JBB8	Q9JBB8	human	immun
573	46	36.2	543	1	CH60_CHLPR	CH60_CHLPR	chlamydia c	646	45.5	35.8	203	2	Q9JBB9	Q9JBB9	human	immun
574	46	36.2	544	1	CH60_CHLPP	CH60_CHLPP	chlamydia p	647	45.5	35.8	203	2	Q9JBC5	Q9JBC5	human	immun
575	46	36.2	544	1	CH61_CHLCV	CH61_CHLCV	chlamydia p	648	45.5	35.8	203	2	Q9JBC9	Q9JBC9	human	immun
576	46	36.2	544	2	Q6XNR4	Q6XNR4	chlamydia p	649	45.5	35.8	203	2	Q9JBD2	Q9JBD2	human	immun
577	46	36.2	549	2	Q8MXA4	Q8MXA4	schistosoma	650	45.5	35.8	203	2	Q9JBF3	Q9JBF3	human	immun
578	46	36.2	550	2	Q8DK21	Q8DK21	synecococc	651	45.5	35.8	204	2	Q6QAA6	Q6QAA6	human	immun
579	46	36.2	560	1	CH62_ANASP	CH62_ANASP	anabaena sp	652	45.5	35.8	204	2	Q6QAA6	Q6QAA6	human	immun
580	46	36.2	572	1	DPY4_HUMAN	DPY4_HUMAN	homo saplen	653	45.5	35.8	204	2	Q9JBD7	Q9JBD7	human	immun
581	46	36.2	575	2	Q9Y1U8	Q9Y1U8	toxoplasma	654	45.5	35.8	204	2	Q9JBF5	Q9JBF5	human	immun
582	46	36.2	577	2	Q27723	Q27723	plasmodium	655	45.5	35.8	205	2	Q6QAA8	Q6QAA8	human	immun
583	46	36.2	579	2	Q97480	Q97480	plasmodium	656	45.5	35.8	205	2	Q6RHM3	Q6RHM3	human	immun
584	46	36.2	579	2	Q7RFT8	Q7RFT8	plasmodium	657	45.5	35.8	205	2	Q6RHM4	Q6RHM4	human	immun
585	46	36.2	580	2	Q81JUN9	Q81JUN9	plasmodium	658	45.5	35.8	205	2	Q6RHM4	Q6RHM4	human	immun
586	46	36.2	580	2	Q9VAB9	Q9VAB9	drosophila	659	45.5	35.8	206	1	Q6AL66	Q6AL66	human	immun
587	46	36.2	609	2	Q7SAN8	Q7SAN8	neurospora	660	45.5	35.8	207	2	Q6SUF2	Q6SUF2	human	immun
588	46	36.2	643	1	SYT_PASMTU	SYT_PASMTU	paeteurella	661	45.5	35.8	207	2	Q6SUF4	Q6SUF4	human	immun
589	46	36.2	644	2	Q9FM17	Q9FM17	arabidopsis	662	45.5	35.8	208	2	Q6SUF3	Q6SUF3	human	immun
590	46	36.2	705	2	Q64JVS	Q64JVS	plasmodium	663	45.5	35.8	215	2	Q9YXG5	Q9YXG5	human	immun
591	46	36.2	712	2	Q83P57	Q83P57	shigella fl	664	45.5	35.8	216	2	Q6OR12	Q6OR12	human	immun
592	46	36.2	797	2	Q8A688	Q8A688	bacteroides	665	45.5	35.8	217	2	Q73094	Q73094	human	immun
593	46	36.2	867	2	Q6BP01	Q6BP01	brachydanio	666	45.5	35.8	217	2	Q73095	Q73095	human	immun
594	46	36.2	923	2	Q7ZVM0	Q7ZVM0	brachydanio	667	45.5	35.8	217	2	Q73097	Q73097	human	immun
595	46	36.2	959	2	Q88NM8	Q88NM8	pseudomonas	668	45.5	35.8	217	2	Q73106	Q73106	human	immun
596	46	36.2	963	2	Q91411	Q91411	pseudomonas	669	45.5	35.8	217	2	Q73109	Q73109	human	immun
597	46	36.2	970	2	Q886B0	Q886B0	pseudomonas	670	45.5	35.8	218	2	Q73109	Q73109	human	immun
598	46	36.2	971	2	Q7RBD3	Q7RBD3	plasmodium	671	45.5	35.8	218	2	Q73109	Q73109	human	immun
599	46	36.2	979	2	Q6C909	Q6C909	yarrowia li	672	45.5	35.8	219	2	Q73096	Q73096	human	immun
600	46	36.2	1052	1	MSIP_RAT	MSIP_RAT	rattus norv	673	45.5	35.8	219	2	Q73098	Q73098	human	immun
601	46	36.2	1057	2	Q81I33	Q81I33	plasmodium	674	45.5	35.8	219	2	Q73110	Q73110	human	immun
602	46	36.2	1284	2	Q7WRJ5	Q7WRJ5	anabaena ci	675	45.5	35.8	219	2	Q73111	Q73111	human	immun
603	46	36.2	2787	2	Q961A9	Q961A9	microcyctis	676	45.5	35.8	219	2	Q73112	Q73112	human	immun
604	46	36.2	2795	2	Q8RTG5	Q8RTG5	microcyctis	677	45.5	35.8	219	2	Q73113	Q73113	human	immun
605	46	36.2	2795	2	Q9RNB1	Q9RNB1	microcyctis	678	45.5	35.8	219	2	Q73114	Q73114	human	immun
606	46	36.2	7389	1	BRAL_MOUSE	BRAL_MOUSE	mus muscu	679	45.5	35.8	219	2	Q73115	Q73115	human	immun
607	45.5	35.8	70	1	SLYX_AGRIS	SLYX_AGRIS	agrobacteri	680	45.5	35.8	219	2	Q73116	Q73116	human	immun
608	45.5	35.8	138	2	SLYX_RHIME	SLYX_RHIME	rhizobium m	681	45.5	35.8	219	2	Q73117	Q73117	human	immun
609	45.5	35.8	177	2	Q9YU26	Q9YU26	microcyctis	682	45.5	35.8	219	2	Q73117	Q73117	human	immun
610	45.5	35.8	177	2	Q8AFU9	Q8AFU9	human immun	683	45.5	35.8	219	2	Q73117	Q73117	human	immun
611	45.5	35.8	177	2	Q8AFU9	Q8AFU9	human immun	684	45.5	35.8	220	2	Q73117	Q73117	human	immun
612	45.5	35.8	179	2	Q7ZPM0	Q7ZPM0	human immun	685	45.5	35.8	221	2	Q73117	Q73117	human	immun
613	45.5	35.8	183	2	Q7ZNA1	Q7ZNA1	human immun	686	45.5	35.8	221	2	Q73117	Q73117	human	immun
614	45.5	35.8	183	2	Q9DV55	Q9DV55	human immun	687	45.5	35.8	225	2	Q73083	Q73083	human	immun
615	45.5	35.8	187	2	Q6UDP2	Q6UDP2	human immun	688	45.5	35.8	225	2	Q73084	Q73084	human	immun

689	45.5	35.8	225	2	Q73085	Q73085 human immun	762	45.5	35.8	1434	2	Q9PX54	Q9PX54 cache valle
690	45.5	35.8	225	2	Q73086	Q73086 human immun	763	45.5	35.8	18519	2	Q8ISF6	Q8ISF6 caenorhabdi
691	45.5	35.8	225	2	Q73087	Q73087 human immun	764	45.5	35.8	18534	2	Q8ISF7	Q8ISF7 caenorhabdi
692	45.5	35.8	225	2	Q73088	Q73088 human immun	765	45	35.4	66	2	Q8ER91	Q8ER91 oceanobacil
693	45.5	35.8	244	2	Q61XG6	Q61XG6 human immun	766	45	35.4	91	2	Q8PI21	Q8PI21 streptococc
694	45.5	35.8	244	2	Q61XH1	Q61XH1 human immun	767	45	35.4	91	2	Q8D275	Q8D275 streptococc
695	45.5	35.8	248	2	Q9W1T6	Q9W1T6 human immun	768	45	35.4	91	2	Q8E072	Q8E072 streptococc
696	45.5	35.8	257	2	Q81XY3	Q81XY3 homo sapien	769	45	35.4	91	2	Q8EBE8	Q8EBE8 streptococc
697	45.5	35.8	258	2	Q8ACR6	Q8ACR6 human immun	770	45	35.4	104	2	Q980B8	Q980B8 sulfolobus
698	45.5	35.8	258	2	Q9WDM2	Q9WDM2 human immun	771	45	35.4	106	2	Q37878	Q37878 lactobacill
699	45.5	35.8	267	2	Q6JMB2	Q6JMB2 human immun	772	45	35.4	106	2	Q8K894	Q8K894 streptococc
700	45.5	35.8	284	2	Q741V8	Q741V8 lactobacill	773	45	35.4	118	2	Q67859	Q67859 aquifex aeo
701	45.5	35.8	289	2	Q83CA6	Q83CA6 coxiella bu	774	45	35.4	128	2	Q26723	Q26723 methanobact
702	45.5	35.8	293	2	Q9J4P0	Q9J4P0 human immun	775	45	35.4	136	2	Q842E7	Q842E7 streptococc
703	45.5	35.8	303	2	Q9J4N0	Q9J4N0 human immun	776	45	35.4	154	2	Q8GXV2	Q8GXV2 arabidopsi
704	45.5	35.8	311	2	Q9TNU1	Q9TNU1 human immun	777	45	35.4	164	2	Q7VB06	Q7VB06 prochloroco
705	45.5	35.8	343	2	Q9IU97	Q9IU97 human immun	778	45	35.4	180	2	Q70NS3	Q70NS3 helicobacte
706	45.5	35.8	347	2	Q6CX56	Q6CX56 Kluveromyc	779	45	35.4	180	2	Q70NS4	Q70NS4 helicobacte
707	45.5	35.8	349	2	Q9IU88	Q9IU88 human immun	780	45	35.4	180	2	Q70NS6	Q70NS6 helicobacte
708	45.5	35.8	359	2	P87965	P87965 human immun	781	45	35.4	180	2	Q70NS9	Q70NS9 helicobacte
709	45.5	35.8	392	2	Q9APR4	Q9APR4 uncultured	782	45	35.4	180	2	Q70NT0	Q70NT0 helicobacte
710	45.5	35.8	397	2	O11547	O11547 human immun	783	45	35.4	180	2	Q70NT3	Q70NT3 helicobacte
711	45.5	35.8	405	2	Q66LAS	Q66LAS human immun	784	45	35.4	180	2	Q70NT5	Q70NT5 helicobacte
712	45.5	35.8	410	2	Q8Q2F9	Q8Q2F9 human immun	785	45	35.4	180	2	Q70NT7	Q70NT7 helicobacte
713	45.5	35.8	422	2	Q8ZGX3	Q8ZGX3 yersinia pe	786	45	35.4	180	2	Q70NT9	Q70NT9 helicobacte
714	45.5	35.8	425	1	BIOA_SERMA	BIOA_SERMA	787	45	35.4	180	2	Q70NU0	Q70NU0 helicobacte
715	45.5	35.8	426	2	Q66D66	Q66D66 yersinia ma	788	45	35.4	180	2	Q70NU1	Q70NU1 helicobacte
716	45.5	35.8	426	2	Q8BD003	Q8BD003 yersinia pe	789	45	35.4	180	2	Q70NU2	Q70NU2 helicobacte
717	45.5	35.8	430	2	Q6W332	Q6W332 human immun	790	45	35.4	180	2	Q70NU6	Q70NU6 helicobacte
718	45.5	35.8	438	2	Q90C05	Q90C05 human immun	791	45	35.4	180	2	Q70NU7	Q70NU7 helicobacte
719	45.5	35.8	455	2	Q7ZBH6	Q7ZBH6 simian-huma	792	45	35.4	180	2	Q70NU9	Q70NU9 helicobacte
720	45.5	35.8	455	2	Q7ZB10	Q7ZB10 simian-huma	793	45	35.4	180	2	Q70NV0	Q70NV0 helicobacte
721	45.5	35.8	456	2	Q7ZBJ2	Q7ZBJ2 simian-huma	794	45	35.4	180	2	Q70NV1	Q70NV1 helicobacte
722	45.5	35.8	490	2	Q24430	Q24430 glycine max	795	45	35.4	180	2	Q70NV2	Q70NV2 helicobacte
723	45.5	35.8	490	2	Q84P28	Q84P28 glycine max	796	45	35.4	180	2	Q70NV5	Q70NV5 helicobacte
724	45.5	35.8	496	2	Q93X19	Q93X19 solanum tub	797	45	35.4	180	2	Q70NV7	Q70NV7 helicobacte
725	45.5	35.8	501	2	Q6U9B2	Q6U9B2 bacterioph	798	45	35.4	180	2	Q70NV8	Q70NV8 helicobacte
726	45.5	35.8	582	1	MSBA_VIBPA	MSBA_VIBPA	799	45	35.4	180	2	Q8KV27	Q8KV27 uncultured
727	45.5	35.8	603	2	Q6YV77	Q6YV77 oryza sativ	800	45	35.4	184	2	Q8KV43	Q8KV43 uncultured
728	45.5	35.8	644	2	Q80814	Q80814 arabidopsi	801	45	35.4	184	2	Q8KV69	Q8KV69 uncultured
729	45.5	35.8	759	2	Q99TL6	Q99TL6 staphylococ	802	45	35.4	184	2	Q8KV91	Q8KV91 uncultured
730	45.5	35.8	759	2	Q7A0Q5	Q7A0Q5 staphylococ	803	45	35.4	184	2	Q8KV00	Q8KV00 uncultured
731	45.5	35.8	759	2	Q7A586	Q7A586 staphylococ	804	45	35.4	184	2	Q6BH37	Q6BH37 lachnospira
732	45.5	35.8	759	2	Q6G8T2	Q6G8T2 staphylococ	805	45	35.4	184	2	Q6H858	Q6H858 clostridium
733	45.5	35.8	759	2	Q6GG67	Q6GG67 staphylococ	806	45	35.4	185	2	Q8KPC6	Q8KPC6 flexispira
734	45.5	35.8	795	2	Q99BY6	Q99BY6 human immun	807	45	35.4	185	2	Q8IG33	Q8IG33 caenorhabdi
735	45.5	35.8	799	2	Q7ZGR4	Q7ZGR4 human immun	808	45	35.4	186	2	Q8KVN6	Q8KVN6 uncultured
736	45.5	35.8	833	2	Q9QKH9	Q9QKH9 human immun	809	45	35.4	186	2	Q6BH18	Q6BH18 prevotella
737	45.5	35.8	833	2	Q9QKI3	Q9QKI3 human immun	810	45	35.4	186	2	Q6GJ48	Q6GJ48 staphylococ
738	45.5	35.8	841	2	Q9DVL7	Q9DVL7 human immun	811	45	35.4	186	2	Q7X3Q5	Q7X3Q5 staphylococ
739	45.5	35.8	849	2	Q6H1S7	Q6H1S7 human immun	812	45	35.4	190	2	Q6DKB7	Q6DKB7 xenopus lae
740	45.5	35.8	854	2	Q6S7Z0	Q6S7Z0 human immun	813	45	35.4	194	2	HAML_CLOPE	HAML_CLOPE
741	45.5	35.8	854	2	Q9W8E4	Q9W8E4 human immun	814	45	35.4	204	1	Q294E5	Q294E5 archaeoglob
742	45.5	35.8	855	2	Q8UL67	Q8UL67 human immun	815	45	35.4	207	2	Q6XLM7	Q6XLM7 brassica ra
743	45.5	35.8	859	2	Q902S4	Q902S4 human immun	816	45	35.4	215	2	Q6XLM5	Q6XLM5 brassica ol
744	45.5	35.8	859	2	Q6JNW4	Q6JNW4 human immun	817	45	35.4	216	2	Q6XLM8	Q6XLM8 brassica ra
745	45.5	35.8	861	2	Q6JNP2	Q6JNP2 human immun	818	45	35.4	226	1	VMEL_PEDV7	VMEL_PEDV7
746	45.5	35.8	861	2	Q80367	Q80367 human immun	819	45	35.4	226	1	VMEL_PEDVB	VMEL_PEDVB
747	45.5	35.8	863	2	Q6BCE8	Q6BCE8 human immun	820	45	35.4	226	1	Q91AU9	Q91AU9 porcine epi
748	45.5	35.8	867	2	Q8UB10	Q8UB10 human immun	821	45	35.4	226	2	Q692M0	Q692M0 porcine epi
749	45.5	35.8	868	2	Q8JC35	Q8JC35 human immun	822	45	35.4	226	2	Q98F05	Q98F05 thizobium l
750	45.5	35.8	868	2	Q6BC31	Q6BC31 human immun	823	45	35.4	230	2	Q7SYQ2	Q7SYQ2 xenopus lae
751	45.5	35.8	897	2	Q997B5	Q997B5 cache valle	824	45	35.4	233	2	Q662V2	Q662V2 borellia ga
752	45.5	35.8	897	2	Q997B7	Q997B7 cache valle	825	45	35.4	238	2	Q8ZU62	Q8ZU62 pyrobaculum
753	45.5	35.8	897	2	Q997B8	Q997B8 cache valle	826	45	35.4	258	2	Q88XH7	Q88XH7 lactobacill
754	45.5	35.8	897	2	Q91ZJ9	Q91ZJ9 cache valle	827	45	35.4	260	1	DCX_HUMAN	DCX_HUMAN
755	45.5	35.8	897	2	Q91ZK0	Q91ZK0 cache valle	828	45	35.4	281	2	Q65E39	Q65E39 bacillus li
756	45.5	35.8	897	2	Q91ZK1	Q91ZK1 cache valle	829	45	35.4	292	2	Q48432	Q48432 lactobacill
757	45.5	35.8	897	2	Q916I0	Q916I0 cache valle	830	45	35.4	294	2	Q48433	Q48433 lactobacill
758	45.5	35.8	1058	2	Q9FLR5	Q9FLR5 arabidopsi	831	45	35.4	296	2	Q73JN0	Q73JN0 treponema d
759	45.5	35.8	1434	2	Q9J6L5	Q9J6L5 cache valle	832	45	35.4	303	2	Q895V5	Q895V5 clostridium
760	45.5	35.8	1434	2	Q9J6L6	Q9J6L6 cache valle	833	45	35.4	307	2	Q9M2H8	Q9M2H8 arabidopsi
761	45.5	35.8	1434	2	Q9J6L7	Q9J6L7 cache valle	834	45	35.4	307	2		

835	45	35.4	321	2	Q8JB39	Q8JB39 human immun	908	45	35.4	877	1	SYA_WOLPM	P61709 wolbachia p
836	45	35.4	330	2	Q7P275	Q7P275 fusobacteri	909	45	35.4	877	2	Q7Z627	Q7Z627 homo sapien
837	45	35.4	334	2	Q7MNH9	Q7MNH9 bordetella	910	45	35.4	878	2	Q80W39	Q80W39 mus musculu
838	45	35.4	345	2	Q9A0Y0	Q9A0Y0 streptococc	911	45	35.4	894	2	Q9BMD2	Q9BMD2 homo sapien
839	45	35.4	357	2	Q89ZZ9	Q89ZZ9 bacteroides	912	45	35.4	896	2	Q8XZ06	Q8XZ06 ralsconia s
840	45	35.4	368	2	Q754L5	Q754L5 aebdya goss	913	45	35.4	897	2	Q8YWP3	Q8YWP3 anabaena sp
841	45	35.4	376	1	XYNA_BACOV	P49942 bacteroides	914	45	35.4	902	2	Q7PX97	Q7PX97 anophelies g
842	45	35.4	377	2	Q9FNC6	Q9FNC6 arabisolapis	915	45	35.4	930	2	Q93IL7	Q93IL7 colipochelrix
843	45	35.4	386	2	Q8EM80	Q8EM80 mycoplasma	916	45	35.4	974	2	Q6PG27	Q6PG27 homo sapien
844	45	35.4	387	2	Q6SEF78	Q6SEF78 bacillus li	917	45	35.4	1025	2	Q7Z7W5	Q7Z7W5 coprinus ci
845	45	35.4	399	2	Q8LG40	Q8LG40 arabisolapis	918	45	35.4	1052	1	MSIP_CRIGR	Q9Z2A8 citreulius
846	45	35.4	399	2	Q67XY1	Q67XY1 arabisolapis	919	45	35.4	1052	1	MSIP_HUMAN	Q14703 homo sapien
847	45	35.4	400	2	Q8XW53	Q8XW53 ralsconia s	920	45	35.4	1052	1	MSIP_MOUSE	Q9WCZ2 mus musculu
848	45	35.4	401	1	APCM_THEMEA	Q9X295 thermotoga	921	45	35.4	1052	2	Q6PG67	Q6PG67 mus musculu
849	45	35.4	402	2	Q90IM7	Q90IM7 human immun	922	45	35.4	1055	2	Q80U80	Q80U80 mus musculu
850	45	35.4	423	2	Q6XS08	Q6XS08 human immun	923	45	35.4	1060	2	Q9P789	Q9P789 schizosacch
851	45	35.4	429	2	Q8DX40	Q8DX40 streptococc	924	45	35.4	1060	2	Q9P789	Q9P789 schizosacch
852	45	35.4	444	2	Q73FT9	Q73FT9 wolbachia p	925	45	35.4	1374	2	Q6F1H8	Q6F1H8 mesoplasma
853	45	35.4	451	2	Q7NRE9	Q7NRE9 chromobacte	926	45	35.4	1493	2	Q68D66	Q68D66 homo sapien
854	45	35.4	459	2	Q9KLN6	Q9KLN6 vibrio chol	927	45	35.4	1549	2	SMC4_CAEEL	Q90060 caenorhadi
855	45	35.4	460	2	Q76H22	Q76H22 bartonella	928	45	35.4	1723	2	Q9Y4F4	Q9Y4F4 homo sapien
856	45	35.4	466	2	Q6B8C6	Q6B8C6 drosophila	929	45	35.4	1752	2	Q6B7X2	Q6B7X2 debaryomyce
857	45	35.4	468	2	Q9JWX2	Q9JWX2 neisseria m	930	45	35.4	1946	2	Q6B072	Q6B072 apis mellif
858	45	35.4	470	2	Q93707	Q93707 sulfolobus	931	45	35.4	2471	2	Q6CQ08	Q6CQ08 kluyveromyc
859	45	35.4	473	1	LCBI_CRIGR	Q54695 citreulius	932	45	35.4	2572	2	Q7PRV6	Q7PRV6 anophelies g
860	45	35.4	473	1	LCBI_MOUSE	Q35704 mus musculu	933	45	35.4	2811	2	Q7Q9V2	Q7Q9V2 anophelies g
861	45	35.4	473	2	Q8BH11	Q8BH11 m mus musculu	934	45	35.4	3432	2	Q87WM7	Q87WM7 pseudomonas
862	45	35.4	473	2	Q8C295	Q8C295 mus musculu	935	45	35.4	5085	2	Q7OLM4	Q7OLM4 bacillus br
863	45	35.4	483	2	Q6V9I8	Q6V9I8 trypanosoma	936	45	35.4	7180	1	RIAB_CVMJH	RIAB_CVMJH
864	45	35.4	483	2	Q94KU1	Q94KU1 spinacia ol	937	45	35.4	7756	2	Q7OLM5	Q7OLM5 m replicase
865	45	35.4	494	2	Q9M072	Q9M072 drosophila	938	45	35.0	84	2	Q40374	Q40374 human immun
866	45	35.4	495	1	1A1C_ARATH	Q94790 arabidopsis	939	45	35.0	84	2	Q40376	Q40376 human immun
867	45	35.4	514	2	Q964E9	Q964E9 ipomoea bat	940	45	35.0	84	2	Q40380	Q40380 human immun
868	45	35.4	516	2	Q81DB5	Q81DB5 bacillus ce	941	45	35.0	84	2	Q40382	Q40382 human immun
869	45	35.4	516	2	Q9CK28	Q9CK28 pasteurella	942	45	35.0	84	2	Q40384	Q40384 human immun
870	45	35.4	519	2	Q6PA21	Q6PA21 xenopus lae	943	45	35.0	84	2	Q40386	Q40386 human immun
871	45	35.4	528	2	Q6F339	Q6F339 oryza sativ	944	45	35.0	84	2	Q40389	Q40389 human immun
872	45	35.4	535	2	Q9MBL8	Q9MBL8 corynebacte	945	45	35.0	84	2	Q40391	Q40391 human immun
873	45	35.4	538	2	Q6KE85	Q6KE85 corynebacte	946	45	35.0	84	2	Q40393	Q40393 human immun
874	45	35.4	539	1	CH60_FUSNN	Q85EX7 fusobacteri	947	45	35.0	84	2	Q40395	Q40395 human immun
875	45	35.4	539	1	CH60_FUSNP	Q8G100 fusobacteri	948	45	35.0	84	2	Q40401	Q40401 human immun
876	45	35.4	543	1	CH62_SYNEL	Q57002 synechococc	949	45	35.0	84	2	Q40402	Q40402 human immun
877	45	35.4	545	1	CH60_HELHP	Q7X317 helicobacte	950	45	35.0	84	2	Q40414	Q40414 human immun
878	45	35.4	545	1	CH60_MYCPE	Q8CXQ7 mycoplasma	951	45	35.0	84	2	Q40423	Q40423 human immun
879	45	35.4	546	1	CH60_HELBP	Q9N5F0 helicobacte	952	45	35.0	84	2	Q40424	Q40424 human immun
880	45	35.4	546	1	CH60_HELFP	P42383 helicobacte	953	45	35.0	84	2	Q40425	Q40425 human immun
881	45	35.4	546	1	Q8RNU2	Q8RNU2 helicobacte	954	45	35.0	84	2	Q40428	Q40428 human immun
882	45	35.4	547	1	CH61_RHOPA	Q9J1D1 drosophila	955	45	35.0	84	2	Q40430	Q40430 human immun
883	45	35.4	548	2	Q9VJDI	P60364 rhodospheudo	956	45	35.0	84	2	Q40433	Q40433 human immun
884	45	35.4	560	1	DTXN_CORBE	P00589 corynebacte	957	45	35.0	84	2	Q40435	Q40435 human immun
885	45	35.4	560	1	DTXN_COROM	P00587 corynebacte	958	45	35.0	84	2	Q40441	Q40441 human immun
886	45	35.4	560	2	Q6YIX8	Q6YIX8 corynebacte	959	45	35.0	84	2	Q40442	Q40442 human immun
887	45	35.4	560	2	Q6YIX9	Q6YIX9 corynebacte	960	45	35.0	93	2	Q91293	Q91293 human immun
888	45	35.4	560	2	Q6NKL5	Q6NKL5 corynebacte	961	45	35.0	146	2	Q9UWV7	Q9UWV7 sulfolobus
889	45	35.4	567	1	DTX_CORBE	P00588 corynebacte	962	45	35.0	149	1	LRBP_BACSU	P96653 bacillus su
890	45	35.4	582	2	Q8BU59	Q8BU59 mus musculu	963	45	35.0	157	2	Q70RE3	Q70RE3 human immun
891	45	35.4	593	2	Q8A796	Q8A796 bacteroides	964	45	35.0	158	2	Q9MWV3	Q9MWV3 human immun
892	45	35.4	595	2	Q89BH2	Q89BH2 bradyrhizob	965	45	35.0	159	2	Q9JER4	Q9JER4 human immun
893	45	35.4	630	2	Q973J8	Q973J8 sulfolobus	966	45	35.0	159	2	Q9JER4	Q9JER4 human immun
894	45	35.4	636	2	Q7L4T5	Q7L4T5 homo sapien	967	45	35.0	168	2	Q7OR09	Q7OR09 human immun
895	45	35.4	649	2	Q7RTS4	Q7RTS4 plasmodium	968	45	35.0	169	2	Q91WR3	Q91WR3 human immun
896	45	35.4	652	2	Q7XRMO	Q7XRMO oryza sativ	969	45	35.0	171	2	Q7OR20	Q7OR20 human immun
897	45	35.4	663	2	Q8DSM8	Q8DSM8 streptococc	970	45	35.0	175	2	Q61429	Q61429 human immun
898	45	35.4	663	2	Q8BVD6	Q8BVD6 mus musculu	971	45	35.0	175	2	Q6U430	Q6U430 human immun
899	45	35.4	674	2	Q91Y31	Q91Y31 mus musculu	972	45	35.0	175	2	Q6U431	Q6U431 human immun
900	45	35.4	731	2	Q7RH47	Q7RH47 plasmodium	973	45	35.0	175	2	Q6U432	Q6U432 human immun
901	45	35.4	755	2	Q9M1Z2	Q9M1Z2 arabidopsis	974	45	35.0	175	2	Q6U433	Q6U433 human immun
902	45	35.4	778	2	Q8B2_HUMAN	Q15057 homo sapien	975	45	35.0	177	2	Q892D2	Q892D2 clostridium
903	45	35.4	778	2	Q6IVG4	Q6IVG4 oryctolagus	976	45	35.0	177	2	Q698V0	Q698V0 human immun
904	45	35.4	795	2	Q9NEX4	Q9NEX4 caenorhadi	977	45	35.0	178	2	Q8UPR4	Q8UPR4 human immun
905	45	35.4	799	2	Q7Z3K9	Q7Z3K9 homo sapien	978	45	35.0	178	2	Q8UPR6	Q8UPR6 human immun
906	45	35.4	865	2	Q6MCD7	Q6MCD7 paracanthamyd	979	45	35.0	178	2	Q8UPR8	Q8UPR8 human immun
907	45	35.4	872	1	S3B2_HUMAN	Q13435 homo sapien	980	45	35.0	178	2	Q8UPR1	Q8UPR1 human immun

```
981 44.5 35.0 179 2 090cm9 human immun
982 44.5 35.0 186 2 090rs9 human immun
983 44.5 35.0 188 2 0929s3 human immun
984 44.5 35.0 188 2 092dv3 human immun
985 44.5 35.0 194 2 0922s4 human immun
986 44.5 35.0 194 2 092qm0 human immun
987 44.5 35.0 194 2 09dv51 human immun
988 44.5 35.0 195 2 0681e4 human immun
989 44.5 35.0 195 2 06v8b3 human immun
990 44.5 35.0 195 2 09dvh9 human immun
991 44.5 35.0 196 2 07skv3 human immun
992 44.5 35.0 196 2 09jhb9 human immun
993 44.5 35.0 196 2 09jbi3 human immun
994 44.5 35.0 196 2 09jbi4 human immun
995 44.5 35.0 196 2 09jbi6 human immun
996 44.5 35.0 196 2 09jbi2 human immun
997 44.5 35.0 196 2 09jbi5 human immun
998 44.5 35.0 197 2 06sut4 human immun
999 44.5 35.0 198 2 08qaa4 human immun
1000 44.5 35.0 198 2 06ey26 human immun
```

## ALIGNMENTS

## RESULT 1

```
06SR10 PRELIMINARY; PRT; 143 AA.
ID 06SR10
AC 06SR10;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-PH2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
CX NCBI_TaxID=264388;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451891; AAS44759.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;
```

```
Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 MADNGITVEELKQLLEQNLV 25
DB 1 MADNGITVEELKQLLEQNLV 22
```

## RESULT 2

```
06SR14 PRELIMINARY; PRT; 143 AA.
ID 06SR14
AC 06SR14;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-PH1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
CX NCBI_TaxID=264387;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
```

```
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451890; AAS44755.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;
```

```
Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 MADNGITVEELKQLLEQNLV 25
DB 1 MADNGITVEELKQLLEQNLV 22
```

## RESULT 3

```
06SR18 PRELIMINARY; PRT; 143 AA.
ID 06SR18
AC 06SR18;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
CX NCBI_TaxID=264386;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451889; AAS44751.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;
```

```
Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 MADNGITVEELKQLLEQNLV 25
DB 1 MADNGITVEELKQLLEQNLV 22
```

## RESULT 4

```
06SRJ2 PRELIMINARY; PRT; 143 AA.
ID 06SRJ2
AC 06SRJ2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-YM3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
CX NCBI_TaxID=264385;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451888; AAS44747.1; -
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON_TER 143
```

SEQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTIVEBELKQLEQMNLY 25  
Db 1 MADNGTIVEBELKQLEQMNLY 22

## RESULT 5

Q6SRJ6 PRELIMINARY; PRT; 143 AA.

AC Q6SRJ6  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-YM2.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
CX NCBI\_TaxID=264384;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451887; AAS44743.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTIVEBELKQLEQMNLY 25  
Db 1 MADNGTIVEBELKQLEQMNLY 22

## RESULT 6

Q6SRK4 PRELIMINARY; PRT; 143 AA.

AC Q6SRK4  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-GD5.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
CX NCBI\_TaxID=264382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451885; AAS44735.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTIVEBELKQLEQMNLY 25

Db 1 MADNGTIVEBELKQLEQMNLY 22

## RESULT 7

Q6SRK8 PRELIMINARY; PRT; 143 AA.

AC Q6SRK8  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-GD4.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
CX NCBI\_TaxID=264381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451884; AAS44731.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTIVEBELKQLEQMNLY 25  
Db 1 MADNGTIVEBELKQLEQMNLY 22

## RESULT 8

Q6SRL2 PRELIMINARY; PRT; 143 AA.

AC Q6SRL2  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-GD3.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
CX NCBI\_TaxID=264380;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451883; AAS44727.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MADNGTIVEBELKQLEQMNLY 25  
Db 1 MADNGTIVEBELKQLEQMNLY 22

## RESULT 9

Q6SRL6 PRELIMINARY; PRT; 143 AA.

```
AC O6SRM6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264379;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451882; AAS44723.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 10
O6SRM0
ID O6SRM0; PRELIMINARY; PRT; 143 AA.
AC O6SRM0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-GD1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264378;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451881; AAS44719.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 11
O6SRM4
ID O6SRM4; PRELIMINARY; PRT; 143 AA.
AC O6SRM4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-KC3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
```

```
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264377;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451880; AAS44715.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 12
O6SRM8
ID O6SRM8; PRELIMINARY; PRT; 143 AA.
AC O6SRM8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-KC1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264376;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY451879; AAS44711.1; -.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AE971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNMNV 25
DB 1 MADNGITVEELKQLEQNMNV 22

RESULT 13
O6SRN2
ID O6SRN2; PRELIMINARY; PRT; 143 AA.
AC O6SRN2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane glycoprotein M (Fragment).
OS SARS coronavirus TW-JC2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; SARS coronavirus TW.
OX NCBI_TaxID=264375;
RN [1]
RP SEQUENCE FROM N.A.
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,
RA Yang J.-Y., Chen H.-Y., Chen Y.-M.Arthur.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
```



DR EMBL; AY451878; AAS44707.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M.1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEQMNLY 25  
DB 1 MADNGTIVBELKQLEQMNLY 22

## RESULT 14

Q6SRN6 PRELIMINARY; PRT; 143 AA.  
AC Q6SRN6;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-Hp2.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_TaxID=264372;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M., Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451877; AAS44703.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M.1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEQMNLY 25  
DB 1 MADNGTIVBELKQLEQMNLY 22

## RESULT 15

Q6SRP0 PRELIMINARY; PRT; 143 AA.  
AC Q6SRP0;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-Hp2.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_TaxID=264372;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M., Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451876; AAS44699.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M.1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEQMNLY 25  
DB 1 MADNGTIVBELKQLEQMNLY 22

## RESULT 16

Q6SRP4 PRELIMINARY; PRT; 143 AA.  
AC Q6SRP4;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-Hp2.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_TaxID=264372;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M., Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451875; AAS44695.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M.1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEQMNLY 25  
DB 1 MADNGTIVBELKQLEQMNLY 22

## RESULT 17

Q6SRP8 PRELIMINARY; PRT; 143 AA.  
AC Q6SRP8;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-Hp1.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_TaxID=264371;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M., Arthur.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451874; AAS44691.1; -  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M.1.  
FT NON TER 143  
SQ SEQUENCE 143 AA; 16423 MW; 1CAB09A94AB971ED CRC64;

Query Match 88.2%; Score 112; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEQMNLY 25  
DB 1 MADNGTIVBELKQLEQMNLY 22

RESULT 18  
ID VME1\_CVHSA STANDARD; PRT: 221 AA.  
AC P59596; Q65885; Q7608; Q7661; Q7685; Q7680; Q7683; Q7726;  
AC Q7776; Q7786; Q7786; Q7786;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).  
GN Name=M;  
OS Human coronavirus (strain SARS) (HCoV-SARS) (SARS-CoV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronaviruses.  
OX NCBI\_TaxID=227859;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Urbani;  
RX MEDLINE=22660724; PubMed=12730500; DOI=10.1126/science.1085952;  
RA Roca P.A., Oberste M.S., Monroe S.S., Nix W.A., Campagnoli R.,  
RA Iacono J.P., Penaranda S., Bankamp B., Maher K., Chen M.-H.,  
RA Tong S., Tamn A., Lowe L., Frace M., Derisi J.L., Chen Q., Wang D.,  
RA Ericman D.D., Peret T.C.T., Burns C., Kaszdek T.G., Rollin P.E.,  
RA Sanchez A., Liffick S., Hollway B., Limor J., McCaustland K.,  
RA Olsen-Rasmussen M., Fouchier R., Guenther S., Osterhaus A.D.M.E.,  
RA Drost C., Pallansch M.A., Anderson L.J., Bellini W.J.;  
RT "Characterization of a novel coronavirus associated with severe acute  
RT respiratory syndrome.";  
RL Science 300:1394-1399(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Tor2;  
RX MEDLINE=22660725; PubMed=12730501; DOI=10.1126/science.1085953;  
RA Maira M.A., Jones S.J.M., Astell C.R., Holt R.A., Brooks-Wilson A.,  
RA Butlerfield Y.S.N., Khattar J., Asano J.K., Barber S.A., Chan S.Y.,  
RA Cloutier A., Coughlin S.M., Freeman D., Glin N., Griffith O.L.,  
RA Leach S.R., Mayo M., McDonald H., Montgomery S.B., Pandolfi P.K.,  
RA Perreault A.S., Robertson A.G., Schein J.E., Siddiqui A., Smailus D.E.,  
RA Stott J.M., Yang G.S., Plummer F., Andonov A., Artsob H., Bastien N.,  
RA Bernard K., Booth T.F., Bowness D., Czud M., Drebot M., Fernando L.,  
RA Flick R., Garbutt M., Gray M., Grolla A., Jones S., Feldman H.,  
RA Meyers A., Kabani A., Li Y., Normand S., Stroher U., Tipples G.A.,  
RA Tyler S., Vogrig R., Ward D., Watson B., Brunham R.C., Krajen G.,  
RA Petric M., Skowronski D.M., Upton C., Roper R.L.;  
RT "The genome sequence of the SARS-associated coronavirus.";  
RL Science 300:1399-1404(2003).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate CUHK-Su10, and Isolate CUHK-W1;  
RX MEDLINE=22737955; PubMed=12853594; DOI=10.1056/NEJM200307103490216;  
RA Tsui S.K.W., Chin S.-S.C., Lo Y.M.D.;  
RT "Coronavirus genomic-sequence variations and the epidemiology of the  
RT severe acute respiratory syndrome.";  
RL N. Engl. J. Med. 349:187-188(2003).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate GZ50, and Isolate HKU-36871;  
RX MEDLINE=22913660; PubMed=12958366; DOI=10.1126/science.1087139;  
RA Guan Y., Zheng B.J., He Y.Q., Liu X.L., Zhuang Z.X., Cheng C.L.,  
RA Luo S.W., Li P.H., Zhang L.J., Guan Y.J., Butt K.M., Wong K.L.,  
RA Chan K.W., Lam W., Shortridge K.F., Yuen K.Y., Peiris J.S.M.,  
RA Poon L.L.M.;  
RT "Isolation and characterization of viruses related to the SARS  
RT coronavirus from animals in southern China.";  
RL Science 302:276-278(2003).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate HKU-39849;  
RX MEDLINE=22758472; PubMed=12876307;  
RA Zeng F.Y., Chan C.W., Chan M.N., Chen J.D., Chow K.Y.C., Hon C.C.C.,  
RA Hui R.K.H., Li J., Li V.Y., Wang C.Y., Wang P.Y., Guan Y., Zheng B.,  
RA Poon L.L.M., Chan K.H., Yuen K.Y., Peiris J.S.M., Leung F.C.;

RT "The complete genome sequence of severe acute respiratory syndrome  
RT coronavirus strain HKU-39849 (HK-39).";  
RL Exp. Biol. Med. 228:866-873(2003).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Sin2500, Isolate Sin2677, Isolate Sin2679,  
RC Isolate Sin2748, and Isolate Sin2774;  
RX MEDLINE=22660704; PubMed=12781537; DOI=10.1016/S0140-6736(03)13414-9;  
RA Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,  
RA Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,  
RA Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,  
RA Liu E.T.;  
RT "Comparative full-length genome sequence analysis of 14 SARS  
RT coronavirus isolates and common mutations associated with putative  
RT origins of infection.";  
RL Lancet 361:1779-1785(2003).  
RN [7]  
RP ERRATUM.  
RX PubMed=12781581;  
RA Ruan Y., Wei C.L., Ling A.E., Vega V.B., Thoreau H., Se Thoe S.Y.,  
RA Chia J.-M., Ng P., Chiu K.P., Lim L., Zhang T., Chan K.P., Oon L.E.L.,  
RA Ng M.L., Leo S.Y., Ng L.F.P., Ren E.C., Stanton L.W., Long P.M.,  
RA Liu E.T.;  
RT Lancet 361:1832-1832(2003).  
RN [8]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate BJ01, Isolate BJ02, Isolate BJ03, Isolate BJ04, and  
RC Isolate GD01;  
RA Qin E., Zhu Q., Yu M., Fan B., Chang G., Si B., Yang B., Peng W.,  
RA Jiang T., Liu B., Deng Y., Liu H., Zhang Y., Wang C., Li Y., Gan Y.,  
RA Li X., Lu F., Tan G., Yang R., Cao W.S., Wang J., Chen W., Cong L.,  
RA Deng Y., Dong W., Han Y., Hu W., Lei W., Li C., Li G., Li H.,  
RA Li S., Li S., Li W., Lin W., Liu J., Liu Z., Lu H.,  
RA Qi Q., Sun Y., Tang L., Tong Z., Wang J., Wang X., Wu Q., Xi Y.,  
RA Xu Z., Yang L., Ye C., Ye J., Zhang B., Zhang F., Zhang J., Zhang X.,  
RA Zhou J., Yang H.;  
RT Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate TW1;  
RA Yen S.-H., Kao C.-L., Tsai C.-Y., Liu C.-J., Chen D.-S., Chen P.-J.;  
RT "The complete genome of SARS coronavirus clone TW1.";  
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate FRA;  
RA Rickmann M., Becker S., Klenk H.-D., Doerr H.W., Stadler K.,  
RA Censini S., Guidotti S., Maignani V., Scarselli M., Mora M.,  
RA Donati C., Han J., Song H.C., Abriani S., Covacci A., Rappelli R.;  
RT "SARS virus is a close relative of type II coronaviruses.";  
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Frankfurt 1;  
RA Thiel V., Hertzog T., Putics A., Ivanov K.A., Schelle B., Bayer S.,  
RA Scheiner B., Weisbach B., Ziebur J.;  
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Shanghai QX1;  
RA Yuan Z., Zhang X., Hu Y., Lan S., Wang H., Zhou Z., Wen Y.;  
RT "Analysis of SARS coronavirus genome in Shanghai isolates.";  
RL Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate ZJ01;  
RA Cong L.-M., Ding G.-Q., Lu Y.-Y., Yan J.-Q., Weng J.-Q., Cheng S.-Y.,  
RA Zhang Y.-J., Mei L.-L., Wang Z.-G., Hu N., Wo J., Yao J., Zhu H.-P.,  
RA Lu Q.-Y., Li M.-H., Gong L.-M., Shi W.;  
RL Submitted (Jun-2003) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate TWC;

RA Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee S.-C., Lin Y.-C.,  
RA Hsu C.-K., Chen H.-Y., Chang J.-G., Chen P.-J., Su I.-J.,  
RT "Genomic sequence of SARS isolate from the first fatal case in  
RT Taiwan."  
RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.  
RN [15]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate Taiwan TC1, Isolate Taiwan TC2, and Isolate Taiwan TC3;  
RA Chang J.-G.C., Lin T.-H., Chen C.-M., Lin C.-S., Chan W.-L.,  
RA Shih W.-C.;  
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.  
RN [16]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate TW1, Isolate TW2, Isolate TW3, Isolate TW4, and  
RC Isolate TW5;  
RA Shu H.-Y., Wu K.-M., Tsai S.-F.;  
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.  
RN [17]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate HSR 1;  
RA Canducci F., Clementi M., Poli G., Vicenzi E.;  
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.  
RN [18]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate TW2, and Isolate TW3;  
RA Yang J.-Y., Lin J.-H., Chiu S.-C., Wang S.-F., Lee H.-C., Lin Y.-C.,  
RA Yao C.-W., Chiu T.-S., Lu J.-J., Chen A., Hsu C.-K., Chen H.-Y.,  
RA Chen P.-J., Su I.-J.,  
RL Submitted (AUG-2003) to the EMBL/Genbank/DBJ databases.  
RN [19]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Isolate AS;  
RA Balotta C., Corvase S., Violin M., Galli M., Moroni M.,  
RA Vigeant G.M., Ruan Y.-J., Salemi M.,  
RL Submitted (OCT-2003) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: Component of the viral envelope that plays a central  
CC role in virus morphogenesis and assembly via its interactions with  
CC other viral proteins (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -1- SIMILARITY: Belongs to the coronavirus M protein family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AY278741; AAP13444.1; -;  
DR EMBL; AY274119; AAP1041.1; -;  
DR EMBL; AY278554; AAP13571.1; -;  
DR EMBL; AY282752; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; AY304492; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; AY304495; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; AY278491; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; AY283794; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; AY283795; -; NOT\_ANNOTATED\_CDS.  
Query Match 88.2%; Score 112; DB 1; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2,4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE M protein.  
OS SARS coronavirus GD322.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=291613;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hu Z., Zhao W., Yan H.;  
RT "The analyses on M genes' variation rules of SARS-CoV and their  
RT influence upon the possible B cell epitopes of M genes."  
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AY702026; AAU07933.1; -;  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;  
Query Match 88.2%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2,4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 25-OCT-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein M.  
OS SARS coronavirus NL63-2004.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=273522;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li J., Wei W., Xiao W., Wang M., Wang J., Zhao J., Pei Y.,  
RA Chen Y.;  
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AY595412; AAT52332.1; -;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR002574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;  
Query Match 88.2%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2,4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 25-OCT-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Membrane protein.  
OS SARS coronavirus Sin03-11.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=255729;

```

RN [1]
  SEQUENCE FROM N.A.
RC STRAIN=Sinol-11;
RA Jin W.W., Feng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
  Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.
RL EMBL; AY485278; AAR23256.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match
  Best Local Similarity 100.0%; Score 112; DB 2; Length 221;
  Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLEQNMNV 25
DB 1 MADNGTITVEELKQLEQNMNV 22

RESULT 22
Q6JH42
ID Q6JH42 PRELIMINARY; PRT; 221 AA.
AC Q6JH42;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane protein.
OS SARS coronavirus Sinol-11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirinae.
OX NCBI_TaxID=255730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sinol-11;
RA Jin W.W., Feng J.D., Du Z.L., Hu L.X., Liu Y.X., Liu Y.F., Zhang X.M.,
  Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.
RL EMBL; AY485277; AAR23248.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match
  Best Local Similarity 100.0%; Score 112; DB 2; Length 221;
  Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLEQNMNV 25
DB 1 MADNGTITVEELKQLEQNMNV 22

RESULT 23
Q6R7Y2
ID Q6R7Y2 PRELIMINARY; PRT; 221 AA.
AC Q6R7Y2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane protein M.
OS SARS coronavirus NS-1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirinae.
OX NCBI_TaxID=260743;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS-1;
RA Zhang H., Wei C., Ding R., Wang W., Li W., Wang J., Tao W., Yu X.,
  Guo H., Chen J., Wei W., Li J., Zhang Y., Wang X., Sun Y., Jiao J.,
  Wang Y., Zhou C.;
  Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.

```

```

DR EMBL; AY508724; AAR91590.1;
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match
  Best Local Similarity 100.0%; Score 112; DB 2; Length 221;
  Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLEQNMNV 25
DB 1 MADNGTITVEELKQLEQNMNV 22

RESULT 24
Q6RCW1
ID Q6RCW1 PRELIMINARY; PRT; 221 AA.
AC Q6RCW1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW9.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirinae.
OX NCBI_TaxID=258972;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
  Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
  "Characterization of severe acute respiratory syndrome coronavirus
  genomes in Taiwan: molecular epidemiology and genome evolution.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
RL EMBL; AY502932; AAR87604.1;
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
RW Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match
  Best Local Similarity 100.0%; Score 112; DB 2; Length 221;
  Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLEQNMNV 25
DB 1 MADNGTITVEELKQLEQNMNV 22

RESULT 25
Q6RCX2
ID Q6RCX2 PRELIMINARY; PRT; 221 AA.
AC Q6RCX2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW8.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirinae.
OX NCBI_TaxID=258971;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
  Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
  "Characterization of severe acute respiratory syndrome coronavirus
  genomes in Taiwan: molecular epidemiology and genome evolution.";
RT

```

```

RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502931; AAR87593.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478B CRC64;

Query March      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGITVEELKQLLEQNMIV 25
Db 1 MADNGITVEELKQLLEQNMIV 22

RESULT 26
Q6RCY3 PRELIMINARY; PRT; 221 AA.
AC Q6RCY3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW7.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_Taxid=258970;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502930; AAR87582.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR Envelope protein.
KW SEQUENCE 221 AA; 25016 MW; 6658652E2927478B CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGITVEELKQLLEQNMIV 25
Db 1 MADNGITVEELKQLLEQNMIV 22

RESULT 27
Q6RCZ4 PRELIMINARY; PRT; 221 AA.
AC Q6RCZ4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW6.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_Taxid=258969;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,

```

```

RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502929; AAR87571.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR Envelope protein.
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478B CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGITVEELKQLLEQNMIV 25
Db 1 MADNGITVEELKQLLEQNMIV 22

RESULT 28
Q6RD05 PRELIMINARY; PRT; 221 AA.
AC Q6RD05;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW5.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_Taxid=258968;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL; AY502928; AAR87560.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M; 1.
DR Envelope protein.
KW SEQUENCE 221 AA; 25016 MW; 6658652E2927478B CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGITVEELKQLLEQNMIV 25
Db 1 MADNGITVEELKQLLEQNMIV 22

RESULT 29
Q6RD16 PRELIMINARY; PRT; 221 AA.
AC Q6RD16;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW4.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_Taxid=258967;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL: AY502927; AAR87549.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
DR Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLLEQNMNV 25
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 30
Q6RD27 PRELIMINARY; PRT; 221 AA.
ID Q6RD27
AC Q6RD27;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Putative envelope protein M.
OS SARS coronavirus TMV.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258966;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL: AY502926; AAR87538.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
DR Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLLEQNMNV 25
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 31
Q6RD38 PRELIMINARY; PRT; 221 AA.
ID Q6RD38
AC Q6RD38;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
```

```

OX NCBI_TaxID=258965;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL: AY502925; AAR87527.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
DR Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLLEQNMNV 25
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 32
Q6RD49 PRELIMINARY; PRT; 221 AA.
ID Q6RD49
AC Q6RD49;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative envelope protein M.
OS SARS coronavirus TW11.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=258964;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14983045; DOI=10.1073/pnas.0307904100;
RG National Taiwan University SARS Research Team;
RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
RA Su I.-J., Tsai S.-F., Chen D.-S., Chen P.-J.;
RT "Characterization of severe acute respiratory syndrome coronavirus
RT genomes in Taiwan: molecular epidemiology and genome evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
DR EMBL: AY502924; AAR87516.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR002574; Corona_M.
DR Pfam: PF01635; Corona_M; 1.
DR Envelope protein.
SQ SEQUENCE 221 AA; 25060 MW; DBEBC0ABAD7B7D CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2,4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEELKQLLEQNMNV 25
DB 1 MADNGTITVEELKQLLEQNMNV 22

RESULT 33
Q6RD60 PRELIMINARY; PRT; 221 AA.
ID Q6RD60
AC Q6RD60;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative envelope protein M.
```

```

OS SARS coronavirus TW10.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=258963;
RN
  [1]
  SEQUENCE FROM N.A.
  PubMed:14983045; DOI=10.1073/pnas.0307904100;
  National Taiwan University SARS Research Team;
  RA Yeh S.-H., Wang H.-Y., Tsai C.-Y., Kao C.-L., Yang J.-Y., Liu H.-W.,
  RA Su I.-J., Tsai S.-P., Chen D.-S., Chen P.-J.;
  RT "Characterization of severe acute respiratory syndrome coronavirus
  RT genomes in Taiwan: molecular epidemiology and genome evolution.";
  RL Proc. Natl. Acad. Sci. U.S.A. 101:2542-2547(2004).
  DR EMBL: AY502923; AAR87505.1; -;
  DR GO: GO:0019031; C:Viral envelope; IEA.
  DR GO: GO:0019058; P:Viral infectious cycle; IEA.
  DR InterPro: IPR002574; Corona_M.1.
  DR Pfam: PF01635; Corona_M.1.
  KM Envelope protein.
  SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNLV 25
DB 1 MADNGITVEELKQLEQNLV 22

RESULT 34
0698D3
ID 0698D3 PRELIMINARY; PRT; 221 AA.
AC 0698D3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE , complete genome.
OS SARS coronavirus Shanghai/CX2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=258508;
RN
  [1]
  SEQUENCE FROM N.A.
  RC STRAIN=Shanghai/CX2;
  RA Yan Z., Zhang X., Hu Y., Lan S., Zhou Z., Wang H., Wen Y.;
  RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
  DR EMBL: AY463060; AAR86779.1; -;
  DR GO: GO:0019058; P:Viral infectious cycle; IEA.
  DR InterPro: IPR002574; Corona_M.1.
  DR Pfam: PF01635; Corona_M.1.
  SQ SEQUENCE 221 AA; 25044 MW; 51875ABE9BAE04FC CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNLV 25
DB 1 MADNGITVEELKQLEQNLV 22

RESULT 35
06T1D8
ID 06T1D8 PRELIMINARY; PRT; 221 AA.
AC 06T1D8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Membrane glycoprotein M.
OS SARS coronavirus CHN-12.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.

```

```

OX NCBI_TaxId=260550;
RN
  [1]
  SEQUENCE FROM N.A.
  RP PubMed:14709660;
  RA Chim S.S.C., Tong Y.K., Hung E.C.W., Chiu R.W.K., Lo Y.M.D.;
  RT "Genomic sequencing of a SARS coronavirus isolate that predated the
  RT Metropole Hotel case cluster in Hong Kong.";
  RL Clin. Chem. 50:231-233(2004).
  DR EMBL: AY443095; AAS01068.1; -;
  DR GO: GO:0019058; P:Viral infectious cycle; IEA.
  DR InterPro: IPR002574; Corona_M.1.
  DR Pfam: PF01635; Corona_M.1.
  SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNLV 25
DB 1 MADNGITVEELKQLEQNLV 22

RESULT 36
06TPE4
ID 06TPE4 PRELIMINARY; PRT; 221 AA.
AC 06TPE4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Matrix protein.
OS SARS coronavirus GZ02.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=256753;
RN
  [1]
  SEQUENCE FROM N.A.
  RA Zhou X., Hou J., He M., Ding Y., Wang Z., Li J., Liu Z., Ma S.;
  RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
  DR EMBL: AY390556; AAS0007.1; -;
  DR GO: GO:0005198; F:Structural molecule activity; IEA.
  DR GO: GO:0019058; P:Viral infectious cycle; IEA.
  DR InterPro: IPR002574; Corona_M.1.
  DR Pfam: PF01635; Corona_M.1.
  KM Matrix protein.
  SQ SEQUENCE 221 AA; 25060 MW; 275C37085A0215A8 CRC64;

Query Match      88.2%; Score 112; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MADNGITVEELKQLEQNLV 25
DB 1 MADNGITVEELKQLEQNLV 22

RESULT 37
06UZE9
ID 06UZE9 PRELIMINARY; PRT; 221 AA.
AC 06UZE9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Putative M protein.
OS SARS coronavirus PUMCO3.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxId=253435;
RN
  [1]
  SEQUENCE FROM N.A.
  RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,
  RA Zhou X., Zhang W., Yu Z., Qin C., Liu X., Shen Y., Ni A., Qiang B.;

```

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY357076; ARI1482.1; -  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEBELKQLEQNNLV 25  
DB 1 MADNGTITVEBELKQLEQNNLV 22

RESULT 38  
Q6UZF3 PRELIMINARY; PRT; 221 AA.  
ID Q6UZF3;  
AC Q6UZF3;  
DT 05-JUL-2004 (TEMBLrel. 27, Created)  
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
DE Putative M protein.  
OS SARS coronavirus PUMC02.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=253434;  
RN  
RP SEQUENCE FROM N.A.  
RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,  
RA Zhou X., Zhang W., Yu Z., Qin C., Liu X., Shen Y., Ni A., Qiang B.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY357075; ARI14808.1; -  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEBELKQLEQNNLV 25  
DB 1 MADNGTITVEBELKQLEQNNLV 22

RESULT 39  
Q6V584 PRELIMINARY; PRT; 221 AA.  
ID Q6V584;  
AC Q6V584;  
DT 05-JUL-2004 (TEMBLrel. 27, Created)  
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
DE Putative M protein.  
OS SARS coronavirus PUMC01.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=253433;  
RN  
RP SEQUENCE FROM N.A.  
RA Zou K., Zhu H., Ding K., Wang Z., Liu Y., Wang T., Yang J., Wei G.,  
RA Zhou X., Zhang W., Yu Z., Fan Z., Peng X., Qin C., Liu X., Shen Y.,  
RA Ni A., Qiang B.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY350750; ARI14804.1; -  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEBELKQLEQNNLV 25  
DB 1 MADNGTITVEBELKQLEQNNLV 22

RESULT 40  
Q6VA74 PRELIMINARY; PRT; 221 AA.  
ID Q6VA74;  
AC Q6VA74;  
DT 05-JUL-2004 (TEMBLrel. 27, Created)  
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
DE Putative M protein.  
OS SARS coronavirus CUHK-AG03.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=239243;  
RN  
RP SEQUENCE FROM N.A.  
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.M.,  
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,  
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,  
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,  
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,  
RA Wong C.H., Yiu W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;  
RT "Genomic characterisation of the SARS-coronavirus of the Amoy Gardens outbreak in Hong Kong";  
RL Lancet 362:1807-1808 (2003).  
DR EMBL: AY345988; AAP94763.1; -  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478E CRC64;

Query Match 88.2%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTITVEBELKQLEQNNLV 25  
DB 1 MADNGTITVEBELKQLEQNNLV 22

RESULT 41  
Q6VA85 PRELIMINARY; PRT; 221 AA.  
ID Q6VA85;  
AC Q6VA85;  
DT 05-JUL-2004 (TEMBLrel. 27, Created)  
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
DE Putative M protein.  
OS SARS coronavirus CUHK-AG02.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=239242;  
RN  
RP SEQUENCE FROM N.A.  
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung E.C.M.,  
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,  
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,  
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,  
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,  
RA Wong C.H., Yiu W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;  
RT "Genomic characterisation of the SARS-coronavirus of the Amoy Gardens outbreak in Hong Kong";  
RL Lancet 362:1807-1808 (2003).  
DR EMBL: AY345987; AAP94752.1; -  
DR GO: GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro: IPR002574; Corona\_M.  
DR Pfam: PF01635; Corona\_M; 1.



SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478B CRC64;  
Query Match 88.2%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 MADNGITVEELKQLEQNMNV 25  
DB 1 MADNGITVEELKQLEQNMNV 22  
RESULT 42  
Q6VA96 PRELIMINARY; PRT; 221 AA.  
AC Q6VA96;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE Putative M protein.  
OS SARS coronavirus CUHK-AG01.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=239241;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chim S.S.C., Tsui S.K.W., Chan K.C.A., Au T.C.C., Hung B.C.W.,  
RA Tong Y.K., Chiu R.W.K., Ng E.K.O., Chan P.K.S., Chu C.M., Sung J.J.Y.,  
RA Tam J.S., Fung K.P., Waye M.M.Y., Lee C.Y., Yuen K.Y., Chung S.,  
RA Au-Yang C., Au K.K.A., Chan A.H., Chan C.W., Kou C.Y.C., Lam W.Y.,  
RA Lau S.K., Lau Y.M., Law S.L., Law P.T.W., Li M.L.Y., Wan A.W.K.,  
RA Wong C.H., Yau W.H., Lee N., Wu A., Tse C.H., Chan L.Y.S., Lo Y.M.D.;  
RT "Genomic characterisation of the SARS-coronavirus of the Amoy Gardens  
RT outbreak in Hong Kong";  
RL Lancet 362:1807-1808(2003).  
DR EMBL; AY345986; AAP94741.1;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR02574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25016 MW; 6658652E2927478B CRC64;  
Query Match 88.2%; Score 112; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 MADNGITVEELKQLEQNMNV 25  
DB 1 MADNGITVEELKQLEQNMNV 22  
RESULT 43  
Q692E0 PRELIMINARY; PRT; 221 AA.  
AC Q692E0;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Membrane glycoprotein.  
OS SARS coronavirus TGF.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=284672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chen W., Yan W., Liu M.,  
RT "Isolation and identification of viruses related to the SARS  
RT Coronavirus from swines in China."  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY546624; AAT76152.1;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR02574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25059 MW; 439CD30C104CBFAC CRC64;

Query Match 85.0%; Score 108; DB 2; Length 221;  
Best Local Similarity 95.5%; Pred. No. 7.9e-06;  
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 MADNGITVEELKQLEQNMNV 25  
DB 1 MADNGITVEELKQLEQNMNV 22  
RESULT 44  
Q6QJ38 PRELIMINARY; PRT; 221 AA.  
AC Q6QJ38;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Membrane protein.  
OS SARS coronavirus BJ01.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=228407;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BJ01;  
RA Li T., Li X., Chang Z., Liu L.,  
RT "Identification of SARS-CoV RNA leader sequence."  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY536759; AAS48455.1;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR02574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
SQ SEQUENCE 221 AA; 25059 MW; 439CD30C104CBFAC CRC64;  
Query Match 85.0%; Score 108; DB 2; Length 221;  
Best Local Similarity 95.5%; Pred. No. 7.9e-06;  
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 MADNGITVEELKQLEQNMNV 25  
DB 1 MADNGITVEELKQLEQNMNV 22  
RESULT 45  
Q6SRK0 PRELIMINARY; PRT; 143 AA.  
AC Q6SRK0;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Membrane glycoprotein M (Fragment).  
OS SARS coronavirus TW-YM1.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus; SARS coronavirus TW.  
OX NCBI\_TaxID=264383;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lan Y.-C., Chen Y.-J., Lee C.-M., Liu T.-T., Lu J.-J., Chan Y.-J.,  
RA Yang J.-Y., Chen H.-Y., Chen Y.-M., Artinur.,  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY451886; AAS44739.1;  
DR GO; GO:0019058; P:Viral infectious cycle; IEA.  
DR InterPro; IPR02574; Corona\_M.  
DR Pfam; PF01635; Corona\_M; 1.  
FT NON\_TER 143  
SQ SEQUENCE 143 AA; 16435 MW; 2694FA8363B971F7 CRC64;  
Query Match 83.5%; Score 106; DB 2; Length 143;  
Best Local Similarity 95.5%; Pred. No. 9.5e-06;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 MADNGITVEELKQLEQNMNV 25  
DB 1 MADNGITVEELKQLEQNMNV 22

```

RESULT 46
HOSC_THET2
ID HOSC_THET2 STANDARD; PRT; 376 AA.
AC 087196;
DT 30-MAY-2000 (Rel. 39, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homocitrate synthase (EC 2.3.3.14).
GN Name-lys20; Ordered locus names=TTG1550;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
NCBI_TaxID=262724;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99085673; PubMed=9668782;
RA Kosuge T., Hoshino T.;
RT "lysine is synthesized through the alpha-aminoadipate pathway in
RT Thermus thermophilus."
RL FEWS Microbiol. Lett. 169:361-367(1998).
RN 1;
RP SEQUENCE FROM N.A.
RX PubMed=15064768; DOI=10.1038/nbt956;
RA Henne A., Brueggemann H., Raasch C., Wlezer A., Hartech T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacob C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus."
RL Nat. Biotechnol. 22:547-553(2004).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + 2-oxoglutarate = 2-
CC hydroxybutyrate+L-2,4-tricarboxylate + COA.
CC -1- PATHWAY: lysine biosynthesis; alpha-aminoadipic acid pathway;
CC first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate
CC synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB018379; BAA33785.1; -
DR EMBL; AB017306; AAS81892.1; -
DR PIR; T51170; T51170.
DR InterPro: IPR002034; AIPM/Hcit_synth.
DR InterPro: IPR000891; HMG_L-like.
DR Pfam; PF00662; HMG_L-like; 1.
DR PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
DR PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
DR PROSITE; PS00991; PYR_CT; 1.
KM Complete proteome; lysine biosynthesis; Transferrase.
FT CONFLICT 104 104 A -> P (in Ref. 1).
SQ SEQUENCE 376 AA; 42159 MW; 1B8EBA63082FCF06 CRC64;

```

```

AC 068H54;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 60 kDa chaperonin (Fragment).
GN Name-cpn60;
OS Clostridium xyloxyticum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC Clostridium.
OX NCBI_TaxID=29375;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 49623;
RX PubMed=15289485; DOI=10.1101/gr.2649204;
RA Hill J.E., Penny S.L., Crowell K.G., Goh S.H., Hemmingsen S.M.;
RT "cpn60: a chaperonin sequence database."
RL Genome Res. 14:1669-1675(2004).
DR EMBL; AY691242; AAT96592.1; -
DR InterPro: IPR008950; GROEL-ATPase.
FT NON TER 1 184
FT NON TER 184 184
SQ SEQUENCE 184 AA; 19763 MW; 16302D37B6F8508E CRC64;

```

Query Match 44.9%; Score 57; DB 2; Length 184;  
Best Local Similarity 41.7%; Pred. No. 23;  
Matches 10; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

```

RESULT 48
08PLJ9
ID 08PLJ9 PRELIMINARY; PRT; 409 AA.
AC 08PLJ9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Two-component system sensor protein.
GN Name=regS; Ordered locus names=XAC1798;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferriz J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaglini R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Camavar F., Cardozo J., Chambergro F., Clapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Petro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AB011812; AAM36661.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR GO; GO:0000155; P:two-component sensor molecule activity; IEA.

```

DR GO:0007165; P:signal transduction; IEA.  
 DR InterPro: IPR003594; APbnd APase.  
 DR InterPro: IPR004358; Bact\_sens\_pr\_C.  
 DR InterPro: IPR005467; Hsb\_Kinase.  
 DR InterPro: IPR003661; Hsb\_Kin\_N.  
 DR InterPro: IPR009082; Hsb\_Kin\_homodm.  
 DR Pfam: PF02518; HATPase\_c/1.  
 DR Pfam: PF00512; HsKKA; 1.  
 DR PRINTS: PR00344; BCTRSNSOR.  
 DR SMART: SM00387; HATPase\_c/1.  
 DR SMART: SM00388; HsKKA; 1.  
 DR POSITIVE: PSS0109; HIS\_KIN; 1.  
 KM Complete proteome; Kinase; Phosphorylation; Sensory transduction;  
 KM Transferrase.  
 SO SEQUENCE 409 AA; 44065 MW; F481A6B6F4A570DE CRC64;  
 Query Match 43.7%; Score 55.5; DB 2; Length 409;  
 Best Local Similarity 54.5%; Pred. No. 78;  
 Matches 12; Conservative 5; Mismatches 4; Indels 1; Gaps 1;  
 Oy 5 ADNGITVE-ELKQLEQNMV 25  
 Db 258 ADNGHLSREVAVXEVLQNMV 279  
 RESULT 49  
 ID RALA\_HUMAN STANDARD; PRT; 206 AA.  
 AC P11233;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ras-related protein Ral-A.  
 GN Name=RALA; Synonyms=RAL;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9296492; PubMed=2662142;  
 RA Charlin P., Tavittian A.;  
 RT "Coding sequences of human rala and ralB cDNAs";  
 RL Nucleic Acids Res. 17:4380-4380(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Platelet;  
 RX MEDLINE=9380251; PubMed=2550440;  
 RA Polakis P.G., Weber R.F., Neville B., Didsbury J.R., Evans T.,  
 RT "Identification of the ral and rac1 gene products, low molecular mass  
 RT GTP-binding proteins from human platelets";  
 RL J. Biol. Chem. 264:16383-16389(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Puhl H.L., Iikeda S.R., Aroncham R.S.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Ryan E., Wilson C.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toehiyuki S., Carninci P., Prange C.,  
 RA Bawa S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP ISOPRENOLD.  
 RX MEDLINE=91236758; PubMed=1903399;  
 RA Kinsella B.T., Erdman R.A., Maltese W.A.;  
 RT "Carboxyl-terminal isoprenylation of ras-related GTP-binding proteins  
 RT encoded by rac1, rac2 and rala";  
 RL J. Biol. Chem. 266:9786-9794(1991).  
 RN [7]  
 RP INTERACTION WITH RALBP1.  
 RX MEDLINE=95403450; PubMed=7673236; DOI=10.1074/jbc.270.38.22473;  
 RA Julien-Plores V., Dorseuil O., Romero F., Letourneur F.,  
 RA Saragosti S., Berger R., Tavittian A., Gacon G., Camonis J.H.,  
 RT "Bridging Ral GTPase to Rho pathways. RLR76, a Ral effector with  
 RT CDC42/Rac GTPase-activating protein activity";  
 RL J. Biol. Chem. 270:22473-22477(1995).  
 CC -1- SUBUNIT: Interacts with RALBP1 via its effector domain.  
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily, Ras family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: X15014; CAA3118.1; -;  
 DR EMBL: M29893; AAA36542.1; -;  
 DR EMBL: AF493910; AAM12624.1; -;  
 DR EMBL: AC004837; -; NOT ANNOTATED\_CDS.  
 DR EMBL: BC039858; AAH39858.1; -;  
 DR PIR: S04596; TVH0UA.  
 DR PDB: 1UAD; X-ray; A/B=9-183.  
 DR Genew: HGNC:9839; RALA.  
 DR MIM: 179550; -;  
 DR GO:0005525; F:GTP binding; TAS.  
 DR GO:0005515; F:protein binding; TAS.  
 DR GO:0006935; P:chemotaxis; TAS.  
 DR GO:0007165; P:signal transduction; TAS.  
 DR InterPro: IPR001806; Ras trnsfrmg.  
 DR InterPro: IPR005225; Small\_GTP.  
 DR Pfam: PF00071; Ras; 1.  
 DR PRINTS: PR00449; RASTRNSFRMG.  
 DR TIGRFAMs: TIGR00231; small\_GTP; 1.  
 KM 3D-structure: GTP-binding; Lipoprotein; Prenylation.  
 FT NP\_BIND 21 28 GTP (By similarity).  
 FT NP\_BIND 68 72 GTP (By similarity).  
 FT NP\_BIND 127 130 GTP (By similarity).  
 FT DOMAIN 43 51 Effector region (By similarity).  
 FT LIPID 203 203 S-geranylgeranyl cysteine.  
 FT CONFLICT 1 2 MA -> MVDYL (in Ref. 2 and 3).  
 SO SEQUENCE 206 AA; 23567 MW; 6974341EA18C1975 CRC64;  
 Query Match 43.3%; Score 55; DB 1; Length 206;  
 Best Local Similarity 41.7%; Pred. No. 47;  
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
 Oy 1 KKQADNGITVEELKQLEQNMV 24

Db 128 KSDLEDRQVSVBEAKRAEQMNV 151

## RESULT 50

Q9LRN6 PRELIMINARY; PRT; 229 AA.

AC Q9LRN6; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Arabidopsis thaliana genomic DNA, chromosome 3, pl clone:MU8.

OS Arabidopsis thaliana (mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=20277480; PubMed=10819329;

RX RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty pl and TAC

RT clones.";

RL DNA Res. 7:131-135(2000).

RL [2]

RN SEQUENCE FROM N.A.

RP Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB028621; BAB01352.1; -.

DR HSP; P06787; IFS5.

DR GO; GO:005509; F:calcium ion binding; IEA.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF-hand\_like.

DR Pfam; PF00036; ehand; 4.

DR PRODOM; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.

DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_1.

DR PROSITE; 229 AA; 26266 MW; 94C011172CA33740 CRC64;

SO SEQUENCE

## Query Match

43.3%; Score 55; DB 2; Length 229;

Best Local Similarity 61.1%; Pred. NO. 52;

Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 NGTIVBELKQLLEQWNL 24

70 NGTIDIELKCKLELKL 87

Search completed: May 11, 2005, 21:27:14

Job time : 131.745 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 21:16:44 ; Search time 32.4468 Seconds  
(without alignments)  
57.516 Million cell updates/sec

Title: US-10-712-812-6  
Perfect score: 127  
Sequence: 1 KKKADNGITVEELKOLLEGWNLV 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/ECTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	55	43.3	205 2 US-08-531-525-31	Sequence 31, Appl
2	55	43.3	205 2 US-08-718-270A-31	Sequence 31, Appl
3	55	43.3	206 3 US-09-078-317-15	Sequence 15, Appl
4	55	43.3	206 3 US-09-454-818-15	Sequence 15, Appl
5	55	43.3	206 4 US-09-709-103-48	Sequence 48, Appl
6	55	43.3	206 4 US-09-439-410A-48	Sequence 48, Appl
7	53	40.6	300 4 US-09-543-681A-7926	Sequence 7926, Ap
8	51.5	40.6	855 4 US-09-206-551-11	Sequence 11, Appl
9	51.5	40.6	855 4 US-09-206-551-12	Sequence 11, Appl
10	50.5	39.8	770 4 US-09-248-796A-17215	Sequence 17215, A
11	50	39.4	100 4 US-09-513-999C-6125	Sequence 6125, Ap
12	50	39.4	300 4 US-09-648-004-26	Sequence 26, Appl
13	50	39.4	300 4 US-10-872-419-26	Sequence 26, Appl
14	50	39.4	536 2 US-08-940-332-2	Sequence 2, Appl1
15	50	39.4	537 4 US-09-543-681A-4729	Sequence 4729, Ap
16	50	39.4	542 4 US-09-949-016-7536	Sequence 7536, Ap
17	50	39.4	545 4 US-09-544-683-2	Sequence 2, Appl1
18	50	39.4	545 4 US-10-192-419-2	Sequence 2, Appl1
19	50	39.4	2472 4 US-09-538-092-1312	Sequence 1312, Ap
20	49	38.6	123 4 US-09-266-965-132	Sequence 132, Appl
21	49	38.6	218 4 US-09-538-092-241	Sequence 241, Appl
22	49	38.6	473 4 US-09-949-016-9830	Sequence 9830, Ap
23	49	38.6	532 4 US-09-489-039A-10011	Sequence 10011, A
24	49	38.6	534 1 US-07-872-644-27	Sequence 27, Appl
25	49	38.6	534 1 US-08-297-494-27	Sequence 27, Appl
26	49	38.6	534 1 US-08-297-510-27	Sequence 27, Appl
27	49	38.6	534 1 US-08-479-532-27	Sequence 27, Appl

28	49	38.6	534 1 US-08-455-526-27	Sequence 27, Appl
29	49	38.6	534 1 US-08-455-525-27	Sequence 27, Appl
30	49	38.6	534 1 US-09-139-491-27	Sequence 27, Appl
31	49	38.6	534 4 US-09-883-825-27	Sequence 27, Appl
32	49	38.6	534 5 PCT-US92-03222-27	Sequence 27, Appl
33	48.5	38.2	434 4 US-09-107-533A-4075	Sequence 4075, Ap
34	48	37.8	159 4 US-09-538-092-266	Sequence 266, Appl
35	48	37.8	208 4 US-09-489-039A-7411	Sequence 7411, Ap
36	48	37.8	313 4 US-09-252-991A-32836	Sequence 32836, A
37	48	37.8	462 4 US-09-538-092-769	Sequence 769, Appl
38	48	37.8	1297 3 US-09-540-245A-17	Sequence 17, Appl
39	47.5	37.4	149 4 US-09-270-767-45884	Sequence 45884, A
40	46	36.2	93 4 US-09-621-976-4009	Sequence 4009, A
41	46	36.2	216 4 US-09-710-279-2624	Sequence 2624, Ap
42	46	36.2	274 3 US-09-134-001C-5279	Sequence 5279, Ap
43	46	36.2	365 4 US-09-270-767-43356	Sequence 43356, A
44	46	36.2	397 4 US-09-270-767-43356	Sequence 43356, A
45	46	36.2	415 4 US-09-248-796A-14232	Sequence 14232, A
46	46	36.2	460 4 US-09-759-595-1	Sequence 1, Appl1
47	46	36.2	544 2 US-08-467-822-33	Sequence 33, Appl
48	46	36.2	544 3 US-08-432-697-33	Sequence 33, Appl
49	46	36.2	544 3 US-08-466-248-33	Sequence 33, Appl
50	46	36.2	544 4 US-09-198-452A-153	Sequence 153, Appl
51	46	36.2	544 4 US-09-809-745-3	Sequence 3, Appl1
52	46	36.2	555 4 US-09-438-185A-136	Sequence 136, Appl
53	46	36.2	998 4 US-09-252-991A-19450	Sequence 19450, A
54	45	35.4	114 4 US-09-107-533A-6600	Sequence 6600, Ap
55	45	35.4	119 4 US-09-540-236-2256	Sequence 2256, Ap
56	45	35.4	174 2 US-08-564-972-62	Sequence 62, Appl
57	45	35.4	203 4 US-09-248-796A-14412	Sequence 14412, A
58	45	35.4	260 2 US-08-879-561-8	Sequence 8, Appl1
59	45	35.4	261 4 US-09-949-016-11398	Sequence 11398, A
60	45	35.4	262 4 US-09-857-498A-6	Sequence 6, Appl1
61	45	35.4	292 4 US-09-248-796A-21680	Sequence 21680, A
62	45	35.4	331 2 US-08-564-972-9	Sequence 9, Appl1
63	45	35.4	376 4 US-09-328-352-5970	Sequence 5970, Ap
64	45	35.4	496 4 US-08-840-713-39	Sequence 39, Appl
65	45	35.4	535 2 US-08-564-972-1	Sequence 1, Appl1
66	45	35.4	535 3 US-09-171-969-9	Sequence 9, Appl1
67	45	35.4	535 4 US-09-250-131-2	Sequence 2, Appl1
68	45	35.4	545 2 US-08-467-822-30	Sequence 30, Appl
69	45	35.4	545 3 US-08-432-697-30	Sequence 30, Appl
70	45	35.4	545 3 US-08-466-248-30	Sequence 30, Appl
71	45	35.4	546 3 US-08-470-260-6	Sequence 6, Appl1
72	45	35.4	546 3 US-08-471-491-6	Sequence 6, Appl1
73	45	35.4	546 3 US-08-466-662-6	Sequence 6, Appl1
74	45	35.4	546 4 US-08-256-847C-1	Sequence 1, Appl1
75	45	35.4	546 4 US-08-256-847C-7	Sequence 7, Appl1
76	45	35.4	567 4 US-09-639-245-4	Sequence 4, Appl1
77	45	35.4	615 4 US-08-840-713-35	Sequence 35, Appl
78	45	35.4	617 4 US-08-840-713-37	Sequence 37, Appl
79	45	35.4	714 4 US-09-248-796A-18997	Sequence 18997, A
80	45	35.4	1052 3 US-09-255-507-7	Sequence 7, Appl1
81	45	35.4	1052 3 US-09-360-237-1	Sequence 1, Appl1
82	45	35.4	1052 3 US-09-360-237-3	Sequence 3, Appl1
83	45	35.4	1052 4 US-09-255-501-208	Sequence 208, Appl
84	45	35.4	1052 4 US-09-060-854B-7	Sequence 7, Appl1
85	45	35.4	1052 4 US-09-891-711-4	Sequence 4, Appl1
86	45	35.4	1052 4 US-09-891-711-6	Sequence 6, Appl1
87	45	35.4	1052 4 US-09-949-016-6413	Sequence 6413, Ap
88	45	35.4	1052 4 US-09-060-872A-208	Sequence 208, Appl
89	45	35.4	1052 4 US-09-500-135C-208	Sequence 208, Appl
90	45	35.4	1058 4 US-09-949-016-10687	Sequence 10687, A
91	44.5	35.0	847 4 US-09-476-242-2	Sequence 2, Appl1
92	44	34.6	259 4 US-09-248-796A-20877	Sequence 20877, A
93	44	34.6	555 4 US-09-027-196-2	Sequence 2, Appl1
94	44	34.6	1577 2 US-08-793-824-2	Sequence 2, Appl1
95	44	34.6	1972 4 US-09-252-991A-17515	Sequence 17515, A
96	44	34.6	2186 4 US-09-949-016-10828	Sequence 10828, A
97	44	34.6	2249 4 US-09-538-092-9148	Sequence 914, Appl
98	43.5	34.3	254 4 US-09-270-767-33738	Sequence 33738, A
99	43.5	34.3	254 4 US-09-270-767-48955	Sequence 48955, A
100	43.5	34.3	272 4 US-09-270-767-31963	Sequence 31963, A

101	43.5	34.3	272	4	US-09-270-767-47180	Sequence 47180, A	174	42	33.1	542	4	US-09-270-767-42841	Sequence 42841, A
102	43.5	34.3	540	4	US-09-543-681A-55987	Sequence 55987, Ap	175	42	33.1	545	4	US-09-134-000C-4559	Sequence 4559, Ap
103	43.5	34.3	555	1	US-08-039-777-3	Sequence 3, Appl1	176	42	33.1	576	2	US-08-533-306A-2	Sequence 2, Appl1
104	43.5	34.3	555	1	US-08-611-361A-10385	Sequence 3, Appl1	177	42	33.1	576	2	US-08-742-923A-C	Sequence 2, Appl1
105	43.5	34.3	626	4	US-09-902-540-10385	Sequence 10385, A	178	42	33.1	618	3	US-09-134-001C-3169	Sequence 3169, Ap
106	43	33.9	45	1	US-08-056-200-96	Sequence 96, Appl	179	42	33.1	637	4	US-09-248-796A-16272	Sequence 16272, A
107	43	33.9	45	2	US-08-800-644-96	Sequence 96, Appl	180	42	33.1	816	2	US-08-533-306A-6	Sequence 6, Appl1
108	43	33.9	128	4	US-09-902-540-15331	Sequence 15331, A	181	42	33.1	816	2	US-08-742-923A-6	Sequence 6, Appl1
109	43	33.9	162	4	US-09-543-681A-6627	Sequence 6627, Ap	182	42	33.1	835	3	US-09-291-833-2	Sequence 2, Appl1
110	43	33.9	191	4	US-09-949-016-7105	Sequence 7105, Ap	183	42	33.1	835	3	US-09-458-457-2	Sequence 2, Appl1
111	43	33.9	229	4	US-09-270-767-41871	Sequence 41871, A	184	42	33.1	835	4	US-09-947-199A-2	Sequence 2, Appl1
112	43	33.9	229	4	US-09-270-767-57115	Sequence 57115, A	185	42	33.1	885	2	US-08-533-306A-4	Sequence 4, Appl1
113	43	33.9	276	4	US-09-134-000C-4646	Sequence 4646, Ap	186	42	33.1	885	2	US-08-742-923A-4	Sequence 4, Appl1
114	43	33.9	399	4	US-09-134-000C-6019	Sequence 6019, Ap	187	42	33.1	932	4	US-08-887-533A-45	Sequence 45, Appl
115	43	33.9	486	4	US-09-252-991A-19636	Sequence 19636, A	188	42	33.1	932	4	US-09-527-431-45	Sequence 45, Appl
116	43	33.9	490	4	US-08-956-171B-5212	Sequence 5212, Ap	189	42	33.1	932	4	US-09-446-861-45	Sequence 45, Appl
117	43	33.9	490	4	US-08-781-986A-5212	Sequence 5212, Ap	190	42	33.1	1019	4	US-09-543-681A-4447	Sequence 4447, Ap
118	43	33.9	495	4	US-09-252-991A-23319	Sequence 23319, A	191	42	33.1	1576	4	US-09-949-016-7610	Sequence 7610, Ap
119	43	33.9	543	1	US-08-775-709-17	Sequence 17, Appl	192	42	33.1	1857	4	US-09-917-25A-91	Sequence 91, Appl
120	43	33.9	543	1	US-08-752-929-17	Sequence 17, Appl	193	42	33.1	1972	4	US-08-875-435B-3	Sequence 3, Appl1
121	43	33.9	543	3	US-09-090-793-10	Sequence 10, Appl	194	42	33.1	1972	4	US-08-875-435B-4	Sequence 4, Appl1
122	43	33.9	543	3	US-09-231-899-10	Sequence 10, Appl	195	42	33.1	1972	4	US-09-538-092-1084	Sequence 1084, Ap
123	43	33.9	597	4	US-09-107-532A-7053	Sequence 7053, Ap	196	42	33.1	1984	4	US-09-949-016-7111	Sequence 7111, Ap
124	43	33.9	880	4	US-09-583-110-4739	Sequence 4739, Ap	197	42	33.1	1984	4	US-09-949-016-7112	Sequence 7112, Ap
125	43	33.9	1086	4	US-09-543-681A-7696	Sequence 7696, Ap	198	42	33.1	1984	4	US-09-949-016-7113	Sequence 7113, Ap
126	43	33.9	2188	4	US-09-328-352-7763	Sequence 7763, Ap	199	41.5	32.7	118	4	US-09-248-796A-21838	Sequence 21838, A
127	43	33.9	2517	4	US-09-902-540-15380	Sequence 15380, A	200	41.5	32.7	205	4	US-09-270-767-42795	Sequence 42795, A
128	43	33.9	3290	4	US-09-328-352-5486	Sequence 5486, Ap	201	41.5	32.7	358	3	US-09-500-569-18	Sequence 18, Appl
129	42.5	33.5	210	3	US-09-247-373B-46	Sequence 46, Appl	202	41.5	32.7	358	4	US-09-971-823B-18	Sequence 18, Appl
130	42.5	33.5	226	3	US-09-134-001C-5494	Sequence 5494, Ap	203	41.5	32.7	365	3	US-09-500-569-4	Sequence 4, Appl1
131	42.5	33.5	291	4	US-09-107-532A-6390	Sequence 6390, Ap	204	41.5	32.7	365	4	US-09-971-823B-4	Sequence 4, Appl1
132	42.5	33.5	362	4	US-09-248-796A-20514	Sequence 20514, A	205	41.5	32.7	454	4	US-09-248-796A-14748	Sequence 14748, A
133	42.5	33.5	429	3	US-08-411-768B-4	Sequence 4, Appl1	206	41.5	32.7	463	1	US-07-951-711A-25	Sequence 25, Appl
134	42.5	33.5	429	3	US-09-543-681A-5233	Sequence 5233, Ap	207	41.5	32.7	463	2	US-08-459-548A-25	Sequence 25, Appl
135	42.5	33.5	431	2	US-08-401-068-4	Sequence 4, Appl1	208	41.5	32.7	463	3	US-08-459-595A-25	Sequence 25, Appl
136	42.5	33.5	431	2	US-08-846-338-4	Sequence 4, Appl1	209	41.5	32.7	463	3	US-08-459-504B-25	Sequence 25, Appl
137	42.5	33.5	447	4	US-09-489-039A-13287	Sequence 13287, A	210	41.5	32.7	463	3	US-08-459-444-25	Sequence 0, Appl1
138	42.5	33.5	596	2	US-08-392-806A-2	Sequence 2, Appl1	211	41.5	32.7	463	3	US-09-547-422-25	Sequence 25, Appl
139	42.5	33.5	596	2	US-09-257-490-2	Sequence 2, Appl1	212	41.5	32.7	463	4	US-09-988-462-25	Sequence 25, Appl
140	42	33.1	16	3	US-09-025-596-30	Sequence 30, Appl	213	41.5	32.7	577	4	US-09-902-540-12554	Sequence 12554, A
141	42	33.1	60	3	US-09-400-742-10	Sequence 10, Appl	214	41.5	32.7	577	4	US-09-248-796A-19304	Sequence 19304, A
142	42	33.1	60	3	US-08-618-651A-10	Sequence 10, Appl	215	41.5	32.7	639	3	US-09-347-801-17	Sequence 17, Appl
143	42	33.1	60	3	US-09-115-252-23	Sequence 23, Appl	216	41.5	32.7	639	3	US-09-854-731-17	Sequence 17, Appl
144	42	33.1	60	4	US-09-970-989A-23	Sequence 23, Appl	217	41	32.3	71	1	US-08-606-789-6	Sequence 6, Appl1
145	42	33.1	115	4	US-09-328-352-5509	Sequence 5509, Ap	218	41	32.3	71	2	US-09-111-348-6	Sequence 6, Appl1
146	42	33.1	129	4	US-09-134-000C-4841	Sequence 4841, Ap	219	41	32.3	83	4	US-09-513-995C-5324	Sequence 2, Appl1
147	42	33.1	152	4	US-09-248-796A-22337	Sequence 22337, A	220	41	32.3	84	4	US-09-621-976-6554	Sequence 6554, Ap
148	42	33.1	200	2	US-08-531-525-33	Sequence 33, Appl	221	41	32.3	87	4	US-09-621-976-4000	Sequence 4000, Ap
149	42	33.1	200	2	US-08-718-270A-33	Sequence 33, Appl	222	41	32.3	106	4	US-09-543-681A-7810	Sequence 7810, Ap
150	42	33.1	211	4	US-09-248-796A-22054	Sequence 22054, A	223	41	32.3	113	4	US-09-270-767-46296	Sequence 46296, A
151	42	33.1	222	3	US-09-134-001C-4264	Sequence 4264, Ap	224	41	32.3	113	4	US-09-270-767-61866	Sequence 61866, A
152	42	33.1	268	4	US-09-328-352-8118	Sequence 8118, Ap	225	41	32.3	123	4	US-09-248-796A-23998	Sequence 23998, A
153	42	33.1	275	4	US-09-902-540-12895	Sequence 12895, A	226	41	32.3	123	4	US-09-601-729-9	Sequence 9, Appl1
154	42	33.1	278	3	US-09-400-742-8	Sequence 8, Appl1	227	41	32.3	140	4	US-08-765-381-2	Sequence 2, Appl1
155	42	33.1	278	3	US-08-618-651A-8	Sequence 8, Appl1	228	41	32.3	164	3	US-09-443-218-2	Sequence 2, Appl1
156	42	33.1	278	3	US-09-215-252-7	Sequence 7, Appl1	229	41	32.3	164	4	US-09-443-218-4	Sequence 4, Appl1
157	42	33.1	278	4	US-09-970-989A-7	Sequence 7, Appl1	230	41	32.3	164	4	US-09-443-218-5	Sequence 5, Appl1
158	42	33.1	278	4	US-09-248-796A-20934	Sequence 20934, A	231	41	32.3	164	4	US-09-443-218-7	Sequence 7, Appl1
159	42	33.1	278	4	US-09-449-016-6276	Sequence 6276, Ap	232	41	32.3	194	4	US-09-489-039A-12868	Sequence 12868, A
160	42	33.1	295	4	US-09-270-767-62384	Sequence 62384, A	233	41	32.3	208	3	US-09-134-001C-4449	Sequence 4449, Ap
161	42	33.1	298	4	US-09-270-767-58159	Sequence 58159, A	234	41	32.3	214	4	US-09-853-450-34	Sequence 34, Appl
162	42	33.1	300	4	US-09-949-016-9334	Sequence 9334, Ap	235	41	32.3	235	4	US-09-270-767-42965	Sequence 42965, A
163	42	33.1	328	4	US-09-134-000C-4243	Sequence 4243, Ap	236	41	32.3	269	4	US-09-543-681A-4916	Sequence 4916, Ap
164	42	33.1	339	4	US-09-107-532A-5514	Sequence 5514, Ap	237	41	32.3	272	4	US-09-543-681A-9658	Sequence 9658, Ap
165	42	33.1	349	4	US-09-107-532A-6684	Sequence 6684, Ap	238	41	32.3	276	4	US-09-489-039A-9658	Sequence 9658, Ap
166	42	33.1	380	4	US-09-248-796A-17151	Sequence 17151, A	239	41	32.3	295	4	US-09-543-681A-4711	Sequence 4711, Ap
167	42	33.1	407	4	US-09-248-796A-17916	Sequence 17916, A	240	41	32.3	319	4	US-09-107-532A-5542	Sequence 5542, Ap
168	42	33.1	435	4	US-09-762-194-8	Sequence 8, Appl1	241	41	32.3	329	4	US-09-602-787A-106	Sequence 106, Appl
169	42	33.1	440	4	US-09-762-194-10	Sequence 10, Appl	242	41	32.3	345	4	US-09-248-796A-14637	Sequence 14637, A
170	42	33.1	440	4	US-09-762-194-12	Sequence 2, Appl1	243	41	32.3	390	4	US-09-107-532A-5668	Sequence 5668, Ap
171	42	33.1	504	4	US-09-270-767-46764	Sequence 46764, A	244	41	32.3	397	4	US-09-252-991A-22719	Sequence 22719, A
172	42	33.1	504	4	US-09-270-767-46764	Sequence 46764, A	245	41	32.3	455	3	US-09-035-382-2	Sequence 2, Appl1
173	42	33.1	540	4	US-09-902-540-9824	Sequence 9824, Ap	246	41	32.3				

247	41	32.3	459	4	US-09-602-787A-302	Sequence 302, App	320	40.5	31.9	1813	4	US-09-949-016-8283	Sequence 8283, Ap
248	41	32.3	469	4	US-09-252-991A-27869	Sequence 27869, A	321	40.5	31.9	1813	4	US-09-949-016-8284	Sequence 8285, Ap
249	41	32.3	490	3	US-09-252-149B-26	Sequence 26, App1	322	40.5	31.9	1813	4	US-09-949-016-8285	Sequence 8285, Ap
250	41	32.3	509	4	US-09-248-796A-17566	Sequence 17566, A	323	40.5	31.9	3666	2	US-08-222-617A-12	Sequence 12, App1
251	41	32.3	510	5	PCT-US95-06556-3	Sequence 3, App1	324	40.5	31.9	3727	2	US-08-222-617A-27	Sequence 27, App1
252	41	32.3	510	5	PCT-US95-06556-3	Sequence 3, App1	325	40.5	31.9	3727	2	US-08-222-617A-27	Sequence 27, App1
253	41	32.3	544	1	US-08-187-156-10	Sequence 10, App1	326	40	31.5	50	2	US-08-402-804-10	Sequence 10, App1
254	41	32.3	544	2	US-08-694-865-10	Sequence 10, App1	327	40	31.5	65	3	US-09-134-001C-4419	Sequence 4419, Ap
255	41	32.3	544	2	US-08-878-748-10	Sequence 10, App1	328	40	31.5	72	4	US-09-583-110-4899	Sequence 4899, Ap
256	41	32.3	544	3	US-09-124-491-10	Sequence 10, App1	329	40	31.5	72	4	US-09-107-433-2938	Sequence 2938, Ap
257	41	32.3	544	3	US-09-83-912-10	Sequence 10, App1	330	40	31.5	95	4	US-09-489-039A-7564	Sequence 7564, Ap
258	41	32.3	547	4	US-09-902-540-13219	Sequence 13219, A	331	40	31.5	102	4	US-09-248-796A-14759	Sequence 14759, A
259	41	32.3	579	4	US-09-470-667-6	Sequence 6, App1	332	40	31.5	120	4	US-09-248-796A-28103	Sequence 28103, A
260	41	32.3	699	2	US-08-694-865-16	Sequence 16, App1	333	40	31.5	206	4	US-09-134-000C-3442	Sequence 3442, Ap
261	41	32.3	699	3	US-09-124-491-16	Sequence 16, App1	334	40	31.5	207	2	US-09-022-940-1	Sequence 1, App1
262	41	32.3	699	4	US-09-383-912-16	Sequence 16, App1	335	40	31.5	207	3	US-09-216-386-1	Sequence 1, App1
263	41	32.3	775	4	US-09-248-796A-17675	Sequence 17675, A	336	40	31.5	207	3	US-09-252-991A-31339	Sequence 31339, A
264	41	32.3	780	4	US-09-252-991A-32892	Sequence 32892, A	337	40	31.5	208	2	US-08-844-120-1	Sequence 1, App1
265	41	32.3	784	4	US-09-583-110-5192	Sequence 5192, Ap	338	40	31.5	208	3	US-09-213-394-1	Sequence 1, App1
266	41	32.3	785	4	US-09-248-796A-24492	Sequence 24492, A	339	40	31.5	208	4	US-09-988-982-1	Sequence 1, App1
267	41	32.3	787	4	US-09-107-433-4612	Sequence 4612, Ap	340	40	31.5	230	2	US-09-022-940-3	Sequence 3, App1
268	41	32.3	838	2	US-08-868-786-4	Sequence 4, App1	341	40	31.5	230	3	US-09-216-386-3	Sequence 3, App1
269	41	32.3	924	3	US-08-619-812-8	Sequence 8, App1	342	40	31.5	230	3	US-09-216-143A-6	Sequence 6, App1
270	41	32.3	926	1	US-07-908-253-2	Sequence 2, App1	343	40	31.5	230	4	US-09-984-205-6	Sequence 6, App1
271	41	32.3	926	1	US-08-455-970A-2	Sequence 2, App1	344	40	31.5	248	2	US-08-867-087B-17	Sequence 17, App1
272	41	32.3	926	1	US-08-387-156-6	Sequence 6, App1	345	40	31.5	248	4	US-09-902-540-16288	Sequence 16288, A
273	41	32.3	926	2	US-08-694-865-6	Sequence 6, App1	346	40	31.5	252	4	US-09-252-991A-30813	Sequence 30813, A
274	41	32.3	926	2	US-08-878-748-6	Sequence 6, App1	347	40	31.5	265	3	US-09-199-637A-31	Sequence 31, App1
275	41	32.3	926	2	US-08-535-837-2	Sequence 2, App1	348	40	31.5	291	4	US-09-107-532A-4763	Sequence 4763, Ap
276	41	32.3	926	3	US-09-124-491-6	Sequence 6, App1	349	40	31.5	298	4	US-09-270-767-46126	Sequence 46126, A
277	41	32.3	926	4	US-09-383-912-6	Sequence 6, App1	350	40	31.5	320	2	US-09-027-013-1	Sequence 1, App1
278	41	32.3	926	4	US-08-976-566-2	Sequence 2, App1	351	40	31.5	320	3	US-09-244-233-1	Sequence 1, App1
279	41	32.3	926	6	547657-3	Patent No. 547657	352	40	31.5	345	4	US-09-543-681A-4540	Sequence 4540, Ap
280	41	32.3	926	6	547657-3	Patent No. 547657	353	40	31.5	352	4	US-08-630-915A-12	Sequence 12, App1
281	41	32.3	936	1	US-08-455-970A-12	Sequence 12, App1	354	40	31.5	352	4	US-09-879-957-12	Sequence 12, App1
282	41	32.3	936	4	US-08-976-566-12	Sequence 12, App1	355	40	31.5	352	4	US-09-949-016-6302	Sequence 6302, Ap
283	41	32.3	943	1	US-08-455-970A-10	Sequence 10, App1	356	40	31.5	358	4	US-09-328-352-6375	Sequence 6375, Ap
284	41	32.3	943	4	US-08-976-566-10	Sequence 10, App1	357	40	31.5	367	4	US-09-949-016-9627	Sequence 9627, Ap
285	41	32.3	951	1	US-08-455-970A-14	Sequence 14, App1	358	40	31.5	377	2	US-08-839-581A-31	Sequence 31, App1
286	41	32.3	951	4	US-08-976-566-14	Sequence 14, App1	359	40	31.5	377	3	US-09-023-591A-31	Sequence 31, App1
287	41	32.3	977	1	US-08-387-156-8	Sequence 8, App1	360	40	31.5	391	4	US-09-198-452A-921	Sequence 921, App
288	41	32.3	977	2	US-08-694-865-8	Sequence 8, App1	361	40	31.5	391	4	US-09-438-185A-855	Sequence 855, App
289	41	32.3	977	2	US-08-878-748-8	Sequence 8, App1	362	40	31.5	401	3	US-09-005-298-17	Sequence 17, App1
290	41	32.3	977	3	US-09-124-491-8	Sequence 8, App1	363	40	31.5	401	4	US-08-768-619-17	Sequence 17, App1
291	41	32.3	977	4	US-09-383-912-8	Sequence 8, App1	364	40	31.5	401	5	PCT-US96-09848-31	Sequence 31, App1
292	41	32.3	1069	1	US-07-777-715-9	Sequence 9, App1	365	40	31.5	403	4	US-09-248-796A-14239	Sequence 14239, A
293	41	32.3	1069	1	US-08-170-126-4	Sequence 4, App1	366	40	31.5	406	4	US-09-134-000C-3752	Sequence 3752, Ap
294	41	32.3	1069	3	US-08-954-418-4	Sequence 4, App1	367	40	31.5	407	3	US-09-005-298-15	Sequence 15, App1
295	41	32.3	1098	1	US-07-777-715-7	Sequence 7, App1	368	40	31.5	407	4	US-08-768-619-15	Sequence 15, App1
296	41	32.3	1098	1	US-08-170-126-2	Sequence 2, App1	369	40	31.5	407	5	PCT-US96-09848-15	Sequence 15, App1
297	41	32.3	1098	3	US-08-954-418-2	Sequence 2, App1	370	40	31.5	411	4	US-09-107-532A-4842	Sequence 4842, Ap
298	41	32.3	1132	1	US-08-446-038B-18	Sequence 18, App1	371	40	31.5	424	4	US-09-198-452A-45	Sequence 45, App1
299	41	32.3	1132	1	US-08-446-010B-18	Sequence 18, App1	372	40	31.5	442	3	US-09-134-001C-3033	Sequence 3033, Ap
300	41	32.3	1132	2	US-08-805-445-18	Sequence 18, App1	373	40	31.5	462	3	US-09-189-527-13	Sequence 13, App1
301	41	32.3	1132	2	US-08-064-067D-18	Sequence 18, App1	374	40	31.5	553	4	US-09-902-540-9807	Sequence 9807, Ap
302	41	32.3	1132	2	US-09-066-209-18	Sequence 18, App1	375	40	31.5	572	4	US-09-702-705-1815	Sequence 1815, Ap
303	41	32.3	1142	1	US-08-097-997A-11	Sequence 11, App1	376	40	31.5	572	4	US-09-736-457-1815	Sequence 1815, Ap
304	41	32.3	1142	3	US-08-665-574C-11	Sequence 11, App1	377	40	31.5	611	4	US-09-671-325-1815	Sequence 1815, Ap
305	41	32.3	1142	3	US-08-946-994-11	Sequence 11, App1	378	40	31.5	622	4	US-09-949-016-10606	Sequence 10606, A
306	41	32.3	1154	1	US-08-357-598-7	Sequence 7, App1	379	40	31.5	631	4	US-09-134-000C-6175	Sequence 6175, Ap
307	41	32.3	1154	1	US-08-446-010B-24	Sequence 24, App1	380	40	31.5	651	4	US-09-902-540-11066	Sequence 11066, A
308	41	32.3	1154	2	US-09-003-289-7	Sequence 7, App1	381	40	31.5	651	4	US-09-248-796A-14553	Sequence 14553, A
309	41	32.3	1154	4	PCT-US95-16435-7	Sequence 7, App1	382	40	31.5	680	4	US-09-949-016-7574	Sequence 7574, Ap
310	41	32.3	1765	5	US-09-270-767-45587	Sequence 45587, A	383	40	31.5	708	4	US-09-248-796A-14553	Sequence 14553, A
311	40.5	31.9	100	4	US-09-134-000C-3989	Sequence 3989, Ap	384	40	31.5	774	2	US-07-731-157A-7	Sequence 7, App1
312	40.5	31.9	166	4	US-09-252-991A-24467	Sequence 24467, A	385	40	31.5	774	2	US-08-541-780-7	Sequence 7, App1
313	40.5	31.9	602	4	US-09-540-236-3263	Sequence 3263, Ap	386	40	31.5	825	4	US-09-166-350-12	Sequence 12, App1
314	40.5	31.9	840	4	US-09-252-991A-19561	Sequence 19561, A	387	40	31.5	825	4	US-09-438-185A-29	Sequence 29, App1
315	40.5	31.9	1769	4	US-09-949-016-8280	Sequence 8280, Ap	388	40	31.5	868	4	US-09-538-092-787	Sequence 787, App
316	40.5	31.9	1769	4	US-09-949-016-8281	Sequence 8281, Ap	389	40	31.5	913	3	US-08-971-089-4	Sequence 4, App1
317	40.5	31.9	1769	4	US-09-949-016-8282	Sequence 8282, Ap	390	40	31.5	919	4	US-08-948-796A-19408	Sequence 19408, A
318	40.5	31.9	1784	3	US-09-040-738-2	Sequence 2, App1	391	40	31.5	983	3	US-09-412-554A-2	Sequence 2, App1
319	40.5	31.9	1784	3	US-08-652-426A-2	Sequence 2, App1	392	40	31.5	1007	4	US-09-538-092-736	Sequence 736, App

393	40	31.5	1024	4	US-09-562-737-41	Sequence 41, Appl	466	39	30.7	275	4	US-09-107-532A-6200	Sequence 6200, Ap
394	40	31.5	1024	4	US-09-562-737-44	Sequence 44, Appl	467	39	30.7	281	4	US-09-949-016-8397	Sequence 8397, Ap
395	40	31.5	1052	4	US-09-949-016-11508	Sequence 11508, A	468	39	30.7	289	4	US-09-198-452A-728	Sequence 728, Appl
396	40	31.5	1154	4	US-09-963-137-203	Sequence 203, Appl	469	39	30.7	298	1	US-08-393-985-10	Sequence 10, Appl
397	40	31.5	1231	4	US-09-107-532A-5150	Sequence 5150, Ap	470	39	30.7	301	1	US-08-393-985-12	Sequence 12, Appl
398	40	31.5	1735	4	US-09-902-540-14547	Sequence 14547, A	471	39	30.7	301	4	US-09-248-796A-36282	Sequence 26282, A
399	40	31.5	1788	2	US-08-962-284-2	Sequence 2, Appl1	472	39	30.7	301	4	US-09-538-092-1302	Sequence 1302, Ap
400	40	31.5	2509	4	US-09-252-991A-16642	Sequence 16642, A	473	39	30.7	308	4	US-09-489-032A-9249	Sequence 9249, Ap
401	40	31.5	2636	4	US-09-252-991A-25753	Sequence 25753, A	474	39	30.7	321	4	US-09-328-352-4883	Sequence 4883, Ap
402	39.5	31.1	663	4	US-09-248-796A-21270	Sequence 21270, A	475	39	30.7	326	4	US-09-489-032A-7348	Sequence 7348, Ap
403	39.5	31.1	78	4	US-09-621-976-7280	Sequence 7280, Ap	476	39	30.7	358	4	US-09-248-796A-19081	Sequence 19081, A
404	39.5	31.1	112	4	US-09-603-208A-38	Sequence 38, Appl	477	39	30.7	360	4	US-09-710-279-2150	Sequence 2150, A
405	39.5	31.1	139	4	US-09-538-092-693	Sequence 693, Appl	478	39	30.7	363	4	US-09-107-532A-7017	Sequence 7017, Ap
406	39.5	31.1	247	4	US-09-328-352-5648	Sequence 5648, Ap	479	39	30.7	367	3	US-08-630-915A-3678	Sequence 3678, Ap
407	39.5	31.1	290	3	US-08-936-165A-462	Sequence 462, Appl	480	39	30.7	368	4	US-09-879-957-20	Sequence 20, Appl
408	39.5	31.1	329	3	US-09-308-003-14	Sequence 14, Appl1	481	39	30.7	368	4	US-09-879-957-20	Sequence 6301, Ap
409	39.5	31.1	339	4	US-09-107-532A-4033	Sequence 4033, Ap	482	39	30.7	373	4	US-09-949-016-6301	Sequence 7535, Ap
410	39.5	31.1	406	4	US-09-543-681A-6072	Sequence 6072, Ap	483	39	30.7	373	4	US-09-949-016-7535	Sequence 2106, Ap
411	39.5	31.1	426	1	US-08-197-792-41	Sequence 41, Appl	484	39	30.7	376	4	US-09-710-279-2106	Sequence 2106, Ap
412	39.5	31.1	426	1	US-08-459-850-41	Sequence 41, Appl	485	39	30.7	390	3	US-09-108-020-36	Sequence 36, Appl
413	39.5	31.1	455	4	US-08-459-214-41	Sequence 41, Appl1	486	39	30.7	390	4	US-09-901-151-5	Sequence 5, Appl1
414	39.5	31.1	455	4	US-09-949-016-11525	Sequence 11525, A	487	39	30.7	390	4	US-09-901-151-6	Sequence 36, Appl
415	39.5	31.1	511	4	US-09-489-039A-9306	Sequence 9206, Ap	488	39	30.7	390	4	US-09-685-296-36	Sequence 2, Appl1
416	39.5	31.1	528	3	US-08-889-841B-44	Sequence 5413, Ap	489	39	30.7	397	4	US-09-901-151-2	Sequence 691, App
417	39.5	31.1	528	3	US-08-889-841B-44	Sequence 44, Appl	490	39	30.7	407	4	US-09-438-185A-691	Sequence 21, Appl
418	39.5	31.1	528	4	US-09-419-362-44	Sequence 44, Appl	491	39	30.7	408	1	US-07-951-715A-21	Sequence 21, Appl
419	39.5	31.1	575	4	US-09-248-796A-17643	Sequence 17643, A	492	39	30.7	408	2	US-08-459-448A-21	Sequence 21, Appl
420	39.5	31.1	587	4	US-09-646-028-50	Sequence 50, Appl	493	39	30.7	408	3	US-08-459-595A-21	Sequence 21, Appl
421	39.5	31.1	595	4	US-09-646-028-56	Sequence 56, Appl	494	39	30.7	408	3	US-08-459-595A-21	Sequence 21, Appl
422	39.5	31.1	601	4	US-09-646-028-52	Sequence 52, Appl	495	39	30.7	408	3	US-08-459-444-21	Sequence 21, Appl
423	39.5	31.1	608	4	US-09-603-208A-36	Sequence 36, Appl	496	39	30.7	408	3	US-09-547-422-21	Sequence 21, Appl
424	39.5	31.1	844	4	US-09-991-258-19	Sequence 19, Appl	497	39	30.7	408	4	US-09-988-462-21	Sequence 21, Appl
425	39.5	31.1	855	1	US-08-022-835-6	Sequence 6, Appl1	498	39	30.7	414	4	US-09-901-151-4	Sequence 40, Appl
426	39.5	31.1	855	1	US-08-388-809-6	Sequence 6, Appl1	499	39	30.7	426	3	US-08-676-444-40	Sequence 40, Appl
427	39.5	31.1	855	2	US-08-647-714-6	Sequence 6, Appl1	500	39	30.7	430	4	US-09-328-352-5453	Sequence 7505, Ap
428	39.5	31.1	884	4	US-09-328-352-4598	Sequence 4598, Ap	501	39	30.7	453	4	US-09-543-681A-7700	Sequence 7700, Ap
429	39.5	31.1	1044	4	US-09-107-532A-5229	Sequence 5229, Ap	502	39	30.7	457	4	US-09-248-796A-32325	Sequence 23295, A
430	39.5	31.1	2396	3	US-08-157-005-2	Sequence 2, Appl1	503	39	30.7	464	1	US-07-951-715A-22	Sequence 22, Appl
431	39.5	31.1	2396	3	US-08-747-863-2	Sequence 2, Appl1	504	39	30.7	464	2	US-08-459-448A-22	Sequence 22, Appl
432	39.5	31.1	2396	4	US-09-565-864-2	Sequence 2, Appl1	505	39	30.7	464	3	US-08-459-595A-22	Sequence 22, Appl
433	39.5	31.1	2396	4	US-10-226-065-2	Sequence 2, Appl1	506	39	30.7	464	3	US-08-459-504B-22	Sequence 22, Appl
434	39	30.7	14	1	US-07-872-644-28	Sequence 28, Appl	507	39	30.7	464	3	US-08-459-444-22	Sequence 0, Appl1
435	39	30.7	14	1	US-08-297-494-28	Sequence 28, Appl	508	39	30.7	464	3	US-09-547-422-22	Sequence 0, Appl1
436	39	30.7	14	1	US-08-297-510-28	Sequence 28, Appl	509	39	30.7	464	4	US-09-988-462-22	Sequence 22, Appl
437	39	30.7	14	1	US-08-479-532-28	Sequence 28, Appl	510	39	30.7	483	4	US-09-949-016-7399	Sequence 7399, Ap
438	39	30.7	14	1	US-08-455-526-28	Sequence 28, Appl	511	39	30.7	494	4	US-09-248-796A-15974	Sequence 15974, A
439	39	30.7	14	1	US-08-455-525-28	Sequence 28, Appl	512	39	30.7	539	2	US-08-978-182-3	Sequence 3, Appl1
440	39	30.7	14	3	US-09-139-491-28	Sequence 28, Appl	513	39	30.7	539	2	US-09-205-681-3	Sequence 3, Appl1
441	39	30.7	14	4	US-09-883-825-28	Sequence 28, Appl	514	39	30.7	541	4	US-08-828-199A-2	Sequence 2, Appl1
442	39	30.7	14	5	PCT-US92-03222-28	Sequence 28, Appl	515	39	30.7	545	4	US-09-604-957-4	Sequence 4, Appl1
443	39	30.7	75	2	US-08-715-527-4	Sequence 4, Appl1	516	39	30.7	547	2	US-08-467-822-35	Sequence 35, Appl
444	39	30.7	75	5	PCT-US95-06406A-4	Sequence 4, Appl1	517	39	30.7	547	3	US-08-432-697-35	Sequence 35, Appl
445	39	30.7	83	3	US-09-134-001C-5335	Sequence 5335, Ap	518	39	30.7	547	3	US-08-466-248-35	Sequence 35, Appl
446	39	30.7	93	4	US-09-107-433-3132	Sequence 3132, Ap	519	39	30.7	561	1	US-09-640-305-2	Sequence 2, Appl1
447	39	30.7	95	1	US-07-987-272A-9	Sequence 9, Appl1	520	39	30.7	561	1	US-08-360-672-2	Sequence 2, Appl1
448	39	30.7	97	4	US-09-461-912A-48	Sequence 48, Appl	521	39	30.7	573	2	US-08-706-209-1	Sequence 1, Appl1
449	39	30.7	104	1	US-08-052-681-2	Sequence 2, Appl1	522	39	30.7	573	3	US-08-981-787-1	Sequence 1, Appl1
450	39	30.7	134	4	US-10-000-489-2	Sequence 2, Appl1	523	39	30.7	573	3	US-08-461-722-1	Sequence 1, Appl1
451	39	30.7	136	4	US-09-248-796A-18002	Sequence 18002, A	524	39	30.7	573	3	US-08-336-251-1	Sequence 1, Appl1
452	39	30.7	156	4	US-09-393-627B-26	Sequence 26, Appl	525	39	30.7	573	4	US-09-468-041-1	Sequence 1, Appl1
453	39	30.7	170	4	US-09-134-000C-4756	Sequence 4756, Ap	526	39	30.7	573	4	US-08-981-861-1	Sequence 1, Appl1
454	39	30.7	170	4	US-09-428-796A-19501	Sequence 19501, A	527	39	30.7	573	4	US-09-613-743A-1	Sequence 1, Appl1
455	39	30.7	171	4	US-09-328-352-4783	Sequence 4783, Ap	528	39	30.7	573	4	US-09-847-637B-7	Sequence 7, Appl1
456	39	30.7	198	4	US-09-328-352-6068	Sequence 6068, Ap	529	39	30.7	573	4	US-09-847-637B-8	Sequence 8, Appl1
457	39	30.7	223	4	US-09-543-681A-5667	Sequence 5667, Ap	530	39	30.7	573	4	US-09-809-745-2	Sequence 2, Appl1
458	39	30.7	224	4	US-09-540-236-3782	Sequence 3782, Ap	531	39	30.7	573	5	PCT-US94-06362-1	Sequence 1, Appl1
459	39	30.7	229	4	US-09-270-767-32090	Sequence 32090, A	532	39	30.7	573	5	PCT-US96-11373-1	Sequence 1, Appl1
460	39	30.7	229	4	US-09-270-767-47307	Sequence 47307, A	533	39	30.7	573	5	PCT-US96-11373-1	Sequence 1, Appl1
461	39	30.7	237	4	US-09-107-532A-6583	Sequence 6583, Ap	534	39	30.7	604	4	US-09-949-016-6585	Sequence 6585, Ap
462	39	30.7	241	3	US-08-896-933-32	Sequence 32, Appl	535	39	30.7	604	4	US-09-949-016-10250	Sequence 10250, A
463	39	30.7	241	3	US-09-114-235-32	Sequence 32, Appl	536	39	30.7	637	4	US-09-949-016-10426	Sequence 10426, A
464	39	30.7	241	4	US-09-108-008B-32	Sequence 32, Appl	537	39	30.7	657	4	US-09-949-016-6174	Sequence 6174, Ap
465	39	30.7	244	4	US-09-710-279-994	Sequence 994, Appl	538	39	30.7	678	4	US-09-949-016-10001	Sequence 10001, A



539	39	30.7	691	4	US-09-830-217-12	Sequence 12, Appl	612	38.5	30.3	450	4	US-09-252-991A-24440	Sequence 24440, A
540	39	30.7	691	4	US-10-278-946-12	Sequence 12, Appl	613	38.5	30.3	476	4	US-09-536-977-74	Sequence 74, Appl
541	39	30.7	703	3	US-08-910-925-4	Sequence 4, Appl	614	38.5	30.3	494	4	US-09-252-991A-28022	Sequence 28022, A
542	39	30.7	717	3	US-08-910-925-1	Sequence 1, Appl	615	38.5	30.3	536	4	US-09-595-857B-31	Sequence 31, Appl
543	39	30.7	743	3	US-08-910-925-3	Sequence 3, Appl	616	38.5	30.3	602	4	US-09-248-796A-19204	Sequence 19204, A
544	39	30.7	743	4	US-09-949-016-6261	Sequence 6261, Ap	617	38.5	30.3	635	4	US-09-536-977-68	Sequence 68, Appl
545	39	30.7	748	4	US-09-585-858-25	Sequence 25, Appl	618	38.5	30.3	657	3	US-09-256-194-2	Sequence 2, Appl
546	39	30.7	748	4	US-10-270-878-25	Sequence 25, Appl	619	38.5	30.3	665	3	US-08-448-603A-32	Sequence 32, Appl
547	39	30.7	768	2	US-08-222-617A-5	Sequence 1, Appl	620	38.5	30.3	665	3	US-09-492-739-32	Sequence 32, Appl
548	39	30.7	784	4	US-09-724-586A-1	Sequence 1, Appl	621	38.5	30.3	665	3	US-09-492-739-32	Sequence 32, Appl
549	39	30.7	784	4	US-09-600-823-1	Sequence 1, Appl	622	38.5	30.3	665	3	US-09-492-739-32	Sequence 32, Appl
550	39	30.7	784	4	US-09-724-666-1	Sequence 1, Appl	623	38.5	30.3	675	3	US-09-134-001C-5219	Sequence 5219, Ap
551	39	30.7	972	4	US-09-710-092-2	Sequence 2, Appl	624	38.5	30.3	687	4	US-09-536-977-70	Sequence 70, Appl
552	39	30.7	973	4	US-09-392-714A-24	Sequence 24, Appl	625	38.5	30.3	715	4	US-09-328-352-6830	Sequence 6830, Ap
553	39	30.7	976	3	US-09-104-324B-4	Sequence 4, Appl	626	38.5	30.3	732	4	US-08-671-757A-7	Sequence 7, Appl
554	39	30.7	976	4	US-09-538-092-1339	Sequence 1339, Ap	627	38.5	30.3	732	4	US-08-671-757A-8	Sequence 8, Appl
555	39	30.7	989	4	US-09-902-540-1598	Sequence 15948, A	628	38.5	30.3	732	4	US-09-015-078-7	Sequence 7, Appl
556	39	30.7	1018	4	US-10-101-664A-909	Sequence 909, Ap	629	38.5	30.3	732	4	US-09-015-078-8	Sequence 8, Appl
557	39	30.7	1056	4	US-09-710-092-6	Sequence 6, Appl	630	38.5	30.3	820	4	US-09-536-977-72	Sequence 72, Appl
558	39	30.7	1130	2	US-08-460-309-2	Sequence 2, Appl	631	38.5	30.3	837	1	US-07-923-976-2	Sequence 2, Appl
559	39	30.7	1130	2	US-08-125-077-2	Sequence 2, Appl	632	38.5	30.3	857	2	US-08-448-603A-30	Sequence 30, Appl
560	39	30.7	1130	6	5444158-2	Patent No. 5444158	633	38.5	30.3	857	3	US-09-492-739-30	Sequence 30, Appl
561	39	30.7	1130	6	5444158-2	Patent No. 5444158	634	38.5	30.3	857	3	US-09-492-739-30	Sequence 30, Appl
562	39	30.7	1173	4	US-09-543-681A-7965	Sequence 7965, Ap	635	38.5	30.3	857	4	US-09-566-931A-30	Sequence 30, Appl
563	39	30.7	1237	1	US-08-241-853-2	Sequence 2, Appl	636	38.5	30.3	1019	4	US-09-252-991A-24417	Sequence 24417, A
564	39	30.7	1237	2	US-08-850-917-2	Sequence 2, Appl	637	38.5	30.3	1048	4	US-08-887-534A-85	Sequence 85, Appl
565	39	30.7	1240	3	US-08-930-996A-4	Sequence 4, Appl	638	38.5	30.3	1048	4	US-09-527-431-85	Sequence 85, Appl
566	39	30.7	1270	4	US-09-710-092-10	Sequence 10, Appl	639	38.5	30.3	1048	4	US-09-446-861-85	Sequence 85, Appl
567	39	30.7	1354	3	US-08-685-871-2	Sequence 2, Appl	640	38	29.9	37	3	US-08-974-549A-68	Sequence 68, Appl
568	39	30.7	1426	4	US-09-710-092-14	Sequence 14, Appl	641	38	29.9	37	3	US-08-974-549A-210	Sequence 210, Ap
569	39	30.7	1430	3	US-09-008-172-2	Sequence 6, Appl	642	38	29.9	37	4	US-08-912-951-68	Sequence 68, Appl
570	39	30.7	1430	3	US-09-210-361-6	Sequence 6, Appl	643	38	29.9	37	4	US-09-402-181B-68	Sequence 68, Appl
571	39	30.7	1430	4	US-09-740-374-6	Sequence 6, Appl	644	38	29.9	37	4	US-09-402-181B-210	Sequence 210, Ap
572	39	30.7	1630	4	US-09-902-540-15581	Sequence 15581, A	645	38	29.9	37	4	US-09-721-456-68	Sequence 68, Appl
573	39	30.7	1630	4	US-09-538-092-1077	Sequence 1077, Ap	646	38	29.9	37	4	US-09-721-456-210	Sequence 210, Ap
574	39	30.7	1960	4	US-09-949-016-10872	Sequence 10872, A	647	38	29.9	40	1	US-08-444-005-27	Sequence 27, Appl
575	39	30.7	3072	4	US-09-961-403-7	Sequence 7, Appl	648	38	29.9	42	4	US-09-614-847-134	Sequence 134, Ap
576	39	30.7	3084	4	US-09-562-702A-12	Sequence 12, Appl	649	38	29.9	44	4	US-09-614-847-149	Sequence 149, Ap
577	39	30.7	3084	4	US-09-562-702A-8	Sequence 8, Appl	650	38	29.9	45	2	US-08-219-237B-10	Sequence 10, Appl
578	39	30.7	3089	4	US-09-562-702A-4	Sequence 4, Appl	651	38	29.9	48	4	US-09-614-847-135	Sequence 135, Ap
579	39	30.7	3106	4	US-09-562-702A-10	Sequence 10, Appl	652	38	29.9	50	4	US-09-614-847-150	Sequence 150, Ap
580	39	30.7	3110	4	US-09-562-702A-2	Sequence 2, Appl	653	38	29.9	54	3	US-08-851-843A-21	Sequence 21, Appl
581	39	30.7	3110	4	US-09-562-702A-6	Sequence 6, Appl	654	38	29.9	54	3	US-08-854-050-21	Sequence 21, Appl
582	39	30.7	3110	4	US-09-561-709B-7	Sequence 7, Appl	655	38	29.9	54	3	US-09-430-323-21	Sequence 21, Appl
583	39	30.7	3110	4	US-09-917-254-86	Sequence 86, Appl	656	38	29.9	54	4	US-09-766-253-21	Sequence 21, Appl
584	39	30.7	3110	4	US-09-949-016-5937	Sequence 5937, Ap	657	38	29.9	63	3	US-08-894-626-1	Sequence 1, Appl
585	39	30.7	3111	2	US-08-460-309-4	Sequence 4, Appl	658	38	29.9	64	4	US-09-248-796A-24105	Sequence 24105, A
586	39	30.7	3111	2	US-08-125-077-4	Sequence 4, Appl	659	38	29.9	65	2	US-08-867-087B-31	Sequence 31, Appl
587	38.5	30.3	54	4	US-09-536-977-16	Sequence 16, Appl	660	38	29.9	68	4	US-09-527-236A-22	Sequence 22, Appl
588	38.5	30.3	121	4	US-09-248-796A-19888	Sequence 19888, A	661	38	29.9	70	4	US-09-756-854-22	Sequence 22, Appl
589	38.5	30.3	124	4	US-09-536-977-44	Sequence 44, Appl	662	38	29.9	70	4	US-09-159-277A-5	Sequence 5, Appl
590	38.5	30.3	129	4	US-09-583-110-3496	Sequence 3496, Ap	663	38	29.9	70	4	US-08-844-691A-5	Sequence 5, Appl
591	38.5	30.3	134	4	US-09-107-433-4837	Sequence 4837, Ap	664	38	29.9	77	4	US-08-828-683A-24	Sequence 24, Appl
592	38.5	30.3	132	4	US-09-107-532A-6870	Sequence 6870, Ap	665	38	29.9	84	4	US-09-107-532A-6677	Sequence 6677, Ap
593	38.5	30.3	217	4	US-09-248-796A-21994	Sequence 21994, A	666	38	29.9	84	4	US-09-069-827B-119	Sequence 119, Ap
594	38.5	30.3	218	4	US-09-328-352-6389	Sequence 6389, Ap	667	38	29.9	85	3	US-09-042-785A-26	Sequence 26, Appl
595	38.5	30.3	218	4	US-09-583-110-4540	Sequence 4540, Ap	668	38	29.9	99	4	US-09-370-767-31885	Sequence 31885, A
596	38.5	30.3	222	4	US-09-107-433-4007	Sequence 4007, Ap	669	38	29.9	99	4	US-09-370-767-47102	Sequence 47102, A
597	38.5	30.3	227	4	US-09-328-352-6938	Sequence 6938, Ap	670	38	29.9	120	1	US-08-233-788A-57	Sequence 57, Appl
598	38.5	30.3	234	4	US-09-270-767-43273	Sequence 43273, A	671	38	29.9	124	4	US-09-248-796A-15593	Sequence 15593, A
599	38.5	30.3	308	4	US-09-804-778A-2	Sequence 2, Appl	672	38	29.9	127	4	US-09-107-532A-5159	Sequence 5159, Ap
600	38.5	30.3	324	4	US-09-543-681A-6167	Sequence 6167, Ap	673	38	29.9	137	3	US-09-446-504-34	Sequence 34, Appl
601	38.5	30.3	324	4	US-08-858-003-34	Sequence 34, Appl	674	38	29.9	137	3	US-09-712-266-34	Sequence 34, Appl
602	38.5	30.3	345	3	US-09-078-166-34	Sequence 34, Appl	675	38	29.9	143	4	US-09-328-352-7316	Sequence 7316, Ap
603	38.5	30.3	345	3	US-08-997-467-34	Sequence 34, Appl	676	38	29.9	151	1	US-08-233-788A-159	Sequence 59, Appl
604	38.5	30.3	345	3	US-08-997-467-34	Sequence 34, Appl	677	38	29.9	152	4	US-09-248-796A-15593	Sequence 15593, A
605	38.5	30.3	364	2	US-08-204-288-2	Sequence 2, Appl	678	38	29.9	153	4	US-09-107-532A-5159	Sequence 5159, Ap
606	38.5	30.3	365	2	US-08-715-325-2	Sequence 2, Appl	679	38	29.9	156	4	US-09-710-279-2848	Sequence 2848, Ap
607	38.5	30.3	421	4	US-09-591-279A-31	Sequence 31, Appl	680	38	29.9	158	2	US-08-414-938A-2	Sequence 2, Appl
608	38.5	30.3	425	4	US-09-536-977-46	Sequence 46, Appl	681	38	29.9	160	4	US-09-370-767-57595	Sequence 57595, A
609	38.5	30.3	425	4	US-09-536-977-48	Sequence 48, Appl	682	38	29.9	163	4	US-09-549-016-9631	Sequence 9631, Ap
610	38.5	30.3	425	4	US-09-536-977-50	Sequence 50, Appl	683	38	29.9	165	4	US-09-732-210-131	Sequence 131, Ap
611	38.5	30.3	425	4	US-09-536-977-52	Sequence 52, Appl	684	38	29.9	165	4	US-09-732-210-565	Sequence 565, Ap

685	38	29.9	165	4	US-09-540-236-3123	Sequence 3123, Ap	758	38	29.9	335	2	US-08-409-338-1	Sequence 1, Appl1
686	38	29.9	167	4	US-09-710-279-408	Sequence 408, App	759	38	29.9	335	3	US-08-815-469-6	Sequence 6, Appl1
687	38	29.9	175	4	US-09-107-433-3909	Sequence 3909, Ap	760	38	29.9	335	3	US-09-290-640-2	Sequence 2, Appl1
688	38	29.9	186	4	US-09-134-000C-5379	Sequence 5379, Ap	761	38	29.9	335	3	US-09-006-353A-7	Sequence 7, Appl1
689	38	29.9	189	4	US-09-270-767-31816	Sequence 31816, A	762	38	29.9	335	3	US-08-468-560C-2	Sequence 2, Appl1
690	38	29.9	189	4	US-09-270-767-47033	Sequence 47033, A	763	38	29.9	335	3	US-09-180-100-20	Sequence 20, Appl1
691	38	29.9	201	4	US-09-489-039A-7394	Sequence 7394, Ap	764	38	29.9	335	4	US-09-565-918-3	Sequence 3, Appl1
692	38	29.9	205	4	US-09-107-532A-4830	Sequence 4830, Ap	765	38	29.9	335	4	US-09-573-986-7	Sequence 7, Appl1
693	38	29.9	207	4	US-09-107-532A-4500	Sequence 4500, Ap	766	38	29.9	335	4	US-09-665-618B-2	Sequence 2, Appl1
694	38	29.9	207	4	US-09-270-767-35136	Sequence 35136, A	767	38	29.9	335	4	US-09-557-908-6	Sequence 6, Appl1
695	38	29.9	207	4	US-09-270-767-50353	Sequence 50353, A	768	38	29.9	335	4	US-09-874-138-4	Sequence 4, Appl1
696	38	29.9	208	3	US-09-134-001C-4697	Sequence 4697, Ap	769	38	29.9	335	4	US-09-333-966-6	Sequence 6, Appl1
697	38	29.9	215	4	US-09-502-540-11802	Sequence 11802, A	770	38	29.9	335	4	US-09-949-016-5877	Sequence 5877, Ap
698	38	29.9	223	4	US-09-107-532A-5762	Sequence 5762, Ap	771	38	29.9	335	5	PCT-US95-17083-2	Sequence 2, Appl1
699	38	29.9	228	4	US-09-710-279-3190	Sequence 3190, Ap	772	38	29.9	338	4	US-09-248-796A-15934	Sequence 15934, A
700	38	29.9	229	4	US-09-270-767-43242	Sequence 43242, A	773	38	29.9	345	3	US-09-120-365-73	Sequence 73, Appl1
701	38	29.9	230	2	US-08-844-120-3	Sequence 3, Appl1	774	38	29.9	345	3	US-09-515-039-73	Sequence 73, Appl1
702	38	29.9	230	2	US-09-022-940-5	Sequence 5, Appl1	775	38	29.9	345	3	US-08-827-171B-7	Sequence 7, Appl1
703	38	29.9	230	3	US-09-216-001-3	Sequence 3, Appl1	776	38	29.9	345	4	US-09-598-062-7	Sequence 515, Ap
704	38	29.9	230	3	US-09-216-386-5	Sequence 5, Appl1	777	38	29.9	345	4	US-09-543-681A-5315	Sequence 5315, Ap
705	38	29.9	230	3	US-08-878-862-3	Sequence 3, Appl1	778	38	29.9	351	1	US-09-500-651-2	Sequence 2, Appl1
706	38	29.9	230	3	US-09-213-394-3	Sequence 3, Appl1	779	38	29.9	351	1	US-08-402-217A-2	Sequence 2, Appl1
707	38	29.9	230	4	US-09-988-982-3	Sequence 3, Appl1	780	38	29.9	351	1	US-08-700-178-2	Sequence 2, Appl1
708	38	29.9	234	3	US-09-503-391-22	Sequence 22, Appl1	781	38	29.9	351	2	US-08-813-591-2	Sequence 2, Appl1
709	38	29.9	236	4	US-09-489-039A-11850	Sequence 11850, A	782	38	29.9	351	3	US-08-995-654-2	Sequence 2, Appl1
710	38	29.9	246	3	US-09-451-117-2	Sequence 2, Appl1	783	38	29.9	355	4	US-09-489-039A-12174	Sequence 12174, A
711	38	29.9	246	3	US-09-888-655-2	Sequence 2, Appl1	784	38	29.9	356	4	US-09-489-092-353	Sequence 353, App
712	38	29.9	246	4	US-09-888-501-2	Sequence 2, Appl1	785	38	29.9	361	4	US-09-252-991A-10426	Sequence 30426, A
713	38	29.9	248	4	US-09-270-767-47468	Sequence 47468, A	786	38	29.9	362	4	US-09-134-000C-4306	Sequence 4306, Ap
714	38	29.9	249	4	US-09-270-767-32251	Sequence 32251, A	787	38	29.9	369	4	US-09-328-355-5957	Sequence 3557, Ap
715	38	29.9	250	2	US-08-867-087B-13	Sequence 13, Appl1	788	38	29.9	375	4	US-09-107-532A-3754	Sequence 3754, Ap
716	38	29.9	259	4	US-09-248-796A-16308	Sequence 16308, A	789	38	29.9	383	3	US-09-134-001C-3701	Sequence 3701, Ap
717	38	29.9	261	4	US-09-248-796A-26725	Sequence 26725, A	790	38	29.9	383	3	US-09-504-445-4	Sequence 4, Appl1
718	38	29.9	261	6	5320958-3	Patent No. 5320958	791	38	29.9	383	4	US-09-710-279-3110	Sequence 3110, Ap
719	38	29.9	261	6	5320958-3	Patent No. 5320958	792	38	29.9	384	4	US-09-252-991A-19333	Sequence 19333, A
720	38	29.9	265	4	US-09-710-279-174	Sequence 174, App	793	38	29.9	386	4	US-09-248-796A-15067	Sequence 15067, A
721	38	29.9	266	3	US-08-815-809-5	Sequence 5, Appl1	794	38	29.9	386	4	US-09-248-796A-17815	Sequence 17815, A
722	38	29.9	273	4	US-09-248-796A-16521	Sequence 16521, A	795	38	29.9	387	4	US-09-949-016-7720	Sequence 7720, Ap
723	38	29.9	273	1	US-07-688-352C-30	Sequence 30, Appl1	796	38	29.9	388	2	US-08-382-505-2	Sequence 2, Appl1
724	38	29.9	279	2	US-08-474-379C-30	Sequence 30, Appl1	797	38	29.9	391	4	US-09-270-767-42309	Sequence 42309, A
725	38	29.9	279	3	US-09-146-249A-30	Sequence 30, Appl1	798	38	29.9	396	1	US-07-757-390-14	Sequence 14, Appl1
726	38	29.9	279	3	US-08-206-188B-30	Sequence 30, Appl1	799	38	29.9	396	1	US-08-442-282-14	Sequence 14, Appl1
727	38	29.9	279	5	PCT-US91-02711-29	Sequence 29, Appl1	800	38	29.9	396	1	US-08-442-282-14	Sequence 14, Appl1
728	38	29.9	280	2	US-08-816-155B-43	Sequence 43, Appl1	801	38	29.9	396	2	US-08-939-727-14	Sequence 14, Appl1
729	38	29.9	280	3	US-09-079-587-43	Sequence 43, Appl1	802	38	29.9	396	3	US-09-108-020-38	Sequence 38, Appl1
730	38	29.9	294	4	US-09-328-352-7430	Sequence 7430, Ap	803	38	29.9	396	4	US-09-800-722-207	Sequence 207, Appl1
731	38	29.9	306	4	US-09-583-110-2708	Sequence 2708, Ap	804	38	29.9	396	4	US-09-685-296-38	Sequence 38, Appl1
732	38	29.9	309	4	US-09-538-092-405	Sequence 405, App	805	38	29.9	397	4	US-09-079-030-123	Sequence 123, Appl1
733	38	29.9	312	3	US-09-188-930-142	Sequence 142, App	806	38	29.9	400	3	US-09-150-347-2	Sequence 2, Appl1
734	38	29.9	312	4	US-09-312-283C-142	Sequence 142, App	807	38	29.9	400	4	US-09-665-311-2	Sequence 2, Appl1
735	38	29.9	313	3	US-08-836-561-106	Sequence 106, App	808	38	29.9	415	4	US-09-248-796A-16172	Sequence 16172, A
736	38	29.9	314	4	US-09-434-122-106	Sequence 106, App	809	38	29.9	416	4	US-07-757-390-13	Sequence 13, Appl1
737	38	29.9	314	1	US-08-589-446-6	Sequence 6, Appl1	810	38	29.9	420	1	US-07-757-390-13	Sequence 13, Appl1
738	38	29.9	314	1	US-08-444-882-6	Sequence 6, Appl1	811	38	29.9	420	1	US-08-442-282-13	Sequence 13, Appl1
739	38	29.9	314	1	US-08-444-231-19	Sequence 19, Appl1	812	38	29.9	420	1	US-08-442-281-13	Sequence 13, Appl1
740	38	29.9	314	1	US-08-152-443A-19	Sequence 19, Appl1	813	38	29.9	420	2	US-08-939-727-13	Sequence 13, Appl1
741	38	29.9	314	2	US-08-389-459A-6	Sequence 6, Appl1	814	38	29.9	420	2	US-09-886-319A-24	Sequence 24, Appl1
742	38	29.9	314	3	US-08-987-867A-6	Sequence 6, Appl1	815	38	29.9	420	4	US-09-949-016-5588	Sequence 5588, Ap
743	38	29.9	314	5	PCT-US95-17083-4	Sequence 4, Appl1	816	38	29.9	425	3	US-09-109-204-31	Sequence 31, Appl1
744	38	29.9	333	3	US-09-134-001C-3339	Sequence 3339, Ap	817	38	29.9	425	4	US-09-490-032-31	Sequence 31, Appl1
745	38	29.9	327	3	US-08-679-493A-71	Sequence 71, Appl1	818	38	29.9	426	4	US-09-949-016-10854	Sequence 10854, A
746	38	29.9	327	4	US-08-679-493A-72	Sequence 72, Appl1	819	38	29.9	427	3	US-09-690-265-1	Sequence 1, Appl1
747	38	29.9	327	4	US-09-585-858-53	Sequence 53, Appl1	820	38	29.9	427	4	US-09-949-016-8614	Sequence 8614, Ap
748	38	29.9	327	4	US-10-270-878-53	Sequence 53, Appl1	821	38	29.9	427	4	US-09-949-016-8620	Sequence 8620, Ap
749	38	29.9	329	2	US-08-813-477-2	Sequence 2, Appl1	822	38	29.9	437	4	US-09-134-001C-5342	Sequence 5342, Ap
750	38	29.9	329	2	US-08-813-477-4	Sequence 4, Appl1	823	38	29.9	441	4	US-09-134-000C-6563	Sequence 6563, Ap
751	38	29.9	331	3	US-09-086-483A-3	Sequence 3, Appl1	824	38	29.9	452	4	US-09-543-681A-6544	Sequence 6544, Ap
752	38	29.9	331	4	US-09-580-212-3	Sequence 3, Appl1	825	38	29.9	457	4	US-09-270-767-44381	Sequence 44381, A
753	38	29.9	331	4	US-09-769-402-3	Sequence 3, Appl1	826	38	29.9	458	4	US-09-134-001C-4663	Sequence 4663, Ap
754	38	29.9	335	1	US-07-947-130-2	Sequence 2, Appl1	827	38	29.9	459	3	US-09-759-595-3	Sequence 3, Appl1
755	38	29.9	335	1	US-08-421-822-2	Sequence 2, Appl1	828	38	29.9	469	3	US-09-188-930-339	Sequence 339, App
756	38	29.9	335	1	US-08-421-823-2	Sequence 2, Appl1	829	38	29.9	469	3	US-09-312-283C-339	Sequence 339, App
757	38	29.9	335	2	US-08-219-237B-2	Sequence 2, Appl1	830	38	29.9	471	4	US-09-583-110-3667	Sequence 3667, Ap

831	38	29.9	471	4	US-08-378-213-2	Sequence 2, Appl1	904	38	29.9	850	4	US-09-952-060-4	Sequence 4, Appl1
832	38	29.9	471	4	US-08-378-213-4	Sequence 5, Appl1	905	38	29.9	850	4	US-09-248-796A-18585	Sequence 18585, A
833	38	29.9	471	4	US-08-378-213-5	Sequence 6, Appl1	906	38	29.9	850	3	US-09-150-460B-7	Sequence 7, Appl1
834	38	29.9	471	4	US-08-378-213-6	Sequence 6, Appl1	907	38	29.9	875	4	US-09-952-060-6	Sequence 6, Appl1
835	38	29.9	471	4	US-09-120-044-3	Sequence 3, Appl1	908	38	29.9	875	4	US-09-952-060-8	Sequence 8, Appl1
836	38	29.9	471	4	US-09-120-044-4	Sequence 4, Appl1	909	38	29.9	875	4	US-09-949-016-8492	Sequence 8492, Ap
837	38	29.9	472	4	US-09-107-433-3566	Sequence 3566, Ap	910	38	29.9	900	4	US-09-107-533A-5284	Sequence 5284, Ap
838	38	29.9	480	2	US-08-913-477-17	Sequence 17, Appl	911	38	29.9	904	3	US-09-198-484-2	Sequence 2, Appl1
839	38	29.9	493	4	US-09-134-000C-4034	Sequence 4034, Ap	912	38	29.9	906	2	US-08-609-230A-9	Sequence 9, Appl1
840	38	29.9	493	4	US-09-198-484-4	Sequence 4, Appl1	913	38	29.9	906	4	US-09-328-352-6037	Sequence 6037, Ap
841	38	29.9	501	2	US-08-913-477-23	Sequence 23, Appl	914	38	29.9	907	3	US-08-990-140-4	Sequence 4, Appl1
842	38	29.9	502	4	US-09-635-872A-13	Sequence 13, Appl	915	38	29.9	907	3	US-09-546-238-4	Sequence 28964, A
843	38	29.9	502	4	US-09-636-077A-13	Sequence 13, Appl	916	38	29.9	913	2	US-07-743-357-22	Sequence 22, Appl
844	38	29.9	502	4	US-09-636-060C-13	Sequence 13, Appl	917	38	29.9	915	4	US-09-543-681A-5334	Sequence 5334, Ap
845	38	29.9	502	4	US-09-986-552-13	Sequence 13, Appl	918	38	29.9	921	3	US-09-514-599-2	Sequence 2, Appl1
846	38	29.9	502	4	US-09-110-279-3136	Sequence 3136, Ap	919	38	29.9	921	4	US-09-996-024-2	Sequence 2, Appl1
847	38	29.9	502	4	US-09-636-596C-13	Sequence 13, Appl	920	38	29.9	923	4	US-09-252-991A-28964	Sequence 28964, A
848	38	29.9	502	4	US-10-023-894-16	Sequence 16, Appl	921	38	29.9	925	4	US-09-540-235-3586	Sequence 3586, Ap
849	38	29.9	502	4	US-10-306-686-13	Sequence 13, Appl	922	38	29.9	940	3	US-08-810-712-7	Sequence 7, Appl1
850	38	29.9	509	4	US-09-710-279-2880	Sequence 2880, Ap	923	38	29.9	940	4	US-09-949-016-7767	Sequence 7767, Ap
851	38	29.9	511	4	US-09-107-532A-6471	Sequence 6171, Ap	924	38	29.9	950	4	US-09-328-352-4668	Sequence 4668, Ap
852	38	29.9	513	3	US-09-134-001C-4386	Sequence 4386, Ap	925	38	29.9	971	3	US-09-112-450-2	Sequence 2, Appl1
853	38	29.9	513	3	US-09-134-001C-4629	Sequence 4629, Ap	926	38	29.9	971	3	US-09-112-450-2	Sequence 2, Appl1
854	38	29.9	522	4	US-09-252-991A-21996	Sequence 21996, A	927	38	29.9	971	4	US-09-419-291A-2	Sequence 2, Appl1
855	38	29.9	530	3	US-08-979-608A-8	Sequence 8, Appl1	928	38	29.9	1000	4	US-10-116-048-2	Sequence 20908, A
856	38	29.9	530	4	US-09-517-849-8	Sequence 8, Appl1	929	38	29.9	1005	2	US-07-743-357-1	Sequence 1, Appl1
857	38	29.9	530	4	US-09-616-289-8	Sequence 8, Appl1	930	38	29.9	1010	3	US-09-134-001C-5178	Sequence 5178, Ap
858	38	29.9	540	4	US-09-107-532A-5314	Sequence 5314, Ap	931	38	29.9	1015	3	US-08-463-210-9	Sequence 9, Appl1
859	38	29.9	546	4	US-09-616-289-44	Sequence 44, Appl	932	38	29.9	1015	3	US-09-124-900-3	Sequence 9, Appl1
860	38	29.9	555	4	US-09-107-532A-4722	Sequence 4722, Ap	933	38	29.9	1015	4	US-08-463-028-9	Sequence 9, Appl1
861	38	29.9	557	3	US-08-979-608A-5	Sequence 5, Appl1	934	38	29.9	1016	2	US-07-743-357-2	Sequence 2, Appl1
862	38	29.9	557	4	US-09-517-849-5	Sequence 5, Appl1	935	38	29.9	1016	2	US-07-743-357-4	Sequence 4, Appl1
863	38	29.9	557	4	US-09-616-289-5	Sequence 5, Appl1	936	38	29.9	1016	2	US-07-743-357-5	Sequence 5, Appl1
864	38	29.9	560	4	US-10-205-641-1	Sequence 1, Appl1	937	38	29.9	1023	4	US-10-164-595-20	Sequence 20, Appl
865	38	29.9	561	4	US-09-489-039A-11625	Sequence 11625, A	938	38	29.9	1024	4	US-09-562-737-47	Sequence 47, Appl
866	38	29.9	562	3	US-09-117-217-14	Sequence 14, Appl	939	38	29.9	1058	4	US-09-489-039A-11177	Sequence 11177, A
867	38	29.9	562	4	US-09-735-487-14	Sequence 14, Appl	940	38	29.9	1214	4	US-10-164-595-24	Sequence 24, Appl
868	38	29.9	566	4	US-09-328-352-4809	Sequence 4809, Ap	941	38	29.9	1280	3	US-09-252-991A-29606	Sequence 29606, A
869	38	29.9	571	4	US-09-814-259-32	Sequence 32, Appl	942	38	29.9	1290	3	US-09-150-460B-6	Sequence 6, Appl1
870	38	29.9	572	4	US-09-949-016-6070	Sequence 6070, Ap	943	38	29.9	1291	3	US-09-150-460B-10	Sequence 10, Appl
871	38	29.9	573	4	US-09-902-540-13770	Sequence 13770, A	944	38	29.9	1291	4	US-09-220-641-5	Sequence 5, Appl1
872	38	29.9	574	4	US-09-643-657-18	Sequence 18, Appl	945	38	29.9	1350	4	US-09-952-060-35	Sequence 35, Appl1
873	38	29.9	578	4	US-09-949-016-11503	Sequence 11503, A	946	38	29.9	1722	4	US-09-513-999C-6774	Sequence 6774, Ap
874	38	29.9	579	4	US-09-519-232-6	Sequence 6, Appl1	947	38	29.9	2471	3	US-09-112-450-4	Sequence 4, Appl1
875	38	29.9	592	4	US-09-328-352-5499	Sequence 5499, Ap	948	38	29.9	2471	4	US-09-419-291A-4	Sequence 4, Appl1
876	38	29.9	599	1	US-08-172-318A-4	Sequence 4, Appl1	949	38	29.9	2471	4	US-10-116-048-4	Sequence 11, Appl
877	38	29.9	599	2	US-09-032-315-6	Sequence 6, Appl1	950	38	29.9	2733	4	US-09-949-016-11433	Sequence 11433, A
878	38	29.9	599	2	US-08-993-318A-6	Sequence 6, Appl1	951	38	29.9	3259	4	US-09-949-016-6507	Sequence 6507, Ap
879	38	29.9	599	3	US-09-399-886-6	Sequence 6, Appl1	952	38	29.9	92	2	US-08-448-603A-14	Sequence 14, Appl
880	38	29.9	599	3	US-09-396-260-6	Sequence 6, Appl1	953	37.5	29.5	92	3	US-09-492-739-14	Sequence 14, Appl
881	38	29.9	599	3	US-09-576-281-6	Sequence 6, Appl1	954	37.5	29.5	92	3	US-09-966-931A-14	Sequence 14, Appl
882	38	29.9	619	4	US-09-814-259-32	Sequence 42558, A	955	37.5	29.5	92	4	US-09-966-931A-14	Sequence 14, Appl
883	38	29.9	622	2	US-08-132-990A-4	Sequence 4, Appl1	956	37.5	29.5	121	4	US-09-513-999C-6774	Sequence 6774, Ap
884	38	29.9	622	5	PCT-US92-09382-4	Sequence 4, Appl1	957	37.5	29.5	172	4	US-09-248-796A-21666	Sequence 21666, Ap
885	38	29.9	629	5	PCT-US82-09382-8	Sequence 8, Appl1	958	37.5	29.5	193	4	US-09-248-796A-20441	Sequence 20441, A
886	38	29.9	644	4	US-09-949-016-9507	Sequence 9507, Ap	959	37.5	29.5	196	4	US-09-248-796A-18117	Sequence 18117, A
887	38	29.9	644	4	US-09-538-092-1190	Sequence 1190, Ap	960	37.5	29.5	213	2	US-08-437-013-2	Sequence 2, Appl1
888	38	29.9	658	3	US-09-013-895A-3	Sequence 3, Appl1	961	37.5	29.5	213	4	US-08-737-312-2	Sequence 2, Appl1
889	38	29.9	669	3	US-09-448-868-3	Sequence 3, Appl1	962	37.5	29.5	259	4	US-09-624-125-15	Sequence 15, Appl
890	38	29.9	669	3	US-09-448-868-3	Sequence 3, Appl1	963	37.5	29.5	269	4	US-09-489-039A-10651	Sequence 10651, A
891	38	29.9	682	1	US-08-441-139-2	Sequence 2, Appl1	964	37.5	29.5	282	4	US-09-134-000C-6154	Sequence 6154, Ap
892	38	29.9	688	4	US-09-538-092-794	Sequence 794, Ap	965	37.5	29.5	282	4	US-09-248-796A-20924	Sequence 20924, A
893	38	29.9	735	4	US-10-164-595-80	Sequence 80, Appl	966	37.5	29.5	293	1	US-08-624-125-15	Sequence 15, Appl
894	38	29.9	740	4	US-09-134-000C-6441	Sequence 6441, Ap	967	37.5	29.5	293	4	US-08-937-155-14	Sequence 15, Appl
895	38	29.9	748	4	US-09-949-016-6124	Sequence 6124, Ap	968	37.5	29.5	293	4	US-09-323-998E-15	Sequence 15, Appl
896	38	29.9	753	4	US-09-949-016-11393	Sequence 11393, A	969	37.5	29.5	293	4	US-09-323-998E-43	Sequence 43, Appl
897	38	29.9	779	4	US-10-164-595-56	Sequence 56, Appl	970	37.5	29.5	303	4	US-09-252-991A-28605	Sequence 28605, A
898	38	29.9	784	4	US-10-164-595-79	Sequence 79, Appl	971	37.5	29.5	305	1	US-08-624-125-14	Sequence 14, Appl
899	38	29.9	798	3	US-09-150-460B-8	Sequence 8, Appl1	972	37.5	29.5	305	4	US-08-937-155-14	Sequence 14, Appl
900	38	29.9	813	4	US-09-328-352-7421	Sequence 7421, Ap	973	37.5	29.5	305	4	US-09-323-998E-14	Sequence 14, Appl
901	38	29.9	841	4	US-09-861-451A-30	Sequence 54, Appl	974	37.5	29.5	312	4	US-09-270-767-47024	Sequence 47024, A
902	38	29.9	843	4	US-10-164-595-54	Sequence 2, Appl1	975	37.5	29.5	317	3	US-09-327-984A-37	Sequence 37, Appl
903	38	29.9	850	4	US-09-952-060-2	Sequence 2, Appl1	976	37.5	29.5				

977	37.5	29.5	324	4	US-09-2248-7966A-16963	Sequence 16963, A
978	37.5	29.5	375	4	US-09-533-029-12	Sequence 12, Appl
979	37.5	29.5	389	4	US-09-800-170-18	Sequence 18, Appl
980	37.5	29.5	420	4	US-09-551-991A-19117	Sequence 19117, A
981	37.5	29.5	420	4	US-09-591-279A-29	Sequence 29, Appl
982	37.5	29.5	424	1	US-08-179-792-31	Sequence 31, Appl
983	37.5	29.5	424	1	US-08-459-850-31	Sequence 31, Appl
984	37.5	29.5	424	1	US-08-459-214-31	Sequence 31, Appl
985	37.5	29.5	427	4	US-09-328-352-4720	Sequence 4720, Appl
986	37.5	29.5	495	3	US-08-889-841B-25	Sequence 25, Appl
987	37.5	29.5	495	3	US-08-889-841B-28	Sequence 28, Appl
988	37.5	29.5	495	4	US-09-419-362-25	Sequence 25, Appl
989	37.5	29.5	495	4	US-09-419-362-28	Sequence 28, Appl
990	37.5	29.5	501	2	US-08-448-603A-2	Sequence 2, Appl
991	37.5	29.5	501	3	US-09-134-075-2	Sequence 2, Appl
992	37.5	29.5	501	3	US-09-4497-739-2	Sequence 2, Appl
993	37.5	29.5	501	4	US-09-966-921A-2	Sequence 2, Appl
994	37.5	29.5	511	2	US-08-448-603A-1	Sequence 1, Appl
995	37.5	29.5	511	3	US-09-134-075-1	Sequence 1, Appl
996	37.5	29.5	511	3	US-08-889-841B-41	Sequence 41, Appl
997	37.5	29.5	511	3	US-09-492-739-1	Sequence 1, Appl
998	37.5	29.5	511	4	US-09-419-362-41	Sequence 41, Appl
999	37.5	29.5	511	4	US-09-966-921A-1	Sequence 1, Appl
1000	37.5	29.5	534	4	US-09-051-996-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
 US-08-531-525-31  
 Sequence 31, Application US/08531525  
 Patent No. 5840683  
 GENERAL INFORMATION:  
 APPLICANT: Hlavka, Joseph J.  
 APPLICANT: Pincus, Matthew R.  
 APPLICANT: No. 58406831e, John F.  
 APPLICANT: Abajian, Henry B.  
 APPLICANT: Kende, Andrew S.  
 TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action  
 TITLE OF INVENTION: Of P21 Ras  
 NUMBER OF SEQUENCES: 52  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Greenlee and Winner, P.C.  
 STREET: 5370 Manhattan Circle, Suite 201  
 CITY: Boulder  
 STATE: Colorado  
 COUNTRY: US  
 ZIP: 80303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/531,525  
 FILING DATE: 21-SEP-1995  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Feiber, Donna M.  
 REGISTRATION NUMBER: 33,878  
 REFERENCE/DOCKET NUMBER: 37-94  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 499-8080  
 TELEFAX: (303) 499-8081  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 205 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO

ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-531-525-31

Query Match	43.3%;	Score 55;	DB 2;	Length 205;
Best Local Similarity	41.7%;	Pred. No. 2.8;		
Matches	10;	Conservative	4;	Mismatches 10;
				Indels

```

QY      1 KKKMADNGTITVEELKQLLQWNL 24
          | : | | | | | | | |
Db      128 KSDLEDKRQVSVEAKNRAEQWNV 151

```

RESULT 2  
US-08-718-270A-31  
; Sequence 31, Application US/08718270A

```

      GENERAL INFORMATION:
APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 5910478le, John F.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
TITLE OF INVENTION: Peptidomimetics Inhibiting
TITLE OF INVENTION: the Oncogenic Action of P21 Ras
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winmer and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-718-270A-31
Query Match          43.3%; Score 55; DB 2; Length 205;
Best Local Similarity 41.7%; Pred. No. 2.8;
Matches    10; Conservative         4; Mismatches        10; Indels           0; Gaps            0;
```

Db 128 KSDLEDKQVSVBEAKRABQNMV 151

## RESULT 3

US-09-078-317-15  
; Sequence 15, Application US/09078317  
; Patent No. 6017710  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Maxine J.  
; APPLICANT: Rutter, Marc  
; APPLICANT: Buckler, Alan J.  
; TITLE OF INVENTION: RAO Genes and Their Uses  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bozicevic & Reed, LLP  
; STREET: 285 Hamilton Ave, Suite 200  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; FILING DATE: 13-MAY-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Francis, Carol L  
; REGISTRATION NUMBER: 36,513  
; REFERENCE/DOCKET NUMBER: SEQ-18P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-327-3400  
; TELEFAX: 650-327-3231  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 206 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: NO. 6017710e  
; US-09-078-317-15

Query Match 43.3%; Score 55; DB 3; Length 206;  
Best Local Similarity 41.7%; Pred. No. 2.9;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVVELKQLEQNMV 24  
Db 128 KSDLEDKQVSVBEAKRABQNMV 151

## RESULT 4

US-09-454-818-15  
; Sequence 15, Application US/09454818  
; Patent No. 6383792  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Maxine J.  
; APPLICANT: Rutter, Marc  
; APPLICANT: Buckler, Alan J.  
; TITLE OF INVENTION: RAO Genes and Their Uses  
; FILE REFERENCE: AYS-018DIV  
; CURRENT APPLICATION NUMBER: US/09/454,818  
; CURRENT FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: 09/078,317  
; PRIOR FILING DATE: 1998-05-13  
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-454-818-15

Query Match 43.3%; Score 55; DB 3; Length 206;  
Best Local Similarity 41.7%; Pred. No. 2.9;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVVELKQLEQNMV 24  
Db 128 KSDLEDKQVSVBEAKRABQNMV 151

## RESULT 5

US-09-709-103-48  
; Sequence 48, Application US/09709103  
; Patent No. 6733991  
; GENERAL INFORMATION:  
; APPLICANT: Ciemowski, Mary  
; APPLICANT: Duzic, Emil  
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor  
; FILE REFERENCE: 60388-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/709,103  
; CURRENT FILING DATE: 2000-11-08  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; US-09-709-103-48

Query Match 43.3%; Score 55; DB 4; Length 206;  
Best Local Similarity 41.7%; Pred. No. 2.9;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVVELKQLEQNMV 24  
Db 128 KSDLEDKQVSVBEAKRABQNMV 151

## RESULT 6

US-09-439-410A-48  
; Sequence 48, Application US/09439410A  
; Patent No. 6746852  
; GENERAL INFORMATION:  
; APPLICANT: Ciemowski, Mary  
; APPLICANT: Duzic, Emil  
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF  
; FILE REFERENCE: 1919/60388-B  
; CURRENT APPLICATION NUMBER: US/09/439,410A  
; CURRENT FILING DATE: 1999-11-11  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-439-410A-48

Query Match 43.3%; Score 55; DB 4; Length 206;  
Best Local Similarity 41.7%; Pred. No. 2.9;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGITVVELKQLEQNMV 24  
Db 128 KSDLEDKQVSVBEAKRABQNMV 151

## RESULT 7

US-09-543-681A-7926  
; Sequence 7926, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 7926  
; LENGTH: 300  
; TYPE: PRF  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-7926

Query Match 41.7%; Score 53; DB 4; Length 300;  
Best Local Similarity 47.6%; Pred. No. 8.5;  
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KXADNGTIVEELKQLEQNLV 23  
DB 59 KLTDDGAILYEHAKQIIAQFN 79

RESULT 8  
US-09-206-551-11  
; Sequence 11, Application US/09206551B

; Patent No. 6521739  
; GENERAL INFORMATION:  
; APPLICANT: Hahn, Beatrice H.  
; APPLICANT: Gao, Feng  
; APPLICANT: Marx, Preston A.  
; APPLICANT: Shaw, George M.  
; APPLICANT: Smith, Stephen M.  
; APPLICANT: Georges-Courbot, Marie Claude  
; APPLICANT: Lu, Chang Yong  
; TITLE OF INVENTION: Complete Genome Sequences of a Simian  
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped  
; FILE REFERENCE: D6286  
; CURRENT APPLICATION NUMBER: US/09/206,551B  
; CURRENT FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 11  
; LENGTH: 855  
; TYPE: PRF  
; ORGANISM: Simian immunodeficiency virus  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of homologous region of  
; OTHER INFORMATION: A\_U455 lentiviral env protein  
US-09-206-551-11

Query Match 40.6%; Score 51.5; DB 4; Length 855;  
Best Local Similarity 43.5%; Pred. No. 45;  
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 MADNGTIVE-ELKQLEQNLV 25  
DB 401 MGPNGTITLQCRIKQIINNMQRV 423

RESULT 9  
US-09-206-551-12  
; Sequence 12, Application US/09206551B  
; Patent No. 6521739  
; GENERAL INFORMATION:  
; APPLICANT: Hahn, Beatrice H.  
; APPLICANT: Gao, Feng  
; APPLICANT: Marx, Preston A.

; APPLICANT: Shaw, George M.  
; APPLICANT: Smith, Stephen M.  
; APPLICANT: Georges-Courbot, Marie Claude  
; APPLICANT: Lu, Chang Yong  
; TITLE OF INVENTION: Complete Genome Sequences of a Simian  
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped  
; FILE REFERENCE: D6286  
; CURRENT APPLICATION NUMBER: US/09/206,551B  
; CURRENT FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 12  
; LENGTH: 855  
; TYPE: PRF  
; ORGANISM: Simian immunodeficiency virus  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of homologous region of  
; OTHER INFORMATION: B\_HXB2R lentiviral env protein  
US-09-206-551-12

Query Match 40.6%; Score 51.5; DB 4; Length 855;  
Best Local Similarity 43.5%; Pred. No. 45;  
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 MADNGTIVE-ELKQLEQNLV 25  
DB 401 MGPNGTITLQCRIKQIINNMQRV 423

RESULT 10  
US-09-248-796A-17215  
; Sequence 17215, Application US/09248796A

; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 17215  
; LENGTH: 770  
; TYPE: PRF  
; ORGANISM: Candida albicans  
US-09-248-796A-17215

Query Match 39.8%; Score 50.5; DB 4; Length 770;  
Best Local Similarity 34.6%; Pred. No. 56;  
Matches 9; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 KKKMADNGTIVEELKQLE-QNLV 25  
DB 524 EKQIDEGFTAEIDIKHKQWYNIL 549

RESULT 11  
US-09-513-999C-6125  
; Sequence 6125, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclercq, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59\_US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO: 6125  
LENGTH: 100  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-513-999C-6125

Query Match 39.4%; Score 50; DB 4; Length 100;  
Best Local Similarity 55.6%; Pred. No. 6.6;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVBELKQLE 20  
DB 44 KOLENGEINIEBLKQLE 61

RESULT 12  
US-09-648-004-26  
Sequence 26, Application US/09648004  
Patent No. 6498242  
GENERAL INFORMATION:  
APPLICANT: CHEN, QIONG  
APPLICANT: THOMAS, STUART  
APPLICANT: NAGARAJAN, VASANTHA  
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
FILE REFERENCE: CL-1341-A  
CURRENT APPLICATION NUMBER: US/09/648,004  
CURRENT FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/252,553  
PRIOR FILING DATE: 1999-02-19  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Microsoft Office 97  
SEQ ID NO: 26  
LENGTH: 300  
TYPE: PRT  
ORGANISM: Acinetobacter sp.  
US-09-648-004-26

Query Match 39.4%; Score 50; DB 4; Length 300;  
Best Local Similarity 22.7%; Pred. No. 23;  
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KXADNGTIVBELKQLE 23  
DB 20 RMOENPNMTIEDFRSMFDEWH 41

RESULT 13  
US-10-272-419-26  
Sequence 26, Application US/10272419  
Patent No. 6794165  
GENERAL INFORMATION:  
APPLICANT: CHEN, QIONG  
APPLICANT: THOMAS, STUART  
APPLICANT: NAGARAJAN, VASANTHA  
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
FILE REFERENCE: CL1341-A  
CURRENT APPLICATION NUMBER: US/10/272,419  
CURRENT FILING DATE: 2002-10-16  
PRIOR APPLICATION NUMBER: 09/252,553  
PRIOR FILING DATE: 1999-02-19  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Microsoft Office 97  
SEQ ID NO: 26  
LENGTH: 300  
TYPE: PRT  
ORGANISM: Acinetobacter sp.  
US-10-272-419-26

Query Match 39.4%; Score 50; DB 4; Length 300;  
Best Local Similarity 22.7%; Pred. No. 23;  
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KXADNGTIVBELKQLE 23  
DB 20 RMOENPNMTIEDFRSMFDEWH 41

RESULT 14  
US-08-940-332-2  
Sequence 2, Application US/08940332  
Patent No. 5885834  
GENERAL INFORMATION:  
APPLICANT: Epstein, Paul M.  
TITLE OF INVENTION: SYNTHESIS OF ANTISENSE  
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE OF PHOSPHODIESTERASE AND  
TITLE OF INVENTION: INDUCEMENT OF APOPTOSIS IN HUMAN LYMPHOBLASTOID CELLS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ALIX, YALE & RISTAS, LLP  
STREET: 750 MAIN STREET  
CITY: HARTFORD  
STATE: CT  
COUNTRY: USA  
ZIP: 06103-2721  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,332  
FILING DATE: 30-SEP-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/027,207  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Alix, James E.  
REGISTRATION NUMBER: 20,736  
REFERENCE/DOCKET NUMBER: UCON/137/US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (860)527-9211  
TELEFAX: (860)527-5029  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 536 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-940-332-2

Query Match 39.4%; Score 50; DB 2; Length 536;  
Best Local Similarity 55.6%; Pred. No. 44;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVBELKQLE 20  
DB 44 KOLENGEINIEBLKQLE 61

RESULT 15  
US-09-543-681A-4729  
Sequence 4729, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 4729  
LENGTH: 537  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-4729

Query Match 39.4%; Score 50; DB 4; Length 537;  
Best Local Similarity 36.4%; Pred. No. 44;  
Matches 8; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 KXADNGTIVVEELKQLEQNL 24  
DB 111 KXVDNGSASLEDELLDKMHL 132

RESULT 16  
US-09-949-016-7536  
Sequence 7536, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7536  
LENGTH: 542  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7536

Query Match 39.4%; Score 50; DB 4; Length 542;  
Best Local Similarity 55.6%; Pred. No. 44;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVVEELKQLE 20  
DB 50 KQLENGEINIEELKNLE 67

RESULT 17  
US-09-544-683-2  
Sequence 2, Application US/09544683  
Patent No. 6787137  
GENERAL INFORMATION:  
APPLICANT: JACOBS, ANTONIUS A.C.  
APPLICANT: VAN DEN BOSCH, JOHANNES F.  
TITLE OF INVENTION: CAMPYLOBACTER VACCINE  
FILE REFERENCE: JACOBS  
CURRENT APPLICATION NUMBER: US/09/544,683  
CURRENT FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: EP99201086.8  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 2  
LENGTH: 545  
TYPE: PRT  
ORGANISM: Campylobacter jejuni  
US-09-544-683-2

Query Match 39.4%; Score 50; DB 4; Length 545;  
Best Local Similarity 41.7%; Pred. No. 45;  
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 KXADNGTIVVEELKQLEQNLV 25  
DB 166 KXVGKDVITVEEPSINDELNVV 189

RESULT 18  
US-10-192-419-2  
Sequence 2, Application US/10192419  
Patent No. 6790446  
GENERAL INFORMATION:  
APPLICANT: JACOBS, ANTONIUS A.C.  
APPLICANT: VAN DEN BOSCH, JOHANNES F.  
TITLE OF INVENTION: CAMPYLOBACTER VACCINE  
FILE REFERENCE: JACOBS  
CURRENT APPLICATION NUMBER: US/10/192,419  
CURRENT FILING DATE: 2002-07-10  
PRIOR APPLICATION NUMBER: US/09/544,683  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: EP99201086.8  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 2  
LENGTH: 545  
TYPE: PRT  
ORGANISM: Campylobacter jejuni  
US-10-192-419-2

Query Match 39.4%; Score 50; DB 4; Length 545;  
Best Local Similarity 41.7%; Pred. No. 45;  
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 KXADNGTIVVEELKQLEQNLV 25  
DB 166 KXVGKDVITVEEPSINDELNVV 189

RESULT 19  
US-09-538-092-1312  
Sequence 1312, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Giot, Loic  
APPLICANT: Mansfield, Traci A.  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538,092  
CURRENT FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CuratPatSegFormatter Version 0.9  
SEQ ID NO 1312  
LENGTH: 2472  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: Polypeptide Accession Number Q13813  
US-09-538-092-1312

Query Match 39.4%; Score 50; DB 4; Length 2472;  
Best Local Similarity 47.6%; Pred. No. 2.5e+02;  
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;



```

OY      2 KKMADNGTITVEELKQLLEQM 22
          ||::|||::||:
Db      1828 KKLSPDNTIGKEIQRRLAQF 1848

```

```

RESULT 20 US-09-266-965-132
US-09-266-965-132
Sequence 132, Application US/09266965
Patent No. 6495348
GENERAL INFORMATION:
APPLICANT: Sherman, D
APPLICANT: Mao, Y
APPLICANT: Varoglu, M
APPLICANT: He, M
APPLICANT: Sheldon, P
TITLE OF INVENTION: Mltomycin biosynthetic gene clusters
FILE REFERENCE: 600.456US1
CURRENT APPLICATION NUMBER: US/09/266,965
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: PCT/US94/11279
EARLIER FILING DATE: 1994-10-06
EARLIER APPLICATION NUMBER: US 08/133,963
EARLIER FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 132
LENGTH: 123
TYPE: PRT
ORGANISM: Streptomyces lavendulae
US-09-266-965-132

```

Query Match	38.6%	Score 49	DB 4	Length 123
Best Local Similarity	57.1%	Pred. No. 12		
Matches	8	Mismatches	1	Indels
				Gaps 0

```
QY      7 NGTITVEELKÖLLE 20
        |||: ||||:::|
Db      86 NGTVPVEELREWE 99
```

```

RESULT 21
US-09-538-092-241
; Sequence 241: Application US/09538092
; Patent No. 675314
; GENERAL INFORMATION:
; APPLICANT: Glot, Iolc
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO 241
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YER063W
US-09-538-092-241

```

Query Match	38.6%	Score	49	DB	4	Length	218
Best Local Similarity	52.4%	Pred.	No.	22			
Matches	11	Conservative	4	Mismatches	6	Indels	0
						Gaps	0

```
QY      4 MADNGTITVEELKQLEQWNL 24
         ||| :|| :||| :||
Db      1 MADYSSLTVQKDKLLTKRNL 21
```

```

RESULT 22
US-09-949-016-9820
; Sequence 9820, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9820
; LENGTH: 473
; TYPE: prt
; ORGANISM: Human
US-09-949-016-9820

```

Query Match	38.6%	Score 49:	DB 4;	Length 473;
Best Local	35.0%	Pred. No. 53;		
Matches 7;	Conservative	8;	Mismatches	5;
			Indels	0;
			Gaps	0

QY 3 KMADNGTITVEELKQÖLLEQW 22  
45 KLQERSDLTVEKEKEELIEEW 64

```

RESULT 23
US-09-489-039A-10011
; Sequence 10011, Application US/03489039A
; Patent No. 6610636
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10011
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10011

```

Query Match	38.6%	Score 49	DB 4	Length 532
Best Local	Similarity 50.0%	Pred. NO. 60		
Matches	9	Conservative	6	Mismatches 3
				Indels 0
				Gaps 0

```
QY . 1 KKKMADNGTITVEELKOL 18
      | :|||||: ::|: :|
Db 290 KFEEMADNGTFLDEIGEL 307
```

RESULT 24  
US-07-872-644-27  
; Sequence 27, Application US/07872644  
; Patent No. 5389527



RESULT 29  
US-08-455-525-27







```

; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Rbdo: Ligand Interactions
; FILE REFERENCE: 898-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1297
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-540-245A-17

Query Match
Best Local Similarity 40.0%; Pred. No. 2.3e+02; Length 1297;
Matches 8; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKKMADNGTIVBELKQLEQ 20
DB 368 RTKVSPGTGLTIEVRQVDE 387

RESULT 39
US-09-270-767-45884
; Sequence 45884, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45884
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-45884

Query Match
Best Local Similarity 37.4%; Score 47.5; DB 4; Length 149;
Matches 10; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

QY 3 KQAD---NGTIVBELKQLEQ 22
DB 86 KAADPQNGTISARQLRLQNW 108

RESULT 40
US-09-621-976-4009
; Sequence 4009, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4009
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```

; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -58...-1
; US-09-621-976-4009

Query Match
Best Local Similarity 36.2%; Score 46; DB 4; Length 93;
Matches 9; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 3 KQADNGTIVBELKQLEQ 25
DB 8 RLSDGTVFEDVAVKTEQEWML 32

RESULT 41
US-09-710-279-2624
; Sequence 2624, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2624
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-710-279-2624

Query Match
Best Local Similarity 36.2%; Score 46; DB 4; Length 216;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 NGTIVBELKQLEQ 21
DB 59 NGTMTLEAKYQLEE 73

RESULT 42
US-09-134-001C-5279
; Sequence 5279, Application US/09134001C
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5279
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-5279

Query Match
Best Local Similarity 36.2%; Score 46; DB 3; Length 274;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 NGTIVBELKQLEQ 21
```

Db 117 NGMTLEAKYQLE 131

# RESULT 43

US-09-270-767-58705  
 ; Sequence 58705; Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 58705  
 ; LENGTH: 365  
 ; TYPE: PRT  
 ; ORGANISM: *Drosophila melanogaster*  
 ; US-09-270-767-58705

Query Match 36.2%; Score 46; DB 4; Length 365;  
 Best Local Similarity 52.2%; Pred. No. 1.1e+02;  
 Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 1 KKKMADNGTI--TVEELKQLEQ 21

Db 284 KVMMDSPVIRISERLKTLEE 306

# RESULT 44

US-09-270-767-43356  
 ; Sequence 43356; Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 43356  
 ; LENGTH: 397  
 ; TYPE: PRT  
 ; ORGANISM: *Drosophila melanogaster*  
 ; US-09-270-767-43356

Query Match 36.2%; Score 46; DB 4; Length 397;  
 Best Local Similarity 52.2%; Pred. No. 1.1e+02;  
 Matches 12; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 1 KKKMADNGTI--TVEELKQLEQ 21

Db 316 KVMMDSPVIRISERLKTLEE 338

# RESULT 45

US-09-248-796A-14232  
 ; Sequence 14232; Application US/09248796A  
 ; Patent No. 6747137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keith Weinstein et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
 ; FILE REFERENCE: 107196.132  
 ; CURRENT APPLICATION NUMBER: US/09/248,796A  
 ; CURRENT FILING DATE: 1999-02-12  
 ; PRIOR APPLICATION NUMBER: US 60/074,725  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 60/096,409  
 ; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208  
 ; SEQ ID NO 14232  
 ; LENGTH: 415  
 ; TYPE: PRT  
 ; ORGANISM: *Candida albicans*  
 ; US-09-248-796A-14232

Query Match 36.2%; Score 46; DB 4; Length 415;  
 Best Local Similarity 46.7%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 10 ITVEELKQLEQWNL 24

Db 106 ITPKRLKRAIDQWNI 120

# RESULT 46

US-09-759-595-1  
 ; Sequence 1; Application US/09759595  
 ; Patent No. 6818419  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mesche, Holger  
 ; APPLICANT: Li, Shyun  
 ; APPLICANT: Tularik Inc.  
 ; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use  
 ; FILE REFERENCE: 018781-003910US  
 ; CURRENT APPLICATION NUMBER: US/09/759,595  
 ; CURRENT FILING DATE: 2001-01-13  
 ; PRIOR APPLICATION NUMBER: US 60/176,395  
 ; PRIOR FILING DATE: 2000-01-13  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 460  
 ; TYPE: PRT  
 ; ORGANISM: *Homo sapiens*  
 ; US-09-759-595-1

Query Match 36.2%; Score 46; DB 4; Length 460;  
 Best Local Similarity 55.0%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 KKKMADNGTITVEELKQLEQ 21

Db 213 KKLAAVMDITTEELKQFPDQ 232

# RESULT 47

US-08-467-822-33  
 ; Sequence 33; Application US/08467822  
 ; Patent No. 5843460  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Labigne, Agnes  
 ; APPLICANT: Sauerbaum, Sebastien  
 ; APPLICANT: Ferrero, Richard L.  
 ; APPLICANT: Thibierge, Jean-Michel  
 ; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
 ; TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
 ; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ; STREET: 1300 I Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3315  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,822  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ. ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 544 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-822-33

Query Match 36.2%; Score 46; DB 2; Length 544;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KKKADNGTITVEELK 16  
: : : : :  
Db 167 EKVKGKGSITVEAK 181

RESULT 48  
US-08-432-697-33  
Sequence 33, Application US/08432697  
Patent No. 6248330  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerdam, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thiberge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-00000

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ. ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 544 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-432-697-33

Query Match 36.2%; Score 46; DB 3; Length 544;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KKKADNGTITVEELK 16  
: : : : :  
Db 167 EKVKGKGSITVEAK 181

RESULT 49  
US-08-466-248-33  
Sequence 33, Application US/08466248  
Patent No. 6258359  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerdam, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thiberge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,248  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ. ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 544 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-466-248-33

Query Match 36.2%; Score 46; DB 3; Length 544;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KKMADNGTITVEELK 16  
:|:|:|:|:|:|  
Db 167 EKVGKNGSITVEAK 181

## RESULT 50

US-09-198-452A-153  
; Sequence 153, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 153  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: 1...544  
; OTHER INFORMATION: Xaa=unknown or other  
US-09-198-452A-153

Query Match 36.2%; Score 46; DB 4; Length 544;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KKMADNGTITVEELK 16  
:|:|:|:|:|:|  
Db 167 EKVGKNGSITVEAK 181

Search completed: May 11, 2005, 21:28:01  
Job time : 37.4468 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2005, 21:23:25 ; Search time 97.3404 Seconds

(without alignments)  
85.795 Million cell updates/sec

Title: US-10-712-812-6  
Perfect score: 127  
Sequence: 1 KKKMDNGTITVEIKLLEQNNLV 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubppa/US09B\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubppa/US10A\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubppa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppa/US10D\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	88.2	221	16	US-10-839-729-6 Sequence 6, Appl
2	112	88.2	221	16	US-10-839-729-7 Sequence 7, Appl
3	112	88.2	221	16	US-10-839-729-8 Sequence 8, Appl
4	112	88.2	221	16	US-10-839-729-9 Sequence 9, Appl
5	112	88.2	221	17	US-10-699-936-24 Sequence 24, Appl
6	112	88.2	221	17	US-10-699-936-81 Sequence 81, Appl
7	112	88.2	221	17	US-10-699-936-82 Sequence 82, Appl
8	112	88.2	221	17	US-10-699-936-83 Sequence 83, Appl
9	112	88.2	221	17	US-10-808-187-214 Sequence 214, Appl
10	73	57.5	15	6	US-10-839-729-46 Sequence 46, Appl
11	55	43.3	54	9	US-09-864-761-39008 Sequence 39008, A
12	55	43.3	206	10	US-09-873-546-10 Sequence 10, Appl
13	55	43.3	206	14	US-10-153-666-214 Sequence 214, Appl

14	55	43.3	206	14	US-10-021-660-132 Sequence 132, App
15	55	43.3	206	15	US-10-231-913-64 Sequence 64, Appl
16	55	43.3	206	15	US-10-211-462-79 Sequence 79, Appl
17	55	43.3	206	16	US-10-408-765A-2022 Sequence 2022, Ap
18	55	43.3	206	16	US-10-804-491-48 Sequence 48, Appl
19	55	43.3	209	16	US-10-231-913-66 Sequence 66, Appl
20	53.5	42.1	336	16	US-10-425-114-69487 Sequence 69487, A
21	53.5	42.1	486	16	US-10-437-963-158994 Sequence 158994, A
22	53.5	42.1	512	16	US-10-437-963-158996 Sequence 158996, A
23	53.5	42.1	523	15	US-10-425-114-57880 Sequence 57880, A
24	53	41.7	351	15	US-10-282-122A-51593 Sequence 51593, A
25	52	40.9	206	15	US-10-231-913-63 Sequence 63, Appl
26	52	40.9	206	15	US-10-231-913-65 Sequence 65, Appl
27	52	40.9	206	15	US-10-231-913-67 Sequence 67, Appl
28	52	40.9	545	15	US-10-282-122A-54546 Sequence 54546, A
29	51.5	40.6	855	14	US-10-369-294-11 Sequence 11, Appl
30	51.5	40.6	855	14	US-10-369-294-12 Sequence 12, Appl
31	51	40.2	217	16	US-10-478-245-4 Sequence 4, Appl
32	51	40.2	626	15	US-10-282-122A-60575 Sequence 60575, A
33	51	40.2	987	14	US-10-156-761-14515 Sequence 14515, A
34	50	39.4	92	15	US-10-424-599-219887 Sequence 219887, A
35	50	39.4	174	16	US-10-437-963-186189 Sequence 186189, A
36	50	39.4	300	14	US-10-272-419-26 Sequence 26, Appl
37	50	39.4	469	15	US-10-417-700A-49 Sequence 49, Appl
38	50	39.4	516	17	US-10-781-102-1 Sequence 1, Appl
39	50	39.4	536	17	US-10-781-102-3 Sequence 3, Appl
40	50	39.4	536	17	US-10-815-390-1 Sequence 1, Appl
41	50	39.4	545	14	US-10-192-419-2 Sequence 2, Appl
42	50	39.4	546	15	US-10-424-599-203557 Sequence 203557, A
43	50	39.4	549	15	US-10-425-114-54704 Sequence 54704, A
44	50	39.4	673	15	US-10-282-122A-76721 Sequence 76721, A
45	50	39.4	808	15	US-10-104-047-2324 Sequence 2324, Ap
46	50	39.4	1803	16	US-10-343-509-3 Sequence 3, Appl
47	50	39.4	1805	16	US-10-343-509-1 Sequence 1, Appl
48	50	39.4	2477	16	US-10-360-053-28 Sequence 28, Appl
49	50	39.4	2477	17	US-10-408-765A-238 Sequence 238, App
50	49	38.6	60	17	US-10-781-102-13 Sequence 13, Appl
51	49	38.6	123	14	US-09-953-348-132 Sequence 132, App
52	49	38.6	123	14	US-10-267-255-132 Sequence 132, App
53	49	38.6	143	11	US-09-978-360A-641 Sequence 641, App
54	49	38.6	476	15	US-10-354-358-96 Sequence 96, Appl
55	49	38.6	476	15	US-10-264-049-2925 Sequence 2925, Ap
56	49	38.6	485	15	US-10-282-122A-51755 Sequence 51755, A
57	49	38.6	534	9	US-09-883-825-27 Sequence 27, Appl
58	49	38.6	534	16	US-10-697-894-27 Sequence 27, Appl
59	49	38.6	643	9	US-09-815-242-11234 Sequence 11234, A
60	49	38.6	643	15	US-10-282-122A-58503 Sequence 58503, A
61	48	37.8	159	15	US-10-429-812-4 Sequence 4, Appl
62	48	37.8	159	15	US-10-612-779-30 Sequence 30, Appl
63	48	37.8	159	17	US-10-823-397-33 Sequence 33, Appl
64	48	37.8	206	15	US-10-231-913-6 Sequence 6, Appl
65	48	37.8	299	16	US-10-437-963-14248 Sequence 124248, A
66	48	37.8	318	15	US-10-282-122A-5263 Sequence 5263, A
67	48	37.8	401	15	US-10-369-499-10440 Sequence 10440, A
68	48	37.8	423	15	US-10-369-499-6746 Sequence 6746, Ap
69	48	37.8	428	16	US-10-437-963-141938 Sequence 141938, A
70	48	37.8	508	16	US-10-686-947-238 Sequence 238, App
71	48	37.8	508	16	US-10-686-947-266 Sequence 266, App
72	48	37.8	909	16	US-10-686-947-240 Sequence 240, App
73	48	37.8	909	17	US-10-826-812-13 Sequence 13, Appl
74	48	37.8	1297	14	US-10-289-776-17 Sequence 17, Appl
75	48	37.8	1297	17	US-10-826-812-6 Sequence 6, Appl
76	48	37.8	1437	17	US-10-314-657-45 Sequence 45, Appl
77	48	37.8	1437	17	US-10-473-193-45 Sequence 45, Appl
78	47	37.0	659	15	US-10-369-499-2600 Sequence 2600, Ap
79	46.5	36.6	171	16	US-10-437-963-137765 Sequence 137765, A
80	46.5	36.6	210	15	US-10-425-114-40176 Sequence 40176, A
81	46.5	36.6	325	15	US-10-424-599-198782 Sequence 198782, A
82	46.5	36.6	428	15	US-10-282-122A-77230 Sequence 77230, A
83	46.5	36.6	500	16	US-10-437-963-137763 Sequence 137763, A
84	46.5	36.6	849	10	US-09-899-575-23 Sequence 23, Appl
85	46.5	36.6	849	14	US-10-190-435-148 Sequence 148, App
86	46	36.2	137	15	US-10-335-977-9398 Sequence 9398, Ap

87	46	36.2	183	15	US-10-425-114-49684	Sequence 49684, A	160	45	35.4	629	14	US-10-128-714-3099	Sequence 3099, Ap
88	46	36.2	196	16	US-10-437-963-200009	Sequence 200009, A	161	45	35.4	637	16	US-10-296-085A-16	Sequence 16, Appl
89	46	36.2	216	17	US-10-470-048B-286	Sequence 286, App	162	45	35.4	638	16	US-10-296-085A-21	Sequence 21, Appl
90	46	36.2	224	16	US-10-767-701-39143	Sequence 39143, A	163	45	35.4	642	16	US-10-296-085A-38	Sequence 38, Appl
91	46	36.2	315	16	US-10-437-963-116503	Sequence 116503, A	164	45	35.4	642	17	US-10-496-119-6	Sequence 6, Appl
92	46	36.2	325	16	US-10-664-421-143	Sequence 143, App	165	45	35.4	643	16	US-10-296-085A-69	Sequence 69, Appl
93	46	36.2	394	16	US-10-451-467A-510	Sequence 510, App	166	45	35.4	643	17	US-10-496-119-1	Sequence 1, Appl
94	46	36.2	460	14	US-09-759-595-1	Sequence 1, Appl	167	45	35.4	645	14	US-10-130-973A-8	Sequence 8, Appl
95	46	36.2	460	14	US-10-001-254-16	Sequence 16, Appl	168	45	35.4	652	16	US-10-437-963-198055	Sequence 198055, A
96	46	36.2	460	14	US-10-001-254-28	Sequence 28, Appl	169	45	35.4	656	16	US-10-296-085A-39	Sequence 39, Appl
97	46	36.2	477	15	US-10-335-977-9400	Sequence 9400, Ap	170	45	35.4	657	16	US-10-296-085A-68	Sequence 68, Appl
98	46	36.2	513	16	US-10-437-963-173217	Sequence 173217, A	171	45	35.4	660	14	US-10-130-973A-12	Sequence 12, Appl
99	46	36.2	525	15	US-10-425-114-64587	Sequence 64587, A	172	45	35.4	665	14	US-10-130-973A-9	Sequence 9, Appl
100	46	36.2	533	16	US-10-437-963-200006	Sequence 200006, A	173	45	35.4	666	15	US-10-264-227-2631	Sequence 2631, Ap
101	46	36.2	544	9	US-09-841-132-400	Sequence 400, App	174	45	35.4	669	15	US-10-282-122A-72423	Sequence 72423, A
102	46	36.2	544	9	US-09-759-272B-5	Sequence 5, Appl	175	45	35.4	685	14	US-10-128-714-0099	Sequence 8099, Ap
103	46	36.2	544	11	US-09-809-745-3	Sequence 3, Appl	176	45	35.4	778	15	US-10-080-334-238	Sequence 238, App
104	46	36.2	544	15	US-10-289-762-153	Sequence 153, App	177	45	35.4	795	17	US-10-661-388-20	Sequence 20, Appl
105	46	36.2	544	15	US-10-282-122A-54855	Sequence 54855, A	178	45	35.4	862	14	US-10-130-973A-4	Sequence 4, Appl
106	46	36.2	544	15	US-10-282-122A-55161	Sequence 55161, A	179	45	35.4	882	14	US-10-130-973A-3	Sequence 3, Appl
107	46	36.2	544	16	US-10-470-093-5	Sequence 5, Appl	180	45	35.4	887	14	US-10-130-973A-6	Sequence 6, Appl
108	46	36.2	551	15	US-10-369-493-18994	Sequence 18994, A	181	45	35.4	895	16	US-10-296-085A-19	Sequence 19, Appl
109	46	36.2	551	9	US-10-369-493-20184	Sequence 20184, A	182	45	35.4	895	16	US-10-296-085A-20	Sequence 20, Appl
110	46	36.2	572	9	US-09-986-632-10	Sequence 10, Appl	183	45	35.4	896	16	US-10-296-085A-17	Sequence 17, Appl
111	46	36.2	605	15	US-10-369-493-3541	Sequence 3541, Ap	184	45	35.4	896	16	US-10-296-085A-18	Sequence 18, Appl
112	46	36.2	643	15	US-10-282-122A-67033	Sequence 67033, A	185	45	35.4	896	17	US-10-496-119-2	Sequence 2, Appl
113	46	36.2	792	13	US-10-025-380-1127	Sequence 1127, Ap	186	45	35.4	896	17	US-10-496-119-3	Sequence 3, Appl
114	46	36.2	959	9	US-10-282-122A-68042	Sequence 68042, A	187	45	35.4	907	14	US-10-130-973A-5	Sequence 5, Appl
115	46	36.2	963	9	US-09-815-242-11819	Sequence 11819, A	188	45	35.4	1052	9	US-09-060-854B-7	Sequence 7, Appl
116	46	36.2	963	15	US-10-282-122A-66253	Sequence 66253, A	189	45	35.4	1052	9	US-09-891-711-4	Sequence 4, Appl
117	46	36.2	974	15	US-10-369-493-11758	Sequence 13758, A	190	45	35.4	1052	9	US-09-891-711-6	Sequence 6, Appl
118	46	36.2	964	15	US-10-282-122A-69819	Sequence 69819, A	191	45	35.4	1052	15	US-10-665-669-6	Sequence 6, Appl
119	45.5	35.8	114	15	US-10-424-559-221216	Sequence 221216, A	192	45	35.4	1052	16	US-10-829-118-4	Sequence 4, Appl
120	45.5	35.8	175	15	US-10-425-114-44519	Sequence 44519, A	193	45	35.4	1052	16	US-10-829-118-6	Sequence 6, Appl
121	45.5	35.8	202	15	US-10-424-559-213143	Sequence 213143, A	194	45	35.4	1549	15	US-10-369-493-5702	Sequence 5702, Ap
122	45.5	35.8	422	15	US-10-282-122A-78200	Sequence 78200, A	195	45	35.4	1696	16	US-10-408-765A-822	Sequence 822, App
123	45.5	35.8	492	15	US-10-424-559-272777	Sequence 272777, A	196	45	35.4	1720	15	US-10-161-927-8	Sequence 8, Appl
124	45.5	35.8	603	16	US-10-437-963-161888	Sequence 161888, A	197	45	35.4	3332	15	US-10-282-122A-69849	Sequence 69849, A
125	45	35.4	40	17	US-10-781-102-9	Sequence 9, Appl	198	44.5	35.0	159	15	US-10-425-114-43153	Sequence 43153, A
126	45	35.4	60	17	US-10-781-102-8	Sequence 7642, Ap	199	44.5	35.0	171	15	US-10-425-114-47363	Sequence 47363, A
127	45	35.4	97	15	US-10-335-977-7642	Sequence 7641, Ap	200	44.5	35.0	258	15	US-10-424-559-218227	Sequence 218227, A
128	45	35.4	98	15	US-10-335-977-7641	Sequence 7641, Ap	201	44.5	35.0	368	15	US-10-469-993-12	Sequence 12, Appl
129	45	35.4	126	15	US-10-424-559-147359	Sequence 147359, A	202	44.5	35.0	404	16	US-10-437-963-130927	Sequence 130927, A
130	45	35.4	137	15	US-10-425-114-51360	Sequence 51360, A	203	44.5	35.0	410	15	US-10-425-114-81139	Sequence 81139, A
131	45	35.4	148	15	US-10-424-559-188811	Sequence 188811, A	204	44.5	35.0	417	17	US-10-369-493-21116	Sequence 21116, A
132	45	35.4	210	14	US-10-130-973A-13	Sequence 13, Appl	205	44.5	35.0	484	15	US-10-866-527-128	Sequence 128, App
133	45	35.4	215	15	US-10-312-222-36	Sequence 36, Appl	206	44.5	35.0	507	15	US-10-424-559-191824	Sequence 191824, A
134	45	35.4	216	15	US-10-312-222-33	Sequence 33, Appl	207	44.5	35.0	502	15	US-10-425-114-40675	Sequence 40675, A
135	45	35.4	255	16	US-10-484-298-5	Sequence 408, App	208	44.5	35.0	542	15	US-10-424-559-218225	Sequence 218225, A
136	45	35.4	259	15	US-10-424-559-277269	Sequence 277269, A	209	44.5	35.0	549	9	US-09-828-313-39	Sequence 39, Appl
137	45	35.4	260	16	US-10-408-765A-408	Sequence 408, App	210	44.5	35.0	549	16	US-10-768-863A-39	Sequence 39, Appl
138	45	35.4	260	17	US-10-791-155-1	Sequence 1, Appl	211	44.5	35.0	619	9	US-09-891-609-2	Sequence 2, Appl
139	45	35.4	260	17	US-10-791-155-5	Sequence 5, Appl	212	44.5	35.0	646	9	US-09-891-609-2	Sequence 2, Appl
140	45	35.4	273	17	US-10-729-571B-48	Sequence 48, Appl	213	44.5	35.0	842	14	US-10-241-009-2	Sequence 2, Appl
141	45	35.4	277	15	US-10-282-122A-57733	Sequence 57733, A	214	44.5	35.0	842	14	US-10-241-009-2	Sequence 2, Appl
142	45	35.4	325	16	US-10-484-298-8	Sequence 8, Appl	215	44.5	35.0	842	14	US-10-434B-2	Sequence 2, Appl
143	45	35.4	329	14	US-10-029-386-32201	Sequence 32201, A	216	44.5	35.0	842	14	US-10-190-405A-2	Sequence 2, Appl
144	45	35.4	356	15	US-10-424-559-165657	Sequence 165657, A	217	44.5	35.0	847	9	US-09-476-24-2	Sequence 2, Appl
145	45	35.4	440	16	US-10-484-298-6	Sequence 6, Appl	218	44	34.6	39	17	US-10-781-102-11	Sequence 11, Appl
146	45	35.4	448	14	US-10-130-973A-10	Sequence 10, Appl	219	44	34.6	68	15	US-10-424-559-161357	Sequence 161357, A
147	45	35.4	462	15	US-10-282-122A-53097	Sequence 53097, A	220	44	34.6	74	15	US-10-424-559-146899	Sequence 146899, A
148	45	35.4	497	15	US-10-104-047-2347	Sequence 2347, App	221	44	34.6	90	15	US-10-335-977-8761	Sequence 8761, Ap
149	45	35.4	508	16	US-10-466-947-174	Sequence 174, App	222	44	34.6	117	15	US-10-335-977-8761	Sequence 8761, Ap
150	45	35.4	510	16	US-10-484-298-9	Sequence 9, Appl	223	44	34.6	138	15	US-10-425-114-64012	Sequence 64012, A
151	45	35.4	535	14	US-10-224-209-2	Sequence 2, Appl	224	44	34.6	157	15	US-10-369-493-4207	Sequence 207, App
152	45	35.4	535	15	US-10-356-765-1	Sequence 1, Appl	225	44	34.6	180	16	US-10-767-701-60185	Sequence 60185, A
153	45	35.4	546	11	US-09-882-227-418	Sequence 418, App	226	44	34.6	182	15	US-10-424-559-199507	Sequence 199507, A
154	45	35.4	546	11	US-09-921-157-6	Sequence 6, Appl	227	44	34.6	196	16	US-10-437-963-102544	Sequence 102544, A
155	45	35.4	546	15	US-10-282-122A-58603	Sequence 58603, A	228	44	34.6	200	15	US-10-424-559-236486	Sequence 236486, A
156	45	35.4	546	15	US-10-335-977-7645	Sequence 7645, Ap	229	44	34.6	202	15	US-10-424-559-271745	Sequence 271745, A
157	45	35.4	547	16	US-10-437-963-179668	Sequence 179668, A	230	44	34.6	204	15	US-10-424-559-205955	Sequence 205955, A
158	45	35.4	567	16	US-10-792-517-4	Sequence 4, Appl	231	44	34.6	257	15	US-10-425-114-44806	Sequence 44806, A
159	45	35.4	605	14	US-10-130-973A-11	Sequence 11, Appl	232	44	34.6	263	15	US-10-335-977-8763	Sequence 8763, Ap

233	44	34.6	286	16	US-10-437-963-201175	Sequence 201175,	306	43	33.9	469	15	US-10-369-493-2943	Sequence 2943, Ap
234	44	34.6	300	15	US-10-424-599-225900	Sequence 225900,	307	43	33.9	477	15	US-10-161-927-62	Sequence 62, Appl
235	44	34.6	308	15	US-10-369-493-23066	Sequence 23066, A	308	43	33.9	485	14	US-10-055-475-17	Sequence 17, Appl
236	44	34.6	314	15	US-10-425-114-65717	Sequence 65717, A	309	43	33.9	490	8	US-08-781-986A-5212	Sequence 5212, Ap
237	44	34.6	316	15	US-10-425-114-55782	Sequence 55782, A	310	43	33.9	490	15	US-10-329-654-5212	Sequence 5212, Ap
238	44	34.6	327	16	US-10-437-963-135534	Sequence 135534,	311	43	33.9	510	15	US-10-369-493-56	Sequence 56, Appl
239	44	34.6	331	15	US-10-424-599-276035	Sequence 276035,	312	43	33.9	521	10	US-09-820-833A-93	Sequence 93, Appl
240	44	34.6	362	9	US-09-870-759-80	Sequence 80, Appl	313	43	33.9	539	16	US-10-375-010-32	Sequence 32, Appl
241	44	34.6	362	15	US-09-751-708A-80	Sequence 80, Appl	314	43	33.9	540	15	US-10-282-122A-47926	Sequence 47926, A
242	44	34.6	480	16	US-10-437-963-201442	Sequence 201442,	315	43	33.9	543	14	US-10-331-061-10	Sequence 10, Appl
243	44	34.6	484	15	US-10-282-122A-52836	Sequence 52836, A	316	43	33.9	553	15	US-10-282-122A-52087	Sequence 52087, A
244	44	34.6	491	9	US-09-815-242-5671	Sequence 5671, Ap	317	43	33.9	550	15	US-10-282-122A-50017	Sequence 50017, A
245	44	34.6	504	9	US-09-815-242-12692	Sequence 12692, A	318	43	33.9	552	15	US-10-369-493-2799	Sequence 2799, Ap
246	44	34.6	511	15	US-10-282-122A-44428	Sequence 44428, A	319	43	33.9	555	15	US-10-282-122A-67921	Sequence 67921, A
247	44	34.6	530	15	US-10-282-122A-77659	Sequence 77659, A	320	43	33.9	567	15	US-10-425-114-69463	Sequence 69463, A
248	44	34.6	547	9	US-09-738-626-5755	Sequence 5755, Ap	321	43	33.9	575	15	US-10-240-280-3	Sequence 3, Appl1
249	44	34.6	547	17	US-10-494-541-84	Sequence 541, Appl	322	43	33.9	579	15	US-10-389-566-753	Sequence 753, Appl
250	44	34.6	553	15	US-10-369-493-17467	Sequence 17467, A	323	43	33.9	587	15	US-10-282-122A-57721	Sequence 57721, A
251	44	34.6	555	13	US-10-024-809-2	Sequence 2, Appl1	324	43	33.9	594	15	US-10-369-493-3337	Sequence 3337, Ap
252	44	34.6	557	15	US-10-424-599-236485	Sequence 236485,	325	43	33.9	608	15	US-10-282-122A-71442	Sequence 71442, A
253	44	34.6	571	15	US-10-369-493-39	Sequence 39, Appl	326	43	33.9	625	16	US-10-437-963-152224	Sequence 152224,
254	44	34.6	718	15	US-10-437-963-196494	Sequence 196494,	327	43	33.9	684	15	US-10-282-122A-47915	Sequence 47915, A
255	44	34.6	726	17	US-10-483-680-2	Sequence 2, Appl1	328	43	33.9	775	15	US-10-437-963-169845	Sequence 169845,
256	44	34.6	748	15	US-10-282-122A-48709	Sequence 48709, A	329	43	33.9	821	15	US-10-369-493-2791	Sequence 2791, Ap
257	44	34.6	814	15	US-10-282-122A-52462	Sequence 52462, A	330	43	33.9	871	15	US-09-815-242-13179	Sequence 13179, A
258	44	34.6	1078	16	US-10-437-963-196472	Sequence 196472,	331	43	33.9	887	9	US-10-282-122A-74187	Sequence 74187, A
259	44	34.6	1905	11	US-09-964-956-44	Sequence 44, Appl	332	43	33.9	890	15	US-10-474-776-393	Sequence 393, Appl
260	44	34.6	3196	15	US-10-282-122A-59535	Sequence 59535, A	333	43	33.9	890	16	US-10-473-276-3	Sequence 3, Appl1
261	43.5	34.3	107	15	US-10-424-599-244888	Sequence 244888,	334	43	33.9	1004	15	US-10-296-724-399	Sequence 399, Appl
262	43.5	34.3	148	15	US-10-424-599-155154	Sequence 155154,	335	43	33.9	1093	15	US-10-296-724-393	Sequence 393, Appl
263	43.5	34.3	174	15	US-10-424-599-149808	Sequence 149808,	336	43	33.9	1396	15	US-10-437-963-142027	Sequence 142027,
264	43.5	34.3	269	16	US-10-437-963-203722	Sequence 203722,	337	43	33.9	1441	16	US-10-329-079-11	Sequence 11, Appl
265	43.5	34.3	270	16	US-10-437-963-171875	Sequence 171875,	338	43	33.9	1545	14	US-10-329-079-45	Sequence 45, Appl
266	43.5	34.3	429	15	US-10-282-122A-75835	Sequence 75835, A	339	43	33.9	5547	15	US-10-296-724-405	Sequence 405, Appl
267	43.5	34.3	473	15	US-10-425-114-55734	Sequence 55734, A	340	42.5	33.5	131	16	US-10-437-963-153143	Sequence 153143,
268	43.5	34.3	477	9	US-09-815-242-13991	Sequence 13991, A	341	42.5	33.5	147	15	US-10-424-599-176645	Sequence 176645,
269	43.5	34.3	490	17	US-10-675-086-24	Sequence 24, Appl	342	42.5	33.5	215	15	US-10-424-599-270242	Sequence 270242,
270	43.5	34.3	495	10	US-09-848-806-1	Sequence 1, Appl1	343	42.5	33.5	220	15	US-10-424-599-149696	Sequence 149696,
271	43.5	34.3	500	17	US-10-866-527-38	Sequence 38, Appl	344	42.5	33.5	223	15	US-09-974-298-147	Sequence 147, Appl
272	43.5	34.3	501	10	US-09-848-806-3	Sequence 3, Appl1	345	42.5	33.5	240	9	US-10-767-701-32851	Sequence 32851, A
273	43.5	34.3	512	17	US-10-866-527-108	Sequence 108, App	346	42.5	33.5	260	16	US-10-767-701-32851	Sequence 131111,
274	43.5	34.3	550	16	US-10-437-963-153480	Sequence 153480,	347	42.5	33.5	270	16	US-10-437-963-131111	Sequence 50274, A
275	43.5	34.3	619	15	US-10-369-493-19203	Sequence 19203, A	348	42.5	33.5	272	15	US-10-028-072-130274	Sequence 136, App
276	43.5	34.3	673	14	US-10-156-761-11243	Sequence 11243, A	349	42.5	33.5	278	14	US-10-143-114-136	Sequence 136, App
277	43.5	34.3	999	16	US-10-437-963-117353	Sequence 117353,	350	42.5	33.5	278	14	US-10-140-808-136	Sequence 136, App
278	43.5	34.3	2402	14	US-10-203-224-2	Sequence 2, Appl1	351	42.5	33.5	278	14	US-10-121-049-136	Sequence 136, App
279	43	33.9	42	14	US-10-029-386-31644	Sequence 31644, A	352	42.5	33.5	278	14	US-10-123-904-136	Sequence 136, App
280	43	33.9	71	17	US-10-472-928-3054	Sequence 3054, Ap	353	42.5	33.5	278	14	US-10-175-746-136	Sequence 136, App
281	43	33.9	83	15	US-10-424-599-194945	Sequence 194945,	354	42.5	33.5	278	14	US-10-175-746-136	Sequence 136, App
282	43	33.9	135	16	US-10-767-701-55426	Sequence 55426, A	355	42.5	33.5	278	14	US-10-175-921-136	Sequence 136, App
283	43	33.9	148	16	US-10-437-963-104683	Sequence 104683,	356	42.5	33.5	278	14	US-10-175-921-136	Sequence 136, App
284	43	33.9	161	15	US-10-424-599-201005	Sequence 201005,	357	42.5	33.5	278	14	US-10-137-865-136	Sequence 136, App
285	43	33.9	170	15	US-10-335-977-6498	Sequence 6498, Ap	358	42.5	33.5	278	14	US-10-140-474-136	Sequence 136, App
286	43	33.9	172	15	US-10-335-977-6498	Sequence 6498, Ap	359	42.5	33.5	278	14	US-10-140-474-136	Sequence 136, App
287	43	33.9	172	15	US-10-369-493-21205	Sequence 21205, A	360	42.5	33.5	278	14	US-10-143-114-136	Sequence 136, App
288	43	33.9	172	15	US-10-282-122A-68573	Sequence 68573, A	361	42.5	33.5	278	14	US-10-143-114-136	Sequence 136, App
289	43	33.9	184	10	US-09-873-546-15	Sequence 15, Appl	362	42.5	33.5	278	14	US-10-143-114-136	Sequence 136, App
290	43	33.9	196	9	US-09-764-877-1830	Sequence 1830, Ap	363	42.5	33.5	278	14	US-10-143-114-136	Sequence 136, App
291	43	33.9	196	15	US-10-242-515-1830	Sequence 1830, Ap	364	42.5	33.5	278	14	US-10-121-050-136	Sequence 136, App
292	43	33.9	210	16	US-10-767-701-36983	Sequence 36983, A	365	42.5	33.5	278	14	US-10-141-735-136	Sequence 136, App
293	43	33.9	304	15	US-10-424-599-280749	Sequence 280749,	366	42.5	33.5	278	14	US-10-141-735-136	Sequence 136, App
294	43	33.9	311	14	US-10-219-810-49	Sequence 49, Appl	367	42.5	33.5	278	14	US-10-143-114-136	Sequence 136, App
295	43	33.9	340	15	US-10-424-599-260951	Sequence 260951,	368	42.5	33.5	278	14	US-10-123-236-136	Sequence 136, App
296	43	33.9	343	15	US-10-335-977-6502	Sequence 6502, Ap	369	42.5	33.5	278	14	US-10-123-236-136	Sequence 136, App
297	43	33.9	407	15	US-10-108-260A-4092	Sequence 4092, Ap	370	42.5	33.5	278	14	US-10-140-921-136	Sequence 136, App
298	43	33.9	453	14	US-10-156-761-12790	Sequence 12790, A	371	42.5	33.5	278	14	US-10-140-921-136	Sequence 136, App
299	43	33.9	455	15	US-10-369-493-18160	Sequence 18160, A	372	42.5	33.5	278	14	US-10-121-045-136	Sequence 136, App
300	43	33.9	467	9	US-09-875-573-17	Sequence 17, Appl	373	42.5	33.5	278	14	US-10-123-232-136	Sequence 136, App
301	43	33.9	467	9	US-09-875-573-19	Sequence 19, Appl	374	42.5	33.5	278	14	US-10-123-232-136	Sequence 136, App
302	43	33.9	467	9	US-09-875-573-21	Sequence 21, Appl	375	42.5	33.5	278	14	US-10-123-232-136	Sequence 136, App
303	43	33.9	467	15	US-10-417-700A-39	Sequence 39, Appl	376	42.5	33.5	278	14	US-10-124-819-136	Sequence 136, App
304	43	33.9	468	9	US-09-875-573-23	Sequence 23, Appl	377	42.5	33.5	278	14	US-10-124-822-136	Sequence 136, App
305	43	33.9	468	9	US-09-875-573-25	Sequence 25, Appl	378	42.5	33.5	278	14	US-10-140-925-136	Sequence 136, App
			468	9	US-09-875-573-27	Sequence 27, Appl	378	42.5	33.5	278	14	US-10-160-498-136	Sequence 136, App

379	42.5	33.5	278	14	US-10-124-824-136	Sequence 136, App	452	42.5	33.5	278	14	US-10-124-815-136	Sequence 136, App
380	42.5	33.5	278	14	US-10-127-825A-136	Sequence 136, App	453	42.5	33.5	278	14	US-10-125-921A-136	Sequence 136, App
381	42.5	33.5	278	14	US-10-127-829A-136	Sequence 136, App	454	42.5	33.5	278	14	US-10-125-928A-136	Sequence 136, App
382	42.5	33.5	278	14	US-10-127-835A-136	Sequence 136, App	455	42.5	33.5	278	14	US-10-127-821A-136	Sequence 136, App
383	42.5	33.5	278	14	US-10-127-839A-136	Sequence 136, App	456	42.5	33.5	278	14	US-10-127-822A-136	Sequence 136, App
384	42.5	33.5	278	14	US-10-127-901A-136	Sequence 136, App	457	42.5	33.5	278	14	US-10-127-824A-136	Sequence 136, App
385	42.5	33.5	278	14	US-10-128-693A-136	Sequence 136, App	458	42.5	33.5	278	14	US-10-127-826A-136	Sequence 136, App
386	42.5	33.5	278	14	US-10-131-813A-136	Sequence 136, App	459	42.5	33.5	278	14	US-10-127-827A-136	Sequence 136, App
387	42.5	33.5	278	14	US-10-131-818A-136	Sequence 136, App	460	42.5	33.5	278	14	US-10-127-828A-136	Sequence 136, App
388	42.5	33.5	278	14	US-10-131-823A-136	Sequence 136, App	461	42.5	33.5	278	14	US-10-127-830A-136	Sequence 136, App
389	42.5	33.5	278	14	US-10-131-824A-136	Sequence 136, App	462	42.5	33.5	278	14	US-10-127-832A-136	Sequence 136, App
390	42.5	33.5	278	14	US-10-131-830A-136	Sequence 136, App	463	42.5	33.5	278	14	US-10-127-833A-136	Sequence 136, App
391	42.5	33.5	278	14	US-10-131-837A-136	Sequence 136, App	464	42.5	33.5	278	14	US-10-127-834A-136	Sequence 136, App
392	42.5	33.5	278	14	US-10-137-807A-136	Sequence 136, App	465	42.5	33.5	278	14	US-10-127-836A-136	Sequence 136, App
393	42.5	33.5	278	14	US-10-147-500-136	Sequence 136, App	466	42.5	33.5	278	14	US-10-127-841A-136	Sequence 136, App
394	42.5	33.5	278	14	US-10-147-502-136	Sequence 136, App	467	42.5	33.5	278	14	US-10-127-842A-136	Sequence 136, App
395	42.5	33.5	278	14	US-10-147-515-136	Sequence 136, App	468	42.5	33.5	278	14	US-10-128-687A-136	Sequence 136, App
396	42.5	33.5	278	14	US-10-147-517-136	Sequence 136, App	469	42.5	33.5	278	14	US-10-128-688A-136	Sequence 136, App
397	42.5	33.5	278	14	US-10-147-526-136	Sequence 136, App	470	42.5	33.5	278	14	US-10-128-689A-136	Sequence 136, App
398	42.5	33.5	278	14	US-10-147-527-136	Sequence 136, App	471	42.5	33.5	278	14	US-10-128-694A-136	Sequence 136, App
399	42.5	33.5	278	14	US-10-121-041-136	Sequence 136, App	472	42.5	33.5	278	14	US-10-131-825A-136	Sequence 136, App
400	42.5	33.5	278	14	US-10-121-043-136	Sequence 136, App	473	42.5	33.5	278	14	US-10-123-017-136	Sequence 136, App
401	42.5	33.5	278	14	US-10-121-047-136	Sequence 136, App	474	42.5	33.5	278	14	US-10-131-815A-136	Sequence 136, App
402	42.5	33.5	278	14	US-10-123-215-136	Sequence 136, App	475	42.5	33.5	278	14	US-10-131-817A-136	Sequence 136, App
403	42.5	33.5	278	14	US-10-123-902-136	Sequence 136, App	476	42.5	33.5	278	14	US-10-131-821A-136	Sequence 136, App
404	42.5	33.5	278	14	US-10-123-908-136	Sequence 136, App	477	42.5	33.5	278	14	US-10-131-822A-136	Sequence 136, App
405	42.5	33.5	278	14	US-10-123-909-136	Sequence 136, App	478	42.5	33.5	278	14	US-10-131-828A-136	Sequence 136, App
406	42.5	33.5	278	14	US-10-123-910-136	Sequence 136, App	479	42.5	33.5	278	14	US-10-131-835A-136	Sequence 136, App
407	42.5	33.5	278	14	US-10-124-813-136	Sequence 136, App	480	42.5	33.5	278	14	US-10-137-684A-136	Sequence 136, App
408	42.5	33.5	278	14	US-10-124-817-136	Sequence 136, App	481	42.5	33.5	278	14	US-10-137-689A-136	Sequence 136, App
409	42.5	33.5	278	14	US-10-125-922-136	Sequence 136, App	482	42.5	33.5	278	14	US-10-147-823-136	Sequence 136, App
410	42.5	33.5	278	14	US-10-125-924-136	Sequence 136, App	483	42.5	33.5	278	14	US-10-158-785-136	Sequence 136, App
411	42.5	33.5	278	14	US-10-140-860-136	Sequence 136, App	484	42.5	33.5	278	14	US-10-121-051-136	Sequence 136, App
412	42.5	33.5	278	14	US-10-143-417-136	Sequence 136, App	485	42.5	33.5	278	14	US-10-121-042-136	Sequence 136, App
413	42.5	33.5	278	14	US-10-147-519-136	Sequence 136, App	486	42.5	33.5	278	14	US-10-123-012-136	Sequence 136, App
414	42.5	33.5	278	14	US-10-157-782-136	Sequence 136, App	487	42.5	33.5	278	14	US-10-192-807-136	Sequence 136, App
415	42.5	33.5	278	14	US-10-152-395-136	Sequence 136, App	488	42.5	33.5	278	14	US-10-194-359-136	Sequence 136, App
416	42.5	33.5	278	14	US-10-125-926A-136	Sequence 136, App	489	42.5	33.5	278	14	US-10-137-866-136	Sequence 136, App
417	42.5	33.5	278	14	US-10-125-930A-136	Sequence 136, App	490	42.5	33.5	278	14	US-10-141-702-136	Sequence 136, App
418	42.5	33.5	278	14	US-10-127-831A-136	Sequence 136, App	491	42.5	33.5	278	14	US-10-146-127-136	Sequence 136, App
419	42.5	33.5	278	14	US-10-127-837A-136	Sequence 136, App	492	42.5	33.5	278	14	US-10-146-127-136	Sequence 136, App
420	42.5	33.5	278	14	US-10-127-838B-136	Sequence 136, App	493	42.5	33.5	278	14	US-10-146-788-136	Sequence 136, App
421	42.5	33.5	278	14	US-10-127-842A-136	Sequence 136, App	494	42.5	33.5	278	14	US-10-152-980-136	Sequence 136, App
422	42.5	33.5	278	14	US-10-127-843A-136	Sequence 136, App	495	42.5	33.5	278	14	US-10-153-934-136	Sequence 136, App
423	42.5	33.5	278	14	US-10-127-845A-136	Sequence 136, App	496	42.5	33.5	278	14	US-10-140-807-136	Sequence 136, App
424	42.5	33.5	278	14	US-10-127-846A-136	Sequence 136, App	497	42.5	33.5	278	14	US-10-140-924A-136	Sequence 136, App
425	42.5	33.5	278	14	US-10-127-848A-136	Sequence 136, App	498	42.5	33.5	278	14	US-10-140-926-136	Sequence 136, App
426	42.5	33.5	278	14	US-10-127-849A-136	Sequence 136, App	499	42.5	33.5	278	14	US-10-141-698-136	Sequence 136, App
427	42.5	33.5	278	14	US-10-127-850A-136	Sequence 136, App	500	42.5	33.5	278	14	US-10-141-702-136	Sequence 136, App
428	42.5	33.5	278	14	US-10-128-684A-136	Sequence 136, App	501	42.5	33.5	278	14	US-10-141-704-136	Sequence 136, App
429	42.5	33.5	278	14	US-10-128-685A-136	Sequence 136, App	502	42.5	33.5	278	14	US-10-142-121-136	Sequence 136, App
430	42.5	33.5	278	14	US-10-128-686A-136	Sequence 136, App	503	42.5	33.5	278	14	US-10-142-132-136	Sequence 136, App
431	42.5	33.5	278	14	US-10-128-680A-136	Sequence 136, App	504	42.5	33.5	278	14	US-10-142-167-136	Sequence 136, App
432	42.5	33.5	278	14	US-10-128-691A-136	Sequence 136, App	505	42.5	33.5	278	14	US-10-143-033-136	Sequence 136, App
433	42.5	33.5	278	14	US-10-131-819A-136	Sequence 136, App	506	42.5	33.5	278	14	US-10-144-894A-136	Sequence 136, App
434	42.5	33.5	278	14	US-10-131-829A-136	Sequence 136, App	507	42.5	33.5	278	14	US-10-145-628-136	Sequence 136, App
435	42.5	33.5	278	14	US-10-131-829A-136	Sequence 136, App	508	42.5	33.5	278	14	US-10-145-746-136	Sequence 136, App
436	42.5	33.5	278	14	US-10-146-729-136	Sequence 136, App	509	42.5	33.5	278	14	US-10-145-748-136	Sequence 136, App
437	42.5	33.5	278	14	US-10-146-791-136	Sequence 136, App	510	42.5	33.5	278	14	US-10-145-823-136	Sequence 136, App
438	42.5	33.5	278	14	US-10-147-508A-136	Sequence 136, App	511	42.5	33.5	278	14	US-10-145-826-136	Sequence 136, App
439	42.5	33.5	278	14	US-10-147-508-136	Sequence 136, App	512	42.5	33.5	278	14	US-10-145-870-136	Sequence 136, App
440	42.5	33.5	278	14	US-10-147-512-136	Sequence 136, App	513	42.5	33.5	278	14	US-10-145-876-136	Sequence 136, App
441	42.5	33.5	278	14	US-10-175-752-136	Sequence 136, App	514	42.5	33.5	278	14	US-10-145-959-136	Sequence 136, App
442	42.5	33.5	278	14	US-10-121-040-136	Sequence 136, App	515	42.5	33.5	278	14	US-10-146-725-136	Sequence 136, App
443	42.5	33.5	278	14	US-10-121-056-136	Sequence 136, App	516	42.5	33.5	278	14	US-10-146-725-136	Sequence 136, App
444	42.5	33.5	278	14	US-10-121-061-136	Sequence 136, App	517	42.5	33.5	278	14	US-10-146-795-136	Sequence 136, App
445	42.5	33.5	278	14	US-10-123-815-136	Sequence 136, App	518	42.5	33.5	278	14	US-10-147-495-136	Sequence 136, App
446	42.5	33.5	278	14	US-10-124-818-136	Sequence 136, App	519	42.5	33.5	278	14	US-10-147-501-136	Sequence 136, App
447	42.5	33.5	278	14	US-10-137-868-136	Sequence 136, App	520	42.5	33.5	278	14	US-10-147-504-136	Sequence 136, App
448	42.5	33.5	278	14	US-10-147-492-136	Sequence 136, App	521	42.5	33.5	278	14	US-10-147-506-136	Sequence 136, App
449	42.5	33.5	278	14	US-10-158-782-136	Sequence 136, App	522	42.5	33.5	278	14	US-10-147-509-136	Sequence 136, App
450	42.5	33.5	278	14	US-10-123-905-136	Sequence 136, App	523	42.5	33.5	278	14	US-10-147-510-136	Sequence 136, App
451	42.5	33.5	278	14	US-10-123-907-136	Sequence 136, App	524	42.5	33.5	278	14	US-10-147-511-136	Sequence 136, App

525	42.5	33.5	278	14	US-10-147-529-136	Sequence 136, App	598	42.5	33.5	278	14	US-10-147-480-136	Sequence 136, App
526	42.5	33.5	278	14	US-10-152-397-136	Sequence 136, App	599	42.5	33.5	278	14	US-10-147-488-136	Sequence 136, App
527	42.5	33.5	278	14	US-10-153-586-136	Sequence 136, App	600	42.5	33.5	278	14	US-10-147-486-136	Sequence 136, App
528	42.5	33.5	278	14	US-10-158-786-136	Sequence 136, App	601	42.5	33.5	278	14	US-10-147-487-136	Sequence 136, App
529	42.5	33.5	278	14	US-10-137-870-136	Sequence 136, App	602	42.5	33.5	278	14	US-10-147-490-136	Sequence 136, App
530	42.5	33.5	278	14	US-10-140-018-136	Sequence 136, App	603	42.5	33.5	278	14	US-10-147-494-136	Sequence 136, App
531	42.5	33.5	278	14	US-10-140-021-136	Sequence 136, App	604	42.5	33.5	278	14	US-10-147-498-136	Sequence 136, App
532	42.5	33.5	278	14	US-10-140-471-136	Sequence 136, App	605	42.5	33.5	278	14	US-10-147-514-136	Sequence 136, App
533	42.5	33.5	278	14	US-10-140-922-136	Sequence 136, App	606	42.5	33.5	278	14	US-10-147-524-136	Sequence 136, App
534	42.5	33.5	278	14	US-10-145-631-136	Sequence 136, App	607	42.5	33.5	278	14	US-10-152-379-136	Sequence 136, App
535	42.5	33.5	278	14	US-10-145-633-136	Sequence 136, App	608	42.5	33.5	278	14	US-10-152-394-136	Sequence 136, App
536	42.5	33.5	278	14	US-10-158-783-136	Sequence 136, App	609	42.5	33.5	278	14	US-10-152-406-136	Sequence 136, App
537	42.5	33.5	278	14	US-10-140-274-136	Sequence 136, App	610	42.5	33.5	278	14	US-10-156-887-136	Sequence 136, App
538	42.5	33.5	278	14	US-10-140-022-136	Sequence 136, App	611	42.5	33.5	278	14	US-10-157-778-136	Sequence 136, App
539	42.5	33.5	278	14	US-10-140-022-136	Sequence 136, App	612	42.5	33.5	278	14	US-10-157-799-136	Sequence 136, App
540	42.5	33.5	278	14	US-10-140-861-136	Sequence 136, App	613	42.5	33.5	278	14	US-10-160-504-136	Sequence 136, App
541	42.5	33.5	278	14	US-10-140-862-136	Sequence 136, App	614	42.5	33.5	278	14	US-10-145-634-136	Sequence 136, App
542	42.5	33.5	278	14	US-10-141-697-136	Sequence 136, App	615	42.5	33.5	278	14	US-10-147-520-136	Sequence 136, App
543	42.5	33.5	278	14	US-10-141-700-136	Sequence 136, App	616	42.5	33.5	278	14	US-10-157-781-136	Sequence 136, App
544	42.5	33.5	278	14	US-10-141-705-136	Sequence 136, App	617	42.5	33.5	278	14	US-10-157-788-136	Sequence 136, App
545	42.5	33.5	278	14	US-10-141-753-136	Sequence 136, App	618	42.5	33.5	278	14	US-10-157-791-136	Sequence 136, App
546	42.5	33.5	278	14	US-10-141-758-136	Sequence 136, App	619	42.5	33.5	278	14	US-10-157-378-136	Sequence 136, App
547	42.5	33.5	278	14	US-10-142-418-136	Sequence 136, App	620	42.5	33.5	278	14	US-10-152-382-136	Sequence 136, App
548	42.5	33.5	278	14	US-10-142-420-136	Sequence 136, App	621	42.5	33.5	278	14	US-10-152-383-136	Sequence 136, App
549	42.5	33.5	278	14	US-10-142-422-136	Sequence 136, App	622	42.5	33.5	278	14	US-10-152-384-136	Sequence 136, App
550	42.5	33.5	278	14	US-10-142-427-136	Sequence 136, App	623	42.5	33.5	278	14	US-10-152-387-136	Sequence 136, App
551	42.5	33.5	278	14	US-10-142-760-136	Sequence 136, App	624	42.5	33.5	278	14	US-10-152-389-136	Sequence

671	42.5	33.5	278	14	US-10-152-391-136	Sequence 136, App	744	42.5	33.5	278	15	US-10-152-381-136	Sequence 136, App
672	42.5	33.5	278	14	US-10-152-399-136	Sequence 136, App	745	42.5	33.5	278	15	US-10-152-400-136	Sequence 136, App
673	42.5	33.5	278	14	US-10-156-848-136	Sequence 136, App	746	42.5	33.5	278	15	US-10-153-585-136	Sequence 136, App
674	42.5	33.5	278	14	US-10-157-785-136	Sequence 136, App	747	42.5	33.5	278	15	US-10-157-780-136	Sequence 136, App
675	42.5	33.5	278	14	US-10-157-794-136	Sequence 136, App	748	42.5	33.5	278	15	US-10-157-800-136	Sequence 136, App
676	42.5	33.5	278	14	US-10-157-796-136	Sequence 136, App	749	42.5	33.5	278	15	US-10-157-801-136	Sequence 136, App
677	42.5	33.5	278	14	US-10-160-500-136	Sequence 136, App	750	42.5	33.5	278	15	US-10-157-802-136	Sequence 136, App
678	42.5	33.5	278	14	US-10-121-046-136	Sequence 136, App	751	42.5	33.5	278	15	US-10-158-784-136	Sequence 136, App
679	42.5	33.5	278	14	US-10-123-156-136	Sequence 136, App	752	42.5	33.5	278	15	US-10-158-789-136	Sequence 136, App
680	42.5	33.5	278	14	US-10-123-214-136	Sequence 136, App	753	42.5	33.5	278	15	US-10-192-011-136	Sequence 136, App
681	42.5	33.5	278	14	US-10-125-805-136	Sequence 136, App	754	42.5	33.5	278	15	US-10-139-963-136	Sequence 136, App
682	42.5	33.5	278	14	US-10-124-821-136	Sequence 136, App	755	42.5	33.5	278	15	US-10-140-020-136	Sequence 136, App
683	42.5	33.5	278	14	US-10-152-385-136	Sequence 136, App	756	42.5	33.5	278	15	US-10-140-023-136	Sequence 136, App
684	42.5	33.5	278	14	US-10-152-393-136	Sequence 136, App	757	42.5	33.5	278	15	US-10-140-809-136	Sequence 136, App
685	42.5	33.5	278	14	US-10-152-396-136	Sequence 136, App	758	42.5	33.5	278	15	US-10-140-865-136	Sequence 136, App
686	42.5	33.5	278	14	US-10-153-552-136	Sequence 136, App	759	42.5	33.5	278	15	US-10-141-701-136	Sequence 136, App
687	42.5	33.5	278	14	US-10-153-840-136	Sequence 136, App	760	42.5	33.5	278	15	US-10-141-754-136	Sequence 136, App
688	42.5	33.5	278	14	US-10-156-841-136	Sequence 136, App	761	42.5	33.5	278	15	US-10-141-760-136	Sequence 136, App
689	42.5	33.5	278	14	US-10-156-842-136	Sequence 136, App	762	42.5	33.5	278	15	US-10-142-425-136	Sequence 136, App
690	42.5	33.5	278	14	US-10-156-844-136	Sequence 136, App	763	42.5	33.5	278	15	US-10-142-430-136	Sequence 136, App
691	42.5	33.5	278	14	US-10-156-845-136	Sequence 136, App	764	42.5	33.5	278	15	US-10-143-113-136	Sequence 136, App
692	42.5	33.5	278	14	US-10-156-846-136	Sequence 136, App	765	42.5	33.5	278	15	US-10-146-730-136	Sequence 136, App
693	42.5	33.5	278	14	US-10-121-048-136	Sequence 136, App	766	42.5	33.5	278	15	US-10-146-792-136	Sequence 136, App
694	42.5	33.5	278	14	US-10-121-052-136	Sequence 136, App	767	42.5	33.5	278	15	US-10-158-791-136	Sequence 136, App
695	42.5	33.5	278	14	US-10-121-053-136	Sequence 136, App	768	42.5	33.5	278	15	US-10-158-843-136	Sequence 136, App
696	42.5	33.5	278	14	US-10-121-054-136	Sequence 136, App	769	42.5	33.5	278	15	US-10-157-786-136	Sequence 136, App
697	42.5	33.5	278	14	US-10-121-063-136	Sequence 136, App	770	42.5	33.5	278	15	US-10-152-405-136	Sequence 136, App
698	42.5	33.5	278	14	US-10-123-212-136	Sequence 136, App	771	42.5	33.5	278	15	US-10-147-528-136	Sequence 136, App
699	42.5	33.5	278	14	US-10-123-213-136	Sequence 136, App	772	42.5	33.5	278	15	US-10-126-103-151	Sequence 136, App
700	42.5	33.5	278	14	US-10-123-291-136	Sequence 136, App	773	42.5	33.5	278	15	US-10-128-692A-136	Sequence 136, App
701	42.5	33.5	278	14	US-10-123-322-136	Sequence 136, App	774	42.5	33.5	278	15	US-10-140-927-136	Sequence 136, App
702	42.5	33.5	278	14	US-10-123-771-136	Sequence 136, App	775	42.5	33.5	278	15	US-10-147-493-136	Sequence 136, App
703	42.5	33.5	278	14	US-10-123-911-136	Sequence 136, App	776	42.5	33.5	278	15	US-10-145-127-136	Sequence 136, App
704	42.5	33.5	278	14	US-10-124-823-136	Sequence 136, App	777	42.5	33.5	278	15	US-10-160-503-136	Sequence 136, App
705	42.5	33.5	278	14	US-10-125-931-136	Sequence 136, App	778	42.5	33.5	278	15	US-10-143-118-136	Sequence 136, App
706	42.5	33.5	278	14	US-10-125-932-136	Sequence 136, App	779	42.5	33.5	278	15	US-10-144-993-136	Sequence 136, App
707	42.5	33.5	278	15	US-10-127-852A-136	Sequence 136, App	780	42.5	33.5	278	15	US-10-262-839-70	Sequence 70, Appl
708	42.5	33.5	278	15	US-10-127-900A-136	Sequence 136, App	781	42.5	33.5	278	15	US-10-158-787-136	Sequence 136, App
709	42.5	33.5	278	15	US-10-128-685A-136	Sequence 136, App	782	42.5	33.5	278	15	US-10-140-024-136	Sequence 136, App
710	42.5	33.5	278	15	US-10-131-820A-136	Sequence 136, App	783	42.5	33.5	278	15	US-10-147-536-136	Sequence 136, App
711	42.5	33.5	278	15	US-10-142-886-136	Sequence 136, App	784	42.5	33.5	278	15	US-10-431-096-151	Sequence 151, App
712	42.5	33.5	278	15	US-10-146-728-136	Sequence 136, App	785	42.5	33.5	278	16	US-10-152-372-136	Sequence 136, App
713	42.5	33.5	278	15	US-10-146-786-136	Sequence 136, App	786	42.5	33.5	278	17	US-10-931-886-136	Sequence 136, App
714	42.5	33.5	278	15	US-10-147-499-136	Sequence 136, App	787	42.5	33.5	278	17	US-10-158-788-136	Sequence 136, App
715	42.5	33.5	278	15	US-10-157-798-136	Sequence 136, App	788	42.5	33.5	334	15	US-10-425-114-40593	Sequence 40593, A
716	42.5	33.5	278	15	US-10-123-913-136	Sequence 136, App	789	42.5	33.5	334	15	US-10-425-114-45796	Sequence 45796, A
717	42.5	33.5	278	15	US-10-140-473-136	Sequence 136, App	790	42.5	33.5	351	14	US-10-156-615-2	Sequence 2, Appl1
718	42.5	33.5	278	15	US-10-140-806-136	Sequence 136, App	791	42.5	33.5	351	17	US-10-938-016-2	Sequence 2, Appl1
719	42.5	33.5	278	15	US-10-140-810-136	Sequence 136, App	792	42.5	33.5	353	15	US-10-264-049-3045	Sequence 3045, Ap
720	42.5	33.5	278	15	US-10-140-863-136	Sequence 136, App	793	42.5	33.5	377	15	US-10-425-114-45684	Sequence 45684, A
721	42.5	33.5	278	15	US-10-141-699-136	Sequence 136, App	794	42.5	33.5	383	15	US-10-425-114-48982	Sequence 48982, A
722	42.5	33.5	278	15	US-10-141-703-136	Sequence 136, App	795	42.5	33.5	408	15	US-10-424-599-241708	Sequence 241708, A
723	42.5	33.5	278	15	US-10-141-706-136	Sequence 136, App	796	42.5	33.5	424	15	US-10-369-493-232	Sequence 232, App
724	42.5	33.5	278	15	US-10-141-757-136	Sequence 136, App	797	42.5	33.5	429	9	US-09-815-242-10098	Sequence 10098, A
725	42.5	33.5	278	15	US-10-141-762-136	Sequence 136, App	798	42.5	33.5	429	15	US-10-369-443-770	Sequence 770, App
726	42.5	33.5	278	15	US-10-142-428-136	Sequence 136, App	799	42.5	33.5	429	15	US-10-282-122A-56485	Sequence 56485, A
727	42.5	33.5	278	15	US-10-142-429-136	Sequence 136, App	800	42.5	33.5	435	15	US-10-282-122A-59565	Sequence 59565, A
728	42.5	33.5	278	15	US-10-142-884-136	Sequence 136, App	801	42.5	33.5	437	14	US-10-156-761-14620	Sequence 14620, A
729	42.5	33.5	278	15	US-10-143-027-136	Sequence 136, App	802	42.5	33.5	506	17	US-10-866-527-118	Sequence 118, App
730	42.5	33.5	278	15	US-10-143-115-136	Sequence 136, App	803	42.5	33.5	518	16	US-10-437-963-168927	Sequence 168927, A
731	42.5	33.5	278	15	US-10-144-956-136	Sequence 136, App	804	42.5	33.5	546	11	US-09-764-875-1122	Sequence 1122, Ap
732	42.5	33.5	278	15	US-10-144-958-136	Sequence 136, App	805	42.5	33.5	567	11	US-10-424-599-241719	Sequence 241719, A
733	42.5	33.5	278	15	US-10-145-632-136	Sequence 136, App	806	42.5	33.5	568	11	US-09-764-875-832	Sequence 832, App
734	42.5	33.5	278	15	US-10-145-749-136	Sequence 136, App	807	42.5	33.5	600	16	US-10-437-963-104086	Sequence 104086, A
735	42.5	33.5	278	15	US-10-145-753-136	Sequence 136, App	808	42.5	33.5	812	15	US-10-424-599-241731	Sequence 241731, A
736	42.5	33.5	278	15	US-10-145-871-136	Sequence 136, App	809	42.5	33.5	824	15	US-10-425-114-45934	Sequence 45934, A
737	42.5	33.5	278	15	US-10-146-794-136	Sequence 136, App	810	42.5	33.5	883	16	US-10-441-926-2	Sequence 2, Appl1
738	42.5	33.5	278	15	US-10-146-794-136	Sequence 136, App	811	42.5	33.5	883	16	US-10-441-926-2	Sequence 2, Appl1
739	42.5	33.5	278	15	US-10-147-489-136	Sequence 136, App	812	42.5	33.1	16	US-10-020-269-10	Sequence 30, Appl1	
740	42.5	33.5	278	15	US-10-147-507-136	Sequence 136, App	813	42	33.1	44	US-09-877-843-84	Sequence 84, Appl1	
741	42.5	33.5	278	15	US-10-147-535-136	Sequence 136, App	814	42	33.1	60	US-09-9		



817	42	33.1	60	15	US-10-667-464-23	Sequence 23, Appl	890	42	33.1	485	15	US-10-425-114-59189	Sequence 59189, A
818	42	33.1	78	15	US-10-369-493-20021	Sequence 20021, A	891	42	33.1	485	15	US-10-425-114-59993	Sequence 59993, A
819	42	33.1	82	15	US-10-424-599-180924	Sequence 180924, A	892	42	33.1	485	15	US-10-425-114-62688	Sequence 62688, A
820	42	33.1	94	15	US-10-424-599-228445	Sequence 228445, A	893	42	33.1	485	15	US-10-425-114-66115	Sequence 66115, A
821	42	33.1	127	15	US-10-424-599-161945	Sequence 161945, A	894	42	33.1	485	15	US-10-425-114-72073	Sequence 72073, A
822	42	33.1	130	15	US-10-424-599-229140	Sequence 229140, A	895	42	33.1	485	15	US-10-425-114-72092	Sequence 72092, A
823	42	33.1	138	9	US-09-731-487-4	Sequence 4, Appl1	896	42	33.1	485	15	US-10-425-114-72099	Sequence 72099, A
824	42	33.1	155	16	US-10-437-963-166917	Sequence 166917, A	897	42	33.1	490	15	US-10-369-493-16459	Sequence 16459, A
825	42	33.1	163	15	US-10-424-599-148963	Sequence 148963, A	898	42	33.1	518	16	US-10-767-701-46009	Sequence 46009, A
826	42	33.1	169	16	US-10-767-701-52386	Sequence 52386, A	899	42	33.1	518	16	US-10-437-963-195842	Sequence 195842, A
827	42	33.1	185	14	US-10-357-884-4	Sequence 4, Appl1	900	42	33.1	531	15	US-10-425-114-70256	Sequence 70256, A
828	42	33.1	189	16	US-10-767-701-32627	Sequence 32627, A	901	42	33.1	537	15	US-10-425-114-70196	Sequence 70196, A
829	42	33.1	200	15	US-10-425-114-46069	Sequence 46069, A	902	42	33.1	539	15	US-10-425-114-71249	Sequence 71249, A
830	42	33.1	200	15	US-10-425-114-53827	Sequence 53827, A	903	42	33.1	541	15	US-10-282-122A-57145	Sequence 57145, A
831	42	33.1	200	15	US-10-425-114-60270	Sequence 60270, A	904	42	33.1	541	15	US-10-282-122A-57445	Sequence 57445, A
832	42	33.1	200	15	US-10-425-114-60477	Sequence 60477, A	905	42	33.1	546	15	US-10-282-122A-49932	Sequence 49932, A
833	42	33.1	200	15	US-10-425-114-60846	Sequence 60846, A	906	42	33.1	549	16	US-10-437-963-164372	Sequence 164372, A
834	42	33.1	200	15	US-10-425-114-61744	Sequence 61744, A	907	42	33.1	574	16	US-10-437-963-102998	Sequence 102998, A
835	42	33.1	200	15	US-10-425-114-61771	Sequence 61771, A	908	42	33.1	585	15	US-10-282-122A-71330	Sequence 71330, A
836	42	33.1	206	16	US-10-363-829-311	Sequence 311, App	909	42	33.1	596	9	US-09-815-242-5244	Sequence 5244, Ap
837	42	33.1	207	15	US-10-424-599-249257	Sequence 249257, A	910	42	33.1	604	9	US-09-815-242-12525	Sequence 12525, A
838	42	33.1	208	16	US-10-767-701-33537	Sequence 33537, A	911	42	33.1	604	15	US-10-282-122A-43977	Sequence 43977, A
839	42	33.1	218	15	US-10-296-115-772	Sequence 772, App	912	42	33.1	611	15	US-10-369-493-5204	Sequence 5204, Ap
840	42	33.1	219	15	US-10-424-599-216565	Sequence 216565, A	913	42	33.1	621	14	US-10-316-253-44	Sequence 44, Appl
841	42	33.1	225	15	US-10-282-122A-78029	Sequence 78029, A	914	42	33.1	689	15	US-10-424-599-187294	Sequence 187294, A
842	42	33.1	240	15	US-10-120-801-69	Sequence 69, Appl	915	42	33.1	698	15	US-10-369-493-13572	Sequence 13572, A
843	42	33.1	244	15	US-10-369-493-2951	Sequence 2951, Ap	916	42	33.1	698	15	US-10-369-493-18198	Sequence 18198, A
844	42	33.1	244	15	US-10-425-114-35990	Sequence 35990, A	917	42	33.1	703	16	US-10-437-963-166911	Sequence 166911, A
845	42	33.1	261	16	US-10-437-963-15536	Sequence 135536, A	918	42	33.1	722	16	US-10-437-963-166911	Sequence 166911, A
846	42	33.1	262	15	US-10-104-047-3090	Sequence 3090, Ap	919	42	33.1	769	15	US-10-282-122A-48256	Sequence 48256, A
847	42	33.1	275	15	US-10-369-493-7668	Sequence 7668, Ap	920	42	33.1	835	9	US-09-947-199-2	Sequence 2, Appl1
848	42	33.1	278	9	US-09-970-989-7	Sequence 7, Appl1	921	42	33.1	835	16	US-10-626-173-2	Sequence 2, Appl1
849	42	33.1	278	15	US-10-667-494-7	Sequence 7, Appl1	922	42	33.1	899	9	US-09-815-242-5356	Sequence 5356, Ap
850	42	33.1	278	15	US-10-667-462-7	Sequence 7, Appl1	923	42	33.1	924	15	US-10-282-122A-44099	Sequence 44099, A
851	42	33.1	278	15	US-10-667-464-7	Sequence 7, Appl1	924	42	33.1	932	9	US-09-815-242-12615	Sequence 12615, A
852	42	33.1	282	15	US-10-282-122A-62789	Sequence 62789, A	925	42	33.1	932	14	US-10-301-997-45	Sequence 45, Appl
853	42	33.1	282	15	US-10-282-122A-64811	Sequence 64811, A	926	42	33.1	932	16	US-10-818-509-45	Sequence 45, Appl
854	42	33.1	284	13	US-10-369-493-4910	Sequence 4910, Ap	927	42	33.1	934	15	US-10-282-122A-70563	Sequence 70563, A
855	42	33.1	292	13	US-10-042-194-2	Sequence 4910, Ap	928	42	33.1	941	16	US-10-437-963-189199	Sequence 189199, A
856	42	33.1	295	15	US-10-425-114-53449	Sequence 53449, A	929	42	33.1	990	11	US-09-764-875-774	Sequence 774, App
857	42	33.1	302	14	US-10-043-487-248	Sequence 248, App	930	42	33.1	1050	15	US-10-425-114-55722	Sequence 55722, A
858	42	33.1	305	15	US-10-425-114-70080	Sequence 70080, A	931	42	33.1	1059	15	US-10-369-493-1095	Sequence 1095, Ap
859	42	33.1	321	16	US-10-767-701-44602	Sequence 44602, A	932	42	33.1	1238	16	US-10-408-765A-2450	Sequence 2450, Ap
860	42	33.1	321	15	US-10-369-493-1132	Sequence 1132, Ap	933	42	33.1	1245	15	US-10-120-801-67	Sequence 67, Appl
861	42	33.1	324	15	US-10-282-122A-57090	Sequence 57090, A	934	42	33.1	1259	15	US-10-120-801-16	Sequence 16, Appl
862	42	33.1	331	15	US-10-424-599-238604	Sequence 238604, A	935	42	33.1	1294	16	US-10-471-762-9	Sequence 9, Appl
863	42	33.1	337	15	US-10-425-114-38844	Sequence 38844, A	936	42	33.1	1409	15	US-10-369-493-5387	Sequence 5387, Ap
864	42	33.1	351	14	US-10-032-585-7371	Sequence 7371, Ap	937	42	33.1	1681	15	US-10-398-885A-16	Sequence 16, Appl
865	42	33.1	357	15	US-10-282-122A-52822	Sequence 52822, A	938	42	33.1	1879	15	US-10-296-115-1265	Sequence 1265, Ap
866	42	33.1	374	15	US-10-424-599-226137	Sequence 226137, A	939	42	33.1	1938	14	US-10-171-311-164	Sequence 164, App
867	42	33.1	376	15	US-10-374-780A-913	Sequence 913, App	940	42	33.1	1945	10	US-09-927-597-4	Sequence 2, Appl1
868	42	33.1	379	15	US-10-424-599-274676	Sequence 912, App	941	42	33.1	1972	14	US-10-171-311-162	Sequence 162, App
869	42	33.1	383	15	US-10-425-114-53577	Sequence 53577, A	942	42	33.1	1973	16	US-10-341-434-103	Sequence 103, App
870	42	33.1	395	14	US-10-091-007-66	Sequence 66, Appl	943	42	33.1	1973	16	US-10-661-809-22	Sequence 22, Appl
871	42	33.1	397	16	US-10-437-963-143589	Sequence 143589, A	944	42	33.1	1973	16	US-10-661-809-24	Sequence 24, Appl
872	42	33.1	431	15	US-10-369-493-22917	Sequence 22917, A	945	42	33.1	1979	10	US-09-927-597-4	Sequence 4, Appl1
873	42	33.1	436	15	US-10-120-801-68	Sequence 68, Appl	946	42	33.1	1987	14	US-10-132-382-6	Sequence 6, Appl1
874	42	33.1	436	15	US-10-275-595A-16	Sequence 16, Appl	947	42	33.1	2013	14	US-10-132-382-2	Sequence 2, Appl1
875	42	33.1	450	15	US-10-282-122A-65058	Sequence 65058, A	948	42	33.1	2014	14	US-10-132-382-8	Sequence 8, Appl1
876	42	33.1	451	15	US-10-282-122A-67651	Sequence 67651, A	949	42	33.1	2014	15	US-10-220-955-18	Sequence 18, Appl
877	42	33.1	459	15	US-10-369-493-18302	Sequence 18302, A	950	42	33.1	2014	15	US-10-415-011-8	Sequence 8, Appl1
878	42	33.1	460	15	US-10-417-700A-133	Sequence 133, App	951	42	33.1	2040	14	US-10-132-382-4	Sequence 4, Appl1
879	42	33.1	462	15	US-10-282-122A-53413	Sequence 53413, A	952	42	33.1	85	16	US-10-437-963-162000	Sequence 162000, A
880	42	33.1	464	15	US-10-369-493-7005	Sequence 7005, Ap	953	42	33.1	98	16	US-10-767-701-53086	Sequence 53086, A
881	42	33.1	481	15	US-10-425-114-53209	Sequence 53209, A	954	42	33.1	122	15	US-10-424-599-146448	Sequence 146448, A
882	42	33.1	481	15	US-10-425-114-59273	Sequence 59273, A	955	42	33.1	145	16	US-10-767-701-37553	Sequence 37553, A
883	42	33.1	481	16	US-10-425-114-46495	Sequence 46495, A	956	42	33.1	187	16	US-10-767-701-41740	Sequence 41740, A
884	42	33.1	485	15	US-10-425-114-46975	Sequence 46975, A	957	42	33.1	186	15	US-10-425-114-57345	Sequence 57345, A
885	42	33.1	485	15	US-10-425-114-47502	Sequence 47502, A	958	42	33.1	188	16	US-10-767-701-40973	Sequence 40973, A
886	42	33.1	485	15	US-10-425-114-47600	Sequence 47600, A	959	42	33.1	198	15	US-10-425-114-46763	Sequence 46763, A
887	42	33.1	485	15	US-10-425-114-53351	Sequence 53351, A	960	42	33.1	202	15	US-10-364-337-12	Sequence 12, Appl
888	42	33.1	485	15	US-10-425-114-59175	Sequence 59175, A	961	42	33.1	233	15	US-10-424-599-163137	Sequence 163137, A
889	42	33.1	485	15	US-10-425-114-59175	Sequence 59175, A	962	42	33.1	261	15	US-10-424-599-146446	Sequence 146446, A

```

963 41.5 32.7 312 15 US-10-425-114-63097 Sequence 63097, A
964 41.5 32.7 345 16 US-10-437-963-204556 Sequence 204556,
965 41.5 32.7 358 15 US-10-464-610-18 Sequence 18, Appl
966 41.5 32.7 365 15 US-10-464-610-4 Sequence 4, Appl
967 41.5 32.7 365 15 US-10-424-599-163141 Sequence 163141,
968 41.5 32.7 374 16 US-10-437-963-118336 Sequence 118336,
969 41.5 32.7 395 15 US-10-425-114-36771 Sequence 36771, A
970 41.5 32.7 413 14 US-10-156-761-15075 Sequence 15075, A
971 41.5 32.7 425 15 US-10-108-260A-4381 Sequence 4381, Ap
972 41.5 32.7 425 15 US-10-282-122A-68661 Sequence 68661, A
973 41.5 32.7 425 17 US-10-959-539-46 Sequence 46, Appl
974 41.5 32.7 438 15 US-10-424-599-265659 Sequence 265659,
975 41.5 32.7 463 10 US-09-988-462-25 Sequence 25, Appl
976 41.5 32.7 470 15 US-10-425-114-70198 Sequence 70198, A
977 41.5 32.7 472 15 US-10-417-700A-67 Sequence 67, Appl
978 41.5 32.7 508 15 US-10-424-599-242297 Sequence 242297,
979 41.5 32.7 517 15 US-10-425-114-65871 Sequence 65871, A
980 41.5 32.7 527 15 US-10-425-114-51766 Sequence 51766, A
981 41.5 32.7 561 14 US-10-032-585-7306 Sequence 7306, Ap
982 41.5 32.7 639 9 US-09-854-731-17 Sequence 17, Appl
983 41.5 32.7 1312 15 US-10-369-493-1904 Sequence 1904, Ap
984 41.5 32.7 55 15 US-10-424-599-235854 Sequence 235854,
985 41.5 32.7 63 16 US-10-437-963-182278 Sequence 182278,
986 41.5 32.3 64 16 US-10-767-701-61024 Sequence 61024, A
987 41.5 32.3 71 9 US-09-982-809-2 Sequence 2, Appl
988 41.5 32.3 71 14 US-10-161-941-11 Sequence 11, Appl
989 41.5 32.3 74 15 US-10-424-599-144538 Sequence 144538,
990 41.5 32.3 99 16 US-10-437-963-168376 Sequence 168376,
991 41.5 32.3 120 16 US-10-767-701-46401 Sequence 46401, A
992 41.5 32.3 128 16 US-10-424-599-251351 Sequence 251351,
993 41.5 32.3 130 15 US-10-424-599-281789 Sequence 281789,
994 41.5 32.3 133 14 US-10-286-421-28 Sequence 28, Appl
995 41.5 32.3 140 15 US-10-282-122A-77767 Sequence 77767, A
996 41.5 32.3 149 15 US-10-369-493-2146 Sequence 2146, Ap
997 41.5 32.3 156 15 US-10-424-599-184133 Sequence 184133,
998 41.5 32.3 157 15 US-10-424-599-236576 Sequence 236576,
999 41.5 32.3 158 15 US-10-389-566-511 Sequence 511, App
1000 41.5 32.3 160 15 US-10-108-260A-3318 Sequence 3318, Ap

```

## ALIGNMENTS

```

RESULT 1
US-10-839-729-6
; Sequence 6, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 221
; TYPE: PR
; ORGANISM: SARS Coronavirus
US-10-839-729-6

```

```

Query Match      88.2%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 4 MADNGTIVTEELKQLEQNMNV 25
Db 1 MADNGTIVTEELKQLEQNMNV 22

```

```

RESULT 2
US-10-839-729-7
; Sequence 7, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 221
; TYPE: PR
; ORGANISM: SARS Coronavirus
US-10-839-729-7

```

```

Query Match      88.2%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 4 MADNGTIVTEELKQLEQNMNV 25
Db 1 MADNGTIVTEELKQLEQNMNV 22

```

```

RESULT 3
US-10-839-729-8
; Sequence 8, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 221
; TYPE: PR
; ORGANISM: SARS Coronavirus
US-10-839-729-8

```

```

Query Match      88.2%; Score 112; DB 16; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 4 MADNGTIVTEELKQLEQNMNV 25
Db 1 MADNGTIVTEELKQLEQNMNV 22

```

```

RESULT 4
US-10-839-729-9
; Sequence 9, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06

```

NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 221  
TYPE: PRF  
ORGANISM: SARS Coronavirus  
US-10-839-729-9

Query Match 88.2%; Score 112; DB 16; Length 221;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25  
DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 5  
US-10-699-936-24  
Sequence 24, Application US/10699936  
Publication No. US20050095582A1  
GENERAL INFORMATION:  
APPLICANT: Gillim-Ross, Laura  
APPLICANT: Taylor, Jill  
APPLICANT: Scholl, David R.  
APPLICANT: Wentworth, David E.  
APPLICANT: Jollick, Joseph D.  
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory  
FILE REFERENCE: DHI-07986  
CURRENT APPLICATION NUMBER: US/10/699,936  
CURRENT FILING DATE: 2003-11-03  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 24  
LENGTH: 221  
TYPE: PRF  
ORGANISM: SARS-CoV Urban1  
US-10-699-936-24

Query Match 88.2%; Score 112; DB 17; Length 221;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25  
DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 6  
US-10-699-936-81  
Sequence 81, Application US/10699936  
Publication No. US20050095582A1  
GENERAL INFORMATION:  
APPLICANT: Gillim-Ross, Laura  
APPLICANT: Taylor, Jill  
APPLICANT: Scholl, David R.  
APPLICANT: Wentworth, David E.  
APPLICANT: Jollick, Joseph D.  
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory  
FILE REFERENCE: DHI-07986  
CURRENT APPLICATION NUMBER: US/10/699,936  
CURRENT FILING DATE: 2003-11-03  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 81  
LENGTH: 221  
TYPE: PRF  
ORGANISM: SARS coronavirus Tor2  
US-10-699-936-81

Query Match 88.2%; Score 112; DB 17; Length 221;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25  
DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 7  
US-10-699-936-82  
Sequence 82, Application US/10699936  
Publication No. US20050095582A1  
GENERAL INFORMATION:  
APPLICANT: Gillim-Ross, Laura  
APPLICANT: Taylor, Jill  
APPLICANT: Scholl, David R.  
APPLICANT: Wentworth, David E.  
APPLICANT: Jollick, Joseph D.  
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory  
FILE REFERENCE: DHI-07986  
CURRENT APPLICATION NUMBER: US/10/699,936  
CURRENT FILING DATE: 2003-11-03  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 82  
LENGTH: 221  
TYPE: PRF  
ORGANISM: SARS coronavirus Shanghai QXC  
US-10-699-936-82

Query Match 88.2%; Score 112; DB 17; Length 221;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25  
DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 8  
US-10-699-936-83  
Sequence 83, Application US/10699936  
Publication No. US20050095582A1  
GENERAL INFORMATION:  
APPLICANT: Gillim-Ross, Laura  
APPLICANT: Taylor, Jill  
APPLICANT: Scholl, David R.  
APPLICANT: Wentworth, David E.  
APPLICANT: Jollick, Joseph D.  
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory  
FILE REFERENCE: DHI-07986  
CURRENT APPLICATION NUMBER: US/10/699,936  
CURRENT FILING DATE: 2003-11-03  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 83  
LENGTH: 221  
TYPE: PRF  
ORGANISM: SARS coronavirus Shanghai QXC  
US-10-699-936-83

Query Match 88.2%; Score 112; DB 17; Length 221;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVTEELKQLEQNNLV 25  
DB 1 MADNGTIVTEELKQLEQNNLV 22

RESULT 9

US-10-808-187-214  
; Sequence 214, Application US/10808187  
; Publication No. US20050009009A1  
; GENERAL INFORMATION:  
; APPLICANT: PEIRIS, JOSEPH S. M.  
; APPLICANT: YUEN, KWOK YUNG  
; APPLICANT: POON, LIT MAN  
; APPLICANT: GUAN, YI  
; APPLICANT: CHAN, KWOK HUNG  
; APPLICANT: NICHOLLS, JOHN  
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE  
; FILE REFERENCE: V9661.0078  
; CURRENT APPLICATION NUMBER: US/10/808,187  
; CURRENT FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: 60/457,031  
; PRIOR FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: 60/457,730  
; PRIOR FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: 60/459,931  
; PRIOR FILING DATE: 2003-04-02  
; PRIOR APPLICATION NUMBER: 60/460,357  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: 60/461,265  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/462,805  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: 60/468,139  
; PRIOR FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: 60/464,886  
; PRIOR FILING DATE: 2003-04-23  
; PRIOR APPLICATION NUMBER: 60/471,200  
; PRIOR FILING DATE: 2003-05-16  
; NUMBER OF SEQ ID NOS: 2476  
; SOFTWARE: PatentIn ver. 3.2  
; SEQ ID NO 214  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Human severe acute respiratory system virus  
US-10-808-187-214

Query Match 88.2%; Score 112; DB 17; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEOMNLV 25  
DB 22 MADNGTIVBELKQLEOMNLV 43

RESULT 10  
US-10-839-729-46  
; Sequence 46, Application US/10839729  
; Publication No. US20050002953A1  
; GENERAL INFORMATION:  
; APPLICANT: JENS Herold  
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES  
; FILE REFERENCE: BIOBANK 013A  
; CURRENT APPLICATION NUMBER: US/10/839,729  
; CURRENT FILING DATE: 2004-05-04  
; PRIOR APPLICATION NUMBER: 60/468703  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically prepared polypeptide sequence  
US-10-839-729-46

Query Match 57.5%; Score 73; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MADNGTIVBELKQLEOMNLV 18  
DB 1 MADNGTIVBELKQLEOMNLV 15

RESULT 11  
US-09-864-761-39008  
; Sequence 39008, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecmlca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 39008  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC004837.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.6  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN HEILA, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6  
OTHER INFORMATION: SWISSPROT HIT: P11233, EVALUE 5.00e-25  
OTHER INFORMATION: EST\_HUMAN HIT: A1344679.1, EVALUE 6.00e-24  
US-09-864-761-39008

Query Match 43.3%; Score 55; DB 9; Length 54;  
Best Local Similarity 41.7%; Pred. No. 2.5;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGTITVEELKQLEQNL 24  
DB 20 KSDLEDKQVSVSEAKNRABQMN 43

RESULT 12  
US-09-873-546-10  
Sequence 10, Application US/09873546  
Publication No. US20030059771A1  
GENERAL INFORMATION:  
APPLICANT: Clark, Geoff  
APPLICANT: Ellis, Chad  
APPLICANT: Vos, Michelle  
TITLE OF INVENTION: R1g: No. US20030059771A1 Ras-Related Gene  
FILE REFERENCE: NIH-05080  
CURRENT APPLICATION NUMBER: US/09/873,546  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-873-546-10

Query Match 43.3%; Score 55; DB 10; Length 206;  
Best Local Similarity 41.7%; Pred. No. 11;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGTITVEELKQLEQNL 24  
DB 128 KSDLEDKQVSVSEAKNRABQMN 151

RESULT 13  
US-10-153-668-214  
Sequence 214, Application US/10153668  
Publication No. US20030092616A1  
GENERAL INFORMATION:  
APPLICANT: HONDA, Goichi  
APPLICANT: MATSUDA, Akio  
APPLICANT: MURAMATSU, Shuji  
APPLICANT: ISHIZAWA, Kenya  
TITLE OF INVENTION: STAT6 Activating Gene  
FILE REFERENCE: 1254-0207P  
CURRENT APPLICATION NUMBER: US/10/153,668  
CURRENT FILING DATE: 2002-05-24  
PRIOR APPLICATION NUMBER: US 60/293,172  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/316,031  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/328,403  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: JP 2001-157043  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: JP 2001-260681  
PRIOR FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: JP 2001-313175  
PRIOR FILING DATE: 2001-10-10  
NUMBER OF SEQ ID NOS: 488  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 214  
LENGTH: 206

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-153-668-214

Query Match 43.3%; Score 55; DB 14; Length 206;  
Best Local Similarity 41.7%; Pred. No. 11;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGTITVEELKQLEQNL 24  
DB 128 KSDLEDKQVSVSEAKNRABQMN 151

RESULT 14  
US-10-021-660-132  
Sequence 132, Application US/10021660  
Publication No. US20030152926A1  
GENERAL INFORMATION:  
APPLICANT: Murray, Richard  
APPLICANT: Glynn, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: EOS Biotechnology, Inc.  
TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,  
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis  
FILE REFERENCE: 018501-000710US  
CURRENT APPLICATION NUMBER: US/10/021,660  
CURRENT FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US/09/784,356  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/637,977  
PRIOR FILING DATE: 2000-08-11  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatSeq for Windows Version 3.0  
SEQ ID NO 132  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-021-660-132

Query Match 43.3%; Score 55; DB 14; Length 206;  
Best Local Similarity 41.7%; Pred. No. 11;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGTITVEELKQLEQNL 24  
DB 128 KSDLEDKQVSVSEAKNRABQMN 151

RESULT 15  
US-10-231-913-64  
Sequence 64, Application US/10231913  
Publication No. US20040005576A1  
GENERAL INFORMATION:  
APPLICANT: Guo, Xiaojia S.  
APPLICANT: Li, Li  
APPLICANT: Patrajan, Meera  
APPLICANT: Smitke, Richard A.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Vernet, Corine A.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Alsobrook II, John P.  
APPLICANT: Edinger, Schlomil  
APPLICANT: Peyman, John A.  
APPLICANT: Stone, David J.  
APPLICANT: Ellerman, Karen  
APPLICANT: Gangolli, Bena A.  
APPLICANT: Boldog, Ference L.  
APPLICANT: Colman, Steven D.  
APPLICANT: Bisen, Andrew J.

```

; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-64
```

```

Query Match      43.3%; Score 55; DB 15; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
```

```

Qy      1 KKKMADNGTIVVEELKQLLEQNNL 24
Db      128 KSDLEDKQVSVBEAKNRAEQNNV 151
```

```

RESULT 16
US-10-211-462-79
; Sequence 79, Application US/10211462
; Publication No. US2004003495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Gluyne, Richard
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-79
```

```

Query Match      43.3%; Score 55; DB 15; Length 206;
```

```

Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
```

```

Qy      1 KKKMADNGTIVVEELKQLLEQNNL 24
Db      128 KSDLEDKQVSVBEAKNRAEQNNV 151
```

```

RESULT 17
US-10-408-765A-2022
; Sequence 2022, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088,465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2022
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2022
```

```

Query Match      43.3%; Score 55; DB 16; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
```

```

Qy      1 KKKMADNGTIVVEELKQLLEQNNL 24
Db      128 KSDLEDKQVSVBEAKNRAEQNNV 151
```

```

RESULT 18
US-10-804-491-48
; Sequence 48, Application US/10804491
; Publication No. US20040180375A1
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emil
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/804,491
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/09/709,103
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-804-491-48
```

```

Query Match      43.3%; Score 55; DB 16; Length 206;
Best Local Similarity 41.7%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
```

```

Qy      1 KKKMADNGTIVVEELKQLLEQNNL 24
Db      128 KSDLEDKQVSVBEAKNRAEQNNV 151
```

```

RESULT 19
```

US-10-231-913-66  
; Sequence 66, Application US/10231913  
; Publication No. US2004000576A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Xiaojia S.  
; APPLICANT: Li, Li  
; APPLICANT: Patursajan, Meera  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Malyskar, Uriel M.  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vermet, Corine A.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Edinger, Schlonitc  
; APPLICANT: Peyman, John A.  
; APPLICANT: Stone, David J.  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Gangolli, Baha A.  
; APPLICANT: Boldog, Ference L.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Eisen, Andrew J.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Spaderma, Steven K.  
; APPLICANT: Zehrusen, Bryan D.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-216  
; CURRENT APPLICATION NUMBER: US/10/231,913  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: 60/251,660  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: 60/255,029  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/260,326  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/263,800  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/269,942  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/286,183  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: 60/313,627  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/318,712  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 292  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-231-913-66

Query Match 43.3%; Score 55; DB 15; Length 209;  
Best Local Similarity 41.7%; Pred. No. 12;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKADNGTIVTEELKQLEQNL 24  
DB 131 KSDLEDKQVSVBEAKRAEQMNV 154

RESULT 20  
US-10-425-114-69487  
; Sequence 69487, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E

APPLICANT: Tabaeke, Jack E  
APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 69487  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLB73003G04\_FLI.pep  
US-10-425-114-69487

Query Match 42.1%; Score 53.5; DB 15; Length 336;  
Best Local Similarity 57.1%; Pred. No. 32;  
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 7 NGTIVTEELKQLEQ---NML 24  
DB 196 NGTISLEELKQALAKDVPWRL 216

RESULT 21  
US-10-437-963-158994  
; Sequence 158994, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 158994  
; LENGTH: 486  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_58414C.1.pep  
US-10-437-963-158994

Query Match 42.1%; Score 53.5; DB 16; Length 486;  
Best Local Similarity 57.1%; Pred. No. 49;  
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 7 NGTIVTEELKQLEQ---NML 24  
DB 346 NGTISLEELKQALAKDVPWRL 366

RESULT 22  
US-10-437-963-158996  
; Sequence 158996, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad

```

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 158996
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_58416C.1.pep
; US-10-437-963-158996

Query Match      42.1%; Score 53.5; DB 16; Length 512;
Best Local Similarity 57.1%; Pred. No. 52;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY      7 NGTITVEELKQLEQ---NNL 24
DB      372 NGTISLEELKQALAKQVPMRL 392

RESULT 23
US-10-425-114-57880
; Sequence 57880, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57880
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17084F11_FLI.pep
; US-10-425-114-57880

Query Match      42.1%; Score 53.5; DB 15; Length 523;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 12; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY      7 NGTITVEELKQLEQ---NNL 24
DB      383 NGTISLEELKQALAKQVPMRL 403

RESULT 24
US-10-282-122A-51593
; Sequence 51593, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert

```

```

; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51593
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
; US-10-282-122A-51593

Query Match      41.7%; Score 53; DB 15; Length 351;
Best Local Similarity 37.5%; Pred. No. 40;
Matches 9; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY      2 KXQADNGTITVEELKQLEQNNLV 25
DB      127 KCTISNGELISBELKXMDASNIV 150

RESULT 25
US-10-231-913-63
; Sequence 63, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Paturajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Urfel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Verneet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsodrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esba A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zernusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

```



```
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 63
LENGTH: 206
TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-63
```

```
Query Match 40.9%; Score 52; DB 15; Length 206;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 1 KKKMADNGTIVTEELKQLLEQWNL 24
Db 128 KSDLEDKQVSVFEAKNRADQWNV 151
```

```
RESULT 26
US-10-231-913-65
Sequence 65, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patnurajan, Meera
APPLICANT: Shinkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Vellizar T.
APPLICANT: Verneet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Baha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eissen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
```

```
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 65
LENGTH: 206
TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-65
```

```
Query Match 40.9%; Score 52; DB 15; Length 206;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 1 KKKMADNGTIVTEELKQLLEQWNL 24
Db 128 KSDLEDKQVSVFEAKNRADQWNV 151
```

```
RESULT 27
US-10-231-913-67
Sequence 67, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patnurajan, Meera
APPLICANT: Shinkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Vellizar T.
APPLICANT: Verneet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Baha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eissen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
```

```

; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-231-913-67

Query Match      40.9%; Score 52; DB 15; Length 206;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 KKKMADNGTIVTELKQLEQWNL 24
DB 128 KSDLEDKQVSVBEAKSRADQWNV 151

RESULT 28
US-10-282-122A-54546
; Sequence 54546, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54546
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-282-122A-54546

Query Match      40.9%; Score 52; DB 15; Length 545;
Best Local Similarity 41.7%; Pred. No. 91;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
```

```

QY 2 KKKMADNGTIVTELKQLEQWNLV 25
DB 166 EKVKQGVITVEAKSINDELNV 189

RESULT 29
US-10-369-294-11
; Sequence 11, Application US/10369294
; Publication No. US20030162170A1
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; FILE REFERENCE: D6286D
; CURRENT APPLICATION NUMBER: US/10/369,294
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 09/206,551
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
US-10-369-294-11

Query Match      40.6%; Score 51.5; DB 14; Length 855;
Best Local Similarity 43.5%; Pred. No. 1,8e+02;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 MADNGTIVTELKQLEQWNLV 25
DB 401 WGPNGTITLQCRKQIINWQRV 423

RESULT 30
US-10-369-294-12
; Sequence 12, Application US/10369294
; Publication No. US20030162170A1
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; FILE REFERENCE: D6286D
; CURRENT APPLICATION NUMBER: US/10/369,294
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 09/206,551
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 12
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; OTHER INFORMATION: B_HXB2R lentiviral env protein
```

US-10-369-294-12

Query Match 40.6%; Score 51.5; DB 14; Length 855;

Best Local Similarity 43.5%; Pred. No. 1.8e+02; Indels 1; Gaps 1;

Matches 10; Conservative 5; Mismatches 7;

QY 4 MADNGITVEELKQLEQNLV 25

DB 401 MGPNGITLQCRKQIINMQRV 423

RESULT 31

US-10-478-245-4

Sequence 4, Application US/10478245

Publication No. US20040171008A1

GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;

APPLICANT: YUE, Henry; AZIMZAI, Yalda;

APPLICANT: BAUGHN, Mariah R.; BUREFORD, Neil;

APPLICANT: REDDY, Roopa; CHAWLA, Narinder K.;

APPLICANT: DAS, Debopriya; NGUYEN, Daniel B.;

APPLICANT: YAO, Monique G.; ARVIZU, Chandra S.;

APPLICANT: LU, Yan; GANDHI, Ameena R.;

APPLICANT: GRIFPIN, Jennifer A.; ELLIOTT, Vicki S.;

APPLICANT: RAMKUMAR, Javalaxmi; LAL, Preeti G.;

APPLICANT: LU, Dzung Anna M.; LEE, Ernestine A.;

APPLICANT: LEE, Soo Y.; YUE, Huibin; Catherine M.;

APPLICANT: YANG, Junming; TRIBOUNLEY, Catherine M.;

APPLICANT: KABLE, Amy E.; SWARNAKAR, Anita;

TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES

FILE REFERENCE: PI-0427 USN

CURRENT APPLICATION NUMBER: US/10/478,245

CURRENT FILING DATE: 2003-11-18

PRIOR APPLICATION NUMBER: PCT/US02/15688

PRIOR FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: US 60/292,242

PRIOR FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US 60/293,726

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/295,346

PRIOR FILING DATE: 2001-06-01

PRIOR APPLICATION NUMBER: US 60/303,404

PRIOR FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: US 60/314,754

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/351,262

PRIOR FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: US 60/368,799

PRIOR FILING DATE: 2002-03-29

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PERL Program

SEQ ID NO 4

LENGTH: 217

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

OTHER INFORMATION: Incyte ID No: 2715421CD1

US-10-478-245-4

Query Match 40.2%; Score 51; DB 16; Length 217;

Best Local Similarity 50.0%; Pred. No. 44; Indels 1; Gaps 0;

Matches 12; Conservative 4; Mismatches 8;

QY 1 KKKMADNGITVEELKQLEQNLV 24

DB 34 KKKMADNGITVEELKQLEQNLV 57

RESULT 32

US-10-282-122A-60575

Sequence 60575, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangou

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remainder Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 60575

LENGTH: 626

TYPE: PRT

ORGANISM: Listeria monocytogenes

US-10-282-122A-60575

Query Match 40.2%; Score 51; DB 15; Length 626;

Best Local Similarity 50.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;

Matches 10; Conservative 5; Mismatches 5;

QY 2 KKKMADNGITVEELKQLEQ 21

DB 417 KQLADEFELTITLTKQLOQ 436

RESULT 33

US-10-156-761-14515

Sequence 14515, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 14515  
LENGTH: 987  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-14515

Query Match 40.2%; Score 51; DB 14; Length 987;  
Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVVEELKQLEQWNL 22  
DB 650 KTADDEIDVEDIRAKIEQY 669

RESULT 34  
US-10-424-599-219887  
Sequence 219887, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K  
APPLICANT: Zhou Yihua  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223) B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 219887  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_40586C.1.pep  
US-10-424-599-219887

Query Match 39.4%; Score 50; DB 15; Length 92;  
Best Local Similarity 47.4%; Pred. No. 23;  
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 DNGTIVVEELKQLEQWNL 24  
DB 25 NSGFITTEELQALREYVM 43

RESULT 35  
US-10-437-963-186189  
Sequence 186189, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221) B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 186189  
LENGTH: 174  
TYPE: PRT  
ORGANISM: Oryza sativa

FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_83010C.1.pep  
US-10-437-963-186189

Query Match 39.4%; Score 50; DB 16; Length 174;  
Best Local Similarity 55.6%; Pred. No. 48;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 7 NGTIVVEELKQLEQWNL 24  
DB 119 NGVITAEELRRLRLRL 136

RESULT 36  
US-10-272-419-26  
Sequence 26, Application US/10272419  
Publication No. US20030087403A1  
GENERAL INFORMATION:  
APPLICANT: CHEN, QIONG  
APPLICANT: THOMAS, STUART  
APPLICANT: NAGARAJAN, VASANTHA  
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
TITLE OF INVENTION: INTERMEDIATES  
FILE REFERENCE: C1341-A  
CURRENT APPLICATION NUMBER: US/10/272,419  
CURRENT FILING DATE: 2002-10-16  
PRIOR APPLICATION NUMBER: 09/252,553  
PRIOR FILING DATE: 1999-02-19  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 26  
LENGTH: 300  
TYPE: PRT  
ORGANISM: Acinetobacter sp.  
US-10-272-419-26

Query Match 39.4%; Score 50; DB 14; Length 300;  
Best Local Similarity 22.7%; Pred. No. 88;  
Matches 5; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 KXADNGTIVVEELKQLEQWNL 23  
DB 20 RMQENPMNTIEDFRSMPEWM 41

RESULT 37  
US-10-417-700A-49  
Sequence 49, Application US/10417700A  
Publication No. US20040033581A1  
GENERAL INFORMATION:  
APPLICANT: ECOPIA BIOSCIENCES INC.  
APPLICANT: ZAZOPOULOS, Emmanuel  
APPLICANT: STAPPA, Alfredo  
APPLICANT: FARNET, Chris  
TITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribosome  
TITLE OF INVENTION: peptide synthetase systems  
FILE REFERENCE: 3002-14US  
CURRENT APPLICATION NUMBER: US/10/417,700A  
CURRENT FILING DATE: 2003-04-17  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 49  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Pseudomonas syringae pv. syringae strain B301D  
US-10-417-700A-49

Query Match 39.4%; Score 50; DB 15; Length 469;  
Best Local Similarity 64.3%; Pred. No. 1.5e+02;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 ITVEELKQLEQWNL 23  
: : |||||||||

Db 432 LPLNERKQLEQWN 445

## RESULT 38

US-10-781-102-1  
; Sequence 1, Application US/10781102  
; Publication No. US20050048525A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: fidoack, Mark D.  
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
; FILE REFERENCE: PC10350B  
; CURRENT APPLICATION NUMBER: US/10/781,102  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: US 60/177,326  
; PRIOR FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: US 09/663,481  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: UK 9922125.1  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 1  
; LENGTH: 516  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-781-102-1

Query Match 39.4%; Score 50; DB 17; Length 516;  
Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVTEBELKQLE 20  
DB 24 KOLENGEINIEELKQLE 41

## RESULT 39

US-10-781-102-3  
; Sequence 3, Application US/10781102  
; Publication No. US20050048525A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: fidoack, Mark D.  
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
; FILE REFERENCE: PC10350B  
; CURRENT APPLICATION NUMBER: US/10/781,102  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: US 60/177,326  
; PRIOR FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: US 09/663,481  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: UK 9922125.1  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 3  
; LENGTH: 536  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-781-102-3

Query Match 39.4%; Score 50; DB 17; Length 536;  
Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVTEBELKQLE 20  
DB 44 KOLENGEINIEELKQLE 61

RESULT 40  
US-10-815-390-1

; Sequence 1, Application US/10815390  
; Publication No. US20050075795A1  
; GENERAL INFORMATION:  
; APPLICANT: Pandit, Jayvardhan  
; APPLICANT: Pandit, Jayvardhan  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF 3', 5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
; FILE REFERENCE: PC25193A  
; CURRENT APPLICATION NUMBER: US/10/815,390  
; CURRENT FILING DATE: 2004-03-31  
; PRIOR APPLICATION NUMBER: US 60/458,946  
; PRIOR FILING DATE: 2003-03-31  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 1  
; LENGTH: 536  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-815-390-1

Query Match 39.4%; Score 50; DB 17; Length 536;  
Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KXADNGTIVTEBELKQLE 20  
DB 44 KOLENGEINIEELKQLE 61

## RESULT 41

US-10-192-419-2  
; Sequence 2, Application US/10192419  
; Publication No. US20030072766A1  
; GENERAL INFORMATION:  
; APPLICANT: JACOBS, ANTONIUS A.C.  
; APPLICANT: VAN DEN BOSCH, JOHANNES F.  
; APPLICANT: NUTTEN, PETRUS J.M.  
; TITLE OF INVENTION: CAMPYLOBACTER VACCINE  
; FILE REFERENCE: JACOBS  
; CURRENT APPLICATION NUMBER: US/10/192,419  
; CURRENT FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US/09/544,683  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: EP99201086.8  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
US-10-192-419-2

Query Match 39.4%; Score 50; DB 14; Length 545;  
Best Local Similarity 41.7%; Pred. No. 1.7e+02;  
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 KXADNGTIVTEBELKQLEQWNLV 25  
DB 166 EKVGKGVITVEBPXSINDELNVV 189

## RESULT 42

US-10-424-599-203557  
; Sequence 203557, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic David J  
; APPLICANT: Kovalic David J  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

```
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 203557
LENGTH: 546
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_25838C.1.pcp
US-10-424-599-203557

Query Match
Best Local Similarity 39.4%; Score 50; DB 15; Length 546;
Pred. No. 1.7e+02;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 6 DNGTIVEELKQLEQWNL 24
Db 477 NSGFITTELEQLREYNM 495

RESULT 43
US-10-425-114-54704
Sequence 54704, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54704
LENGTH: 549
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: JC-GWFL02220063C09_FLI.pcp
US-10-425-114-54704

Query Match
Best Local Similarity 39.4%; Score 50; DB 15; Length 549;
Pred. No. 1.8e+02;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 6 DNGTIVEELKQLEQWNL 24
Db 480 NSGFITTELEQLREYNM 498

RESULT 44
US-10-282-122A-76721
Sequence 76721, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
```

```
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76721
LENGTH: 673
TYPE: PRT
ORGANISM: Ureaplasma urealyticum
US-10-282-122A-76721

Query Match
Best Local Similarity 39.4%; Score 50; DB 15; Length 673;
Pred. No. 2.2e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 12 VBEKQKLEQWNL 23
Db 8 IDELKQKLEQWNL 19

RESULT 45
US-10-104-047-2324
Sequence 2324, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2324
LENGTH: 808
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2324

Query Match
Best Local Similarity 39.4%; Score 50; DB 15; Length 808;
Pred. No. 2.7e+02;
Matches 12; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy 3 KXADNGTIVEELKQLEQWNLV 25
Db 32 KXADNGTIVEELKQLEQWNLV 56

RESULT 46
US-10-343-509-3
Sequence 3, Application US/10343509
```

```
Publication No. US20040101865A1
GENERAL INFORMATION:
APPLICANT: BASF
TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof
FILE REFERENCE: 0050/51654
CURRENT APPLICATION NUMBER: US/10/343,509
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1803
TYPE: PRT
ORGANISM: Euglena gracilis
US-10-343-509-3

Query Match      39.4%; Score 50; DB 16; Length 1803;
Best Local Similarity 47.8%; Pred. No. 6.8e+02;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY      1 KKKMADNGTITVEELKQLLEQWN 23
DB      963 EKKVADEGLTTL--LQWMLQDMN 983

RESULT 47
US-10-343-509-1
Sequence 1, Application US/10343509
Publication No. US20040101865A1
GENERAL INFORMATION:
APPLICANT: BASF
TITLE OF INVENTION: Pyruvate:NADP+ oxidoreductase and uses thereof
FILE REFERENCE: 0050/51654
CURRENT APPLICATION NUMBER: US/10/343,509
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1805
TYPE: PRT
ORGANISM: Euglena gracilis
US-10-343-509-1

Query Match      39.4%; Score 50; DB 16; Length 1805;
Best Local Similarity 47.8%; Pred. No. 6.8e+02;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY      1 KKKMADNGTITVEELKQLLEQWN 23
DB      965 EKKVADEGLTTL--LQWMLQDMN 985

RESULT 48
US-10-360-053-28
Sequence 28, Application US/10360053
Publication No. US20030170230A1
GENERAL INFORMATION:
APPLICANT: Caterer, Nigel
APPLICANT: Uttenenthal, Lars O
APPLICANT: Nielsen, Rasmus W
TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibio
TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
TITLE OF INVENTION: Thereof
FILE REFERENCE: IMX-0028
CURRENT APPLICATION NUMBER: US/10/360,053
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US60/354,376
PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 28
LENGTH: 2477
TYPE: PRT
ORGANISM: Homo sapien
```

```
US-10-360-053-28

Query Match      39.4%; Score 50; DB 14; Length 2477;
Best Local Similarity 47.6%; Pred. No. 9.8e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      2 KKKMADNGTITVEELKQLLEQW 22
DB      1833 KKLSDNTIGKEEIQORLQAF 1853

RESULT 49
US-10-408-765A-238
Sequence 238, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 238
LENGTH: 2477
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-238

Query Match      39.4%; Score 50; DB 16; Length 2477;
Best Local Similarity 47.6%; Pred. No. 9.8e+02;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      2 KKKMADNGTITVEELKQLLEQW 22
DB      1833 KKLSDNTIGKEEIQORLQAF 1853

RESULT 50
US-10-781-102-13
Sequence 13, Application US/10781102
Publication No. US20050048525A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Fiddock, Mark D.
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
FILE REFERENCE: PC10350B
CURRENT APPLICATION NUMBER: US/10/781,102
CURRENT FILING DATE: 2004-02-18
PRIOR APPLICATION NUMBER: US 60/177,326
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: US 09/663,481
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: UK 9922125.1
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 13
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-10-781-102-13

Query Match      38.6%; Score 49; DB 17; Length 60;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

Qy	3	KWADNGTIVEELKOLLE	20
		:    : :     :	
Db	43	KOLENGEVNIEELKONLE	60

Search completed: May 11, 2005, 21:43:37  
Job time : 106.34 secs